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117827

From: Swope, Sheridan  
Sent: Thursday, March 25, 2004 1:02 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/771,161

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STIC

For 09/771,161, pls search:

SID 2: Full-length and oligo search ( $\geq 20$ NTs) against the NT and AA data bases.

SID 93: Full-length and oligo search ( $\geq 20$ AAs) against the NT and AA data bases.

THANKS SO VERY MUCH TO THE GREAT STAFF OF STIC!!!!

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E03A70 Remsen Bld (Office)  
E03C70 Remsen Bld (Mailbox)

Scan this page

Paul Schuchwitz

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 4/1  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:31:34 ; Search time 76 Seconds  
(without alignments)  
11492.462 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 531

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1065169 seqs, 261661801 residues

Word size: 20

Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	232	43.7	232	9	US-09-771-161A-93	Sequence 93, Appl
2	227	42.7	540	9	US-09-771-161A-184	Sequence 184, Appl
3	227	42.7	540	9	US-09-862-037-28	Sequence 28, Appl
4	227	42.7	540	10	US-09-981-397A-14	Sequence 14, Appl
5	227	42.7	544	9	US-09-925-301-1015	Sequence 1015, Ap
6	128	24.1	540	9	US-09-748-537-1	Sequence 1, Appl
7	128	24.1	540	9	US-09-728-721-2	Sequence 2, Appl
8	128	24.1	540	13	US-10-133-780-1	Sequence 1, Appl
9	128	24.1	540	13	US-10-105-931-2	Sequence 2, Appl
10	128	24.1	540	13	US-10-118-984-2	Sequence 2, Appl
11	128	24.1	540	14	US-10-295-981-2	Sequence 6, Appl
12	109	20.5	109	9	US-09-728-721-6	Sequence 6, Appl
13	109	20.5	109	13	US-10-105-931-6	Sequence 6, Appl
14	109	20.5	109	13	US-10-118-984-6	Sequence 6, Appl
15	109	20.5	109	14	US-10-295-981-6	Sequence 5, Appl
16	98	18.5	131	9	US-09-728-721-5	Sequence 5, Appl
17	98	18.5	131	13	US-10-105-931-5	Sequence 5, Appl
18	98	18.5	131	13	US-10-118-984-5	Sequence 5, Appl
19	98	18.5	131	14	US-10-295-981-5	Sequence 5, Appl
20	92	17.3	92	13	US-10-014-269-21	Sequence 21, Appl
21	92	17.3	92	13	US-10-002-974-21	Sequence 21, Appl
22	92	17.3	92	14	US-10-314-506-21	Sequence 21, Appl
23	90	16.9	90	9	US-09-841-879B-10	Sequence 10, Appl
24	89	16.8	89	9	US-09-931-071-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005-1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724, 676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; TYPE: PRT  
; LENGTH: 232  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

Alignment Scores:  
Pred. No.: 4.95e-230 Length: 232  
Score: 232.00 Matches: 232  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 43.69% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-771-161A-93 (1-232)

QY	320	ATGTATTTCATTACAGTTCAGAGTCTTTCAAGTGCACCTATGTGCAAGAGAA	379
DB	1	MetTyrSerLeuGlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLys	20
QY	380	ATGGAATTATCTCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCC	439
DB	21	MetGluLeuSerSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySer	40
QY	440	TCTCAGCTCCATGAATAAGTGTCTCTCCTGAAACTTCAAGGTCCCTGCAGCTCTCTCAA	499
DB	41	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln	60

500 GACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTTATTTTATGAAGCTGCATCACTGT 559  
Db 61 AsphanaspPheLeuSerArgLysAlaGlnAspCysIyrPheMetLysLeuHisCys 80  
QY 560 CCTGGAATCACAGTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTTCTGTGAT 619  
Db 81 ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp 100  
QY 620 CACAAGACCCTCATCTCTTACGCAATATAAATCACTCTCAACTGCAGGAACTCA 679  
Db 101 HisLysThrThrProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSer 120  
QY 680 GAACCTCTGACGCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTG 739  
Db 121 GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleVal 140  
QY 740 AACCAATGACAGAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCAGGGACTTG 799  
Db 141 AsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgLeu 160  
QY 800 ATCATGAAGAGGACTATGACTTGTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAAAGTCAGA 859  
Db 161 IleMetLysGluAspIyrGluLeuValSerThrLysProThrArgThrSerLysValArg 180  
QY 860 CAATTACTAGACACTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAA 919  
Db 181 GlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 200  
QY 920 TTGAAGATACAAACAAATGGGTCTTACGCTTACCCGCTTACCCGAAATACTGTGGTTCTCAGA 979  
Db 201 LeuLysAspAsnLysGlnMetGlyLeuGlnProIyrProGluIleLeuValSerArg 220  
QY 980 TCACCATCTTAAATTTACTTCAAAATAAAGCATG 1015  
Db 221 SerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232

## RESULT 2

US-09-771-161A-184  
; Sequence 184, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 09/774, 676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 184  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-184

Alignment Scores:  
Pred. No.: 6,75e-225 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-771-161A-184 (1-540)

QY 335 TTACAGAGTCTTTCAGTGCATTCACCTATGTGACAGAGAAATGGATATCTCTG 394

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QY 395 AACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCTCTCTAGCTCCATGAA 454  
Db 334 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCTCCTGAAACTTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTTAA 514  
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATCAAGCTGCATCTGCTCTCGAAATCAAGT 574  
Db 374 SerArgLysAlaGlnAspCysIyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGACCACTTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 634  
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 413  
QY 635 TGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGCCT 694  
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCAGAGTGGATCCAGACAAAGGAAGACATTGTGAACCAAAATGACAGAA 754  
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGGACTTGTATGATGAAGAGGAC 814  
Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGluAsp 473  
QY 815 TATGAATCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTTCAGACAAATTTACTAGAC 874  
Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTCAAAAATGGAAGATAACAA 934  
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAAATGGTCTTTCAGCTTACCCGGAATACTTGTGTTTCTAGATCACCACCTTTTAAAT 994  
Db 514 GlnMetGlyLeuGlnProIyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 534 LeuLeuGlnAsnLysSerMet 540

## RESULT 3

US-09-862-027-28  
; Sequence 28, Application US/09862027  
; Patent No. US20020142428A1  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; TITLE OF INVENTION: No. US20020142428A1 Kinases and Uses Thereof  
; FILE REFERENCE: 35800/234862  
; CURRENT APPLICATION NUMBER: US/09/862, 027  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 09/345,473  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-862-027-28

Alignment Scores:  
Pred. No.: 6,75e-225 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-862-027-28 (1-540)

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Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 353
QY 455 AATAGTGGTTCCTCAAACTTCAAGTCCCTGCGAGCTCTCAAGACAAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
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Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393
QY 575 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATTCGTGATCACAAGACCACTCCA 634
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Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAGAA 754
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QY 935 CAAATGGGTCTTACGCTTACCGGAAATACCTTGTTGGTTCTTAGATCACCATCTTTAAAT 994
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533
QY 995 TTACTTCAAAATAAAAGCATG 1015
Db 534 LeuLeuGlnAsnLysSerMet 540
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RESULT 4

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; Sequence 14, Application US/09981397A
; Publication No.: US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 540
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-09-981-397A-14

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Alignment Scores: 6.75e-225 Length: 540
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 10 Gaps: 0
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US-09-771-161A-2 (1-1669) x US-09-981-397A-14 (1-540)

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Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333
QY 395 AACATACCTGTAAATCATGCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 353
QY 455 AATAGTGGTTCCTCAAACTTCAAGTCCCTGCGAGCTCTCAAGACAAATGATTTTAA 514
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373
QY 515 TCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCACTGCTCGGAATACACAGT 574
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393
QY 575 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATTCGTGATCACAAGACCACTCCA 634
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 413
QY 635 TGCTCTTCAGCAATTAATCAATCCACTCTCAACTGCAGGAACTCAGAACGCTCGAGCT 694
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAGAA 754
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453
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Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAsp 473
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QY 875 ACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATGGAAGATAACAA 934
Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513
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RESULT 5

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US-09-925-301-1015
; Sequence 1015, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
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APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Alignment Scores:  
Pred. No.: 6,75e-225 Length: 544  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-925-301-1015 (1-544)

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QY 455 AATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCTCAAGCAATGATTTTAA 514  
Db 358 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 377  
QY 515 TCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCTCTCTCGAAATCACAGT 574  
Db 378 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 397  
QY 575 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCATCCA 634  
Db 398 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 417  
QY 635 TGCTCTTCAGCAATAAATCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGCT 694  
Db 418 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 437  
QY 695 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATCACAGAA 754  
Db 438 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 457  
QY 755 GCCTGCCTTAAACCAAGTCCAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAGGAC 814  
Db 458 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 477  
QY 815 TATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCCAGCAATTAAGTACACAT 874  
Db 478 TyrGlnLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 497  
QY 875 ACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAAATGAAAGATAACAAA 934  
Db 498 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 517  
QY 935 CAAATGGGTCTTACGCTTACCCGGAAATACCTGTGGTTCTAGATCACCATCTTTAAAT 994  
Db 518 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 537  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 538 LeuLeuGlnAsnLysSerMet 544

RESULT 6  
US-09-748-537-1  
Sequence 1, Application US/09748537  
Patent No. US2002061833A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942

APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-316001  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Alignment Scores:  
Pred. No.: 1,11e-122 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)

QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACCTCTGCAG 691  
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCCTTAAACCAAGTCCAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACTGTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCCAGCAATTAAGTAC 871  
Db 473 AspTyrGlnLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGCATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAAATGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGTCTTCTCAGCTTACCCGGAAATACCTGTGGTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 7  
US-09-728-721-2  
Sequence 2, Application US/09728721  
Patent No. US2002061845A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942

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; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-2

Alignment Scores:
Pred. No.:      1,11e-122      Length:      540
Score:          128.00         Matches:    128
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:     24.11%        Indels:     0
DB:              9            Gaps:        0

US-09-771-161A-2 (1-1669) x US-09-728-721-2 (1-540)
QY 632 CCATGCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGCTCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTATAGCCAGCAGTGCATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAACCAAGTCGTAGATGCCCTTCTCAGGAGCTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAAGAAATTGGCAAGTTATAGTACAAAATTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAATGGTCTTCAGCCTTACCCGGAATACTTGCTGTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 8
US-10-133-780-1
; Sequence 1, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
```

```
; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-780-1

Alignment Scores:
Pred. No.:      1,11e-122      Length:      540
Score:          128.00         Matches:    128
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:     24.11%        Indels:     0
DB:              13            Gaps:        0

US-09-771-161A-2 (1-1669) x US-10-133-780-1 (1-540)
QY 632 CCATGCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGCTCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTATAGCCAGCAGTGCATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAACCAAGTCGTAGATGCCCTTCTCAGGAGCTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAAGAAATTGGCAAGTTATAGTACAAAATTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAATGGTCTTCAGCCTTACCCGGAATACTTGCTGTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 2  
 LENGTH: 540  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-105-931-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 24.11%  
 DB: 13  
 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-2 (1-540)

QY 632 CCATGCTCTTACGCAATAATAATCACTCTCACTCCAGGAACTCAGAACTGCTGCAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCCTTAAACCATGCTAGATGCCCTTCTGTCCAGGACTTGCATCAAGAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATGTTAGTACAGCCTACAGGACCTCAAGACCTCAAAAGTTCAGACAAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAATGGTCTTACGCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10

US-10-118-984-2  
 ; Sequence 2, Application US/10118984  
 ; Publication No. US20020197693A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-118-984-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540

Score: 128.00 Matches: 128  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 24.11%  
 DB: 13  
 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-118-984-2 (1-540)

QY 632 CCATGCTCTTACGCAATAATAATCACTCTCACTCCAGGAACTCAGAACTGCTGCAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCCTGCCTTAAACCATGCTAGATGCCCTTCTGTCCAGGACTTGCATCAAGAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATGAATGTTAGTACAGCCTACAGGACCTCAAGACCTCAAAAGTTCAGACAAATTAAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAATGGTCTTACGCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 11

US-10-295-981-2  
 ; Sequence 2, Application US/10295981  
 ; Publication No. US20030120055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-295-981-2

Alignment Scores:

Pred. No.: 1.11e-122 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 24.11%  
 DB: 14  
 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-295-981-2 (1-540)

QY 632 CCATGCTCTTCACCAATATAATCCACTCTCACTGCGAGGAACCTCAGAAAGCTGCGAG 691  
Db 413 ProCysSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACAGAAAGGAAGACATTCTGAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCTTAACCAAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAATCTGTAGTACCAAGCTCACAAGACCTCAAAAGTCAGACAAATTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCCAAAGGAGAAGATTGCGCAAGTTATAGTACAAAAATTTGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12  
US-09-728-721-6  
; Sequence 6, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728, 721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-6

Alignment Scores:  
Pred. No.: 5.18e-103 Length: 109  
Score: 109.00 Matches: 109  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.53% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-728-721-6 (1-109)  
QY 689 CAGCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAAGT 748  
Db 1 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 20  
QY 749 ACAGAAGCCTGCCTTAAACCAAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAA 808  
Db 21 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLys 40  
QY 809 GAGGACTATGAATTTAGTACCAAGCCTCAAGACCTCAAAAGTCAGACAAATTACTTA 868  
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60  
QY 869 GACACTACTGACATCCAAAGGAGAAGATTGCGCAAGTTATAGTACAAAAATTTGAAAGAT 928  
Db 61 AspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
QY 929 AACAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCT 988  
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100  
QY 989 TTAATTTACTTCAAAATAAAGCATG 1015  
Db 101 LeuAsnLeuLeuGlnAsnLysSerMet 109

QY 809 GAGGACTATGAATTTAGTACCAAGCCTCAAGACCTCAAAAGTCAGACAAATTACTTA 868  
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60  
QY 869 GACACTACTGACATCCAAAGGAGAAGATTGCGCAAGTTATAGTACAAAAATTTGAAAGAT 928  
Db 61 AspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
QY 929 AACAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCT 988  
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100  
QY 989 TTAATTTACTTCAAAATAAAGCATG 1015  
Db 101 LeuAsnLeuLeuGlnAsnLysSerMet 109

RESULT 13  
US-10-105-931-6  
; Sequence 6, Application US/10105931  
; Publication No. US20020150987A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/10/105,931  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-931-6

Alignment Scores:  
Pred. No.: 5.18e-103 Length: 109  
Score: 109.00 Matches: 109  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.53% Indels: 0  
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-6 (1-109)  
QY 689 CAGCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAAGT 748  
Db 1 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 20  
QY 749 ACAGAAGCCTGCCTTAAACCAAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAA 808  
Db 21 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLys 40  
QY 809 GAGGACTATGAATTTAGTACCAAGCCTCAAGACCTCAAAAGTCAGACAAATTACTTA 868  
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60  
QY 869 GACACTACTGACATCCAAAGGAGAAGATTGCGCAAGTTATAGTACAAAAATTTGAAAGAT 928  
Db 61 AspThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAsp 80  
QY 929 AACAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCT 988  
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US-10-118-984-6
; Sequence 6, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-6

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.53% Indels: 0
DB: 13 Gaps: 0

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QY 749 ACAGAACCTGCTTAAACGAGTCGCTAGATGCCCTTCTGTCAGGAGACTTGATCATGAAA 808
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QY 809 GAGGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCACACAATTACTA 868
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QY 929 AACAAACAATGGGTCTTACGCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCT 988
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100
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; Sequence 6, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
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; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
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; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
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US-10-295-981-6

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Db 21 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLys 40
QY 809 GAGGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCACACAATTACTA 868
Db 41 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 60
QY 869 GACACTACTGACATCCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGAT 928
Db 61 AspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 80
QY 929 AACAAACAATGGGTCTTACGCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCT 988
Db 81 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSer 100
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Search completed: March 29, 2004, 14:40:27
Job time : 84 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 06:30:56 ; Search time 649 Seconds  
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Perfect score: 1669

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- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1079	64.6	2709	US-09-925-301-173	Sequence 173, App
3	812	48.7	2501	US-09-981-397A-13	Sequence 13, Appl
4	682	40.9	1931	US-09-748-537-2	Sequence 2, Appli
5	682	40.9	1931	US-09-728-721-1	Sequence 1, Appli
6	682	40.9	1931	US-10-133-780-2	Sequence 1, Appli
7	682	40.9	1931	US-10-105-931-1	Sequence 1, Appli
8	682	40.9	1931	US-10-118-984-1	Sequence 1, Appli
9	682	40.9	1931	US-10-295-981-1	Sequence 1, Appli
10	632	37.9	1620	US-09-728-721-3	Sequence 3, Appli
11	632	37.9	1620	US-10-105-931-3	Sequence 3, Appli
12	632	37.9	1620	US-10-118-984-3	Sequence 3, Appli
13	632	37.9	1620	US-10-295-981-3	Sequence 3, Appli
14	363	21.7	491	US-09-918-995-20565	Sequence 20565, A
15	220	13.2	299	US-09-919-580-544	Sequence 544, App

16	191	11.4	242	14	US-10-066-543-3282	Sequence 3282, Ap
17	60	3.6	60	10	US-09-908-975-13799	Sequence 13799, A
18	60	3.6	60	10	US-09-908-975-31279	Sequence 31279, A
19	60	3.6	60	10	US-09-908-975-31541	Sequence 31541, A
20	50	3.0	50	15	US-10-131-827-4651	Sequence 4651, Ap
21	37	2.2	54	9	US-09-748-537-10	Sequence 10, Appl
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23	24	1.4	804	12	US-10-282-122A-35784	Sequence 35784, A
24	23	1.4	32	9	US-09-748-537-9	Sequence 9, Appli
25	22	1.3	1119	9	US-09-741-669-174	Sequence 174, App
26	22	1.3	1119	9	US-09-860-432-515	Sequence 215, App
27	21	1.3	438	9	US-09-860-432-51	Sequence 51, Appl
28	21	1.3	1942	10	US-09-822-846-166	Sequence 166, App
29	21	1.3	3060	10	US-09-919-039-229	Sequence 229, App
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39	20	1.2	645	15	US-10-027-632-188799	Sequence 188799, A
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42	20	1.2	837	12	US-10-424-599-11942	Sequence 11942, A
43	20	1.2	912	12	US-10-282-122A-21960	Sequence 21960, A
44	20	1.2	1007	15	US-10-027-632-249981	Sequence 249981, A
45	20	1.2	1536	14	US-10-072-438-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TGTAGTAATTGTTAGATTTTCGAGGATCGAGCTCTGAGACATGAGAGAGTAACTTACC 120



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US-09-981-397A-13
; Sequence 13, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981.397A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
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; ORGANISM: Homo sapiens
US-09-981-397A-13

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Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 2, Application US/09748537  
; Patent No. US20020061833A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
; FILE REFERENCE: 07334-316001  
; CURRENT APPLICATION NUMBER: US/09/748,537  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-748-537-2

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QY 453 AAAATAGTGGTTCCTCGAAACTTCAAGGTCCTCCAGGTCCTCAAGACAATGATTTTT 512

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QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTGGAATCACA 572  
Db 1331 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTGGAATCACA 1390  
QY 573 GTTGGGATAGCACATTTCTGGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 632  
Db 1391 GTTGGGATAGCACATTTCTGGATCTCAAGGGCTCATTTCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGGAAACTCAGAACGTCCTCAGC 692  
Db 1451 CATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGGAAACTCAGAACGTCCTCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 1570  
QY 753 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 812  
Db 1571 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 1630  
QY 813 ACTATCAACTTGTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872  
Db 1631 ACTATCAACTTGTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 1690  
QY 873 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
Db 1691 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
QY 933 AACAAATGGTCTTTCAGACCTTACCCGGAATACCTTGTGTTTCTAGATCACCATCTTTAA 992  
Db 1751 AACAAATGGTCTTTCAGACCTTACCCGGAATACCTTGTGTTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTTACTTCAAAATAAAGCATGTAAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1052  
Db 1811 ATTTACTTCAAAATAAAGCATGTAAGTGAAGTGTGTTTCAAGAGAAATGTGTTTCATAA 1870  
QY 1053 AAGGATATTTATA 1065  
Db 1871 AAGGATATTTATA 1883

RESULT 5  
US-09-728-721-1  
; Sequence 1, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-728-721-1



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QY 933 AACAAATGGTCTTCCAGCTTACCCGGAATACTCTGTGGTTCTTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTCCAGCTTACCCGGAATACTCTGTGGTTCTTAGATCACCATCTTTAA 1810
QY 993 ATTACTTCAAAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTGTTTCATAA 1052
Db 1811 ATTACTTCAAAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTGTTTCATAA 1870
QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 7
US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Query Match 40.9%; Score 682; DB 13; Length 1931;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 392
Db 1151 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 1210
QY 393 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 1211 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270
QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 512
Db 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 1330
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCACTGTCTGGAATACACA 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCACTGTCTGGAATACACA 1390
QY 573 GTTGGATAGCACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 632
Db 1391 GTTGGATAGCACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 1450
QY 633 CATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 692
Db 1451 CATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 1510
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTGTGAACCAATGACAG 752
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTGTGAACCAATGACAG 1570
QY 753 AAGCTGCTTAAACGATCGCTAGATGCCCTTCTGTCCAGGCACTTGATCATGAAGAGG 812
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Db 1571 AAGCCTGCCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630
QY 813 ACTATGAACCTTGTAGTACCAAGCCTACAAGACCTCAAAAGTCAACAATTAAGTACAGCA 872
Db 1631 ACTATGAACCTTGTAGTACCAAGCCTACAAGACCTCAAAAGTCAACAATTAAGTACAGCA 1690
QY 873 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 932
Db 1691 CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 1750
QY 933 AACAAATGGTCTTCCAGCTTACCCGGAATACTCTGTGGTTCTTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTCCAGCTTACCCGGAATACTCTGTGGTTCTTAGATCACCATCTTTAA 1810
QY 993 ATTACTTCAAAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTGTTTCATAA 1052
Db 1811 ATTACTTCAAAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTGTTTCATAA 1870
QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 8
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-02-05
; PRIOR FILING DATE: 1998-12-08
; PRIOR FILING DATE: 1998-12-08
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Query Match 40.9%; Score 682; DB 13; Length 1931;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 392
Db 1151 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 1210
QY 393 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 1211 TGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270
QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 512
Db 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCATTCACCTATGTGCAAGAGAAATGGAATATCTC 1330
QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCACTGTCTGGAATACACA 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGTCATCACTGTCTGGAATACACA 1390
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QY 573 GTTGGATAGACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 632  
Db 1391 GTTGGATAGACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 1450  
QY 633 CATGCTCTTTCAGCAATAAATCAACTCTCAACTGCGAGGAACCTCAGAACTGTCGACG 692  
Db 1451 CATGCTCTTTCAGCAATAAATCAACTCTCAACTGCGAGGAACCTCAGAACTGTCGACG 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 1570  
QY 753 AAGCCTGCTTAAACAGTCTAGATGCGCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
Db 1571 AAGCCTGCTTAAACAGTCTAGATGCGCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
QY 813 ACTATGAACCTTGTAGTACCAAGCTTACCAAGGACTTCAAAAGTTCAGAAATTTGAAAGATAA 932  
Db 1631 ACTATGAACCTTGTAGTACCAAGCTTACCAAGGACTTCAAAAGTTCAGAAATTTGAAAGATAA 1690  
QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAA 932  
Db 1691 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAA 1750  
QY 933 AACAAATGGCTCTTACGCTTACCGGAAATTTGCTGTTCTAGATCACCATCTTTAA 992  
Db 1751 AACAAATGGCTCTTACGCTTACCGGAAATTTGCTGTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGAAATTTGCTTCAATAA 1052  
Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGAAATTTGCTTCAATAA 1870  
QY 1053 AAGGATATTTATA 1065  
Db 1871 AAGGATATTTATA 1883

RESULT 9

US-10-295-981-1  
; Sequence 1, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-10-295-981-1  
Query Match 40.9%; Score 682; DB 14; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGTGGCAATTCACCTATGTGACAAGAGAAAAATGGAATATATCTC 392

Db 1151 AGTTACAGAGTGTTCAGTGGCAATTCACCTATGTGACAAGAGAAAAATGGAATATATCTC 1210  
QY 393 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCCTCTCAGCTCCATG 452  
Db 1211 TGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCCTCTCAGCTCCATG 1270  
QY 453 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCGAGCTCCCTCAAGACATATGTTTT 512  
Db 1271 AAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCGAGCTCCCTCAAGACATATGTTTT 1330  
QY 513 TATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCATCTGCTGAAATCACA 572  
Db 1331 TATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCATCTGCTGAAATCACA 1390  
QY 573 GTTGGATAGCACCAATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCACAAGACCACTC 632  
Db 1391 GTTGGATAGCACCAATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCACAAGACCACTC 1450  
QY 633 CATGCTCTTTCAGCAATAAATCCACTCTCAACTGCGAGGAACCTCAGAACTGTCGACG 692  
Db 1451 CATGCTCTTTCAGCAATAAATCCACTCTCAACTGCGAGGAACCTCAGAACTGTCGACG 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 752  
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAG 1570  
QY 753 AAGCCTGCTTAAACAGTCTAGATGCGCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
Db 1571 AAGCCTGCTTAAACAGTCTAGATGCGCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
QY 813 ACTATGAACCTTGTAGTACCAAGCTTACCAAGGACTTCAAAAGTTCAGAAATTTGAAAGATAA 872  
Db 1631 ACTATGAACCTTGTAGTACCAAGCTTACCAAGGACTTCAAAAGTTCAGAAATTTGAAAGATAA 1690  
QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAA 1750  
Db 1691 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATAA 1750  
QY 933 AACAAATGGCTCTTACGCTTACCGGAAATTTGCTGTTCTAGATCACCATCTTTAA 992  
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QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGAAATTTGCTTCAATAA 1052  
Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGTTTTCAGAGAAATTTGCTTCAATAA 1870  
QY 1053 AAGGATATTTATA 1065  
Db 1871 AAGGATATTTATA 1883

RESULT 10

US-09-728-721-3  
; Sequence 3, Application US/09728721  
; Patent No. US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3

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; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-728-721-3

Query Match      37.9%; Score 632; DB 9; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.1e-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392
Db 938 AGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTC 997
QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 998 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 512
Db 1058 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 572
Db 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 1177
QY 573 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 632
Db 1178 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 1237
QY 632 CATGCTCTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCGAGC 692
Db 1238 CATGCTCTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCGAGC 1297
QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGACAG 752
Db 1298 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGACAG 1357
QY 752 AAGCCTGCTTAAACAGCTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 812
Db 1358 AAGCCTGCTTAAACAGCTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 1417
QY 812 ACTATGAACCTTTAGTACCAAGCTCAAGGACTCAAGGAACTCAAGAGTCAAGATTAAGACA 872
Db 1418 ACTATGAACCTTTAGTACCAAGCTCAAGGAACTCAAGAGTCAAGATTAAGACA 1477
QY 872 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db 1478 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 1537
QY 932 AACAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 992
Db 1538 AACAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 1597
QY 992 ATTTACTTCAAAATAAAGCATG 1015
Db 1598 ATTTACTTCAAAATAAAGCATG 1620

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RESULT 11
US-10-105-931-3
; Sequence 3, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 05/019,942
; PRIOR FILING DATE: 1998-02-06

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; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-931-3

Query Match      37.9%; Score 632; DB 13; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.1e-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTC 392
Db 938 AGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTC 997
QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452
Db 998 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 512
Db 1058 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGCTCCCTCAAGACAATGATTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 572
Db 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTGATCAAGACCACTC 1177
QY 573 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 632
Db 1178 GTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCAATCTGTGATCAAGACCACTC 1237
QY 632 CATGCTCTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCGAGC 692
Db 1238 CATGCTCTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCGAGC 1297
QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGACAG 752
Db 1298 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGACAG 1357
QY 752 AAGCCTGCTTAAACAGCTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 812
Db 1358 AAGCCTGCTTAAACAGCTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 1417
QY 812 ACTATGAACCTTTAGTACCAAGCTCAAGGACTCAAGGAACTCAAGAGTCAAGATTAAGACA 872
Db 1418 ACTATGAACCTTTAGTACCAAGCTCAAGGAACTCAAGAGTCAAGATTAAGACA 1477
QY 872 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db 1478 CTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 1537
QY 932 AACAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 992
Db 1538 AACAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 1597
QY 992 ATTTACTTCAAAATAAAGCATG 1015
Db 1598 ATTTACTTCAAAATAAAGCATG 1620

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RESULT 12
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/245,281

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3

Query Match      37.9%; Score 632; DB 13; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.le-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAGAAATGGAATATATCTC 392
Db      |||||
QY 938 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAGAAATGGAATATATCTC 997
Db      |||||

QY 393 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 452
Db      |||||
QY 998 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 1057
Db      |||||

QY 453 AAAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTT 512
Db      |||||
QY 1058 AAAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTT 1117
Db      |||||

QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATACAA 572
Db      |||||
QY 1118 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATACAA 1177
Db      |||||

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATCTC 632
Db      |||||
QY 1178 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATCTC 1237
Db      |||||

QY 633 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCAGC 692
Db      |||||
QY 1238 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCAGC 1297
Db      |||||

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 752
Db      |||||
QY 1418 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 1477
Db      |||||

QY 873 CTACTGACATCCAGGAGAAATTTGCAAAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db      |||||
QY 1478 CTACTGACATCCAGGAGAAATTTGCAAAAGTTATAGTACAAAATTTGAAAGATAACA 1537
Db      |||||

QY 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGTTTCTAGATCACCATTCTTTAA 992
Db      |||||
QY 1538 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGTTTCTAGATCACCATTCTTTAA 1597
Db      |||||

QY 993 ATTTACTTCAAAATAAAGCATG 1015
Db      |||||
QY 1598 ATTTACTTCAAAATAAAGCATG 1620
Db      |||||
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RESULT 13  
US-10-295-981-3  
; Sequence 3, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:

```
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3
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Query Match      37.9%; Score 632; DB 14; Length 1620;
Best Local Similarity 99.9%; Pred. No. 1.le-298;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAGAAATGGAATATATCTC 392
Db      |||||
QY 938 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAGAAATGGAATATATCTC 997
Db      |||||

QY 393 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 452
Db      |||||
QY 998 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 1057
Db      |||||

QY 453 AAAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTT 512
Db      |||||
QY 1058 AAAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTT 1117
Db      |||||

QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATACAA 572
Db      |||||
QY 1118 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATACAA 1177
Db      |||||

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATCTC 632
Db      |||||
QY 1178 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATCTC 1237
Db      |||||

QY 633 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCAGC 692
Db      |||||
QY 1238 CATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCAGC 1297
Db      |||||

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 752
Db      |||||
QY 1298 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAG 1357
Db      |||||

QY 753 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGAACTTGATCATGAAGAGG 812
Db      |||||
QY 1358 AAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGAACTTGATCATGAAGAGG 1417
Db      |||||

QY 813 ACTATGAACTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGACA 872
Db      |||||
QY 1418 ACTATGAACTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGACA 1477
Db      |||||

QY 873 CTACTGACATCCAGGAGAAATTTGCAAAAGTTATAGTACAAAATTTGAAAGATAACA 932
Db      |||||
QY 1478 CTACTGACATCCAGGAGAAATTTGCAAAAGTTATAGTACAAAATTTGAAAGATAACA 1537
Db      |||||

QY 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGTTTCTAGATCACCATTCTTTAA 992
Db      |||||
QY 1538 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGTTTCTAGATCACCATTCTTTAA 1597
Db      |||||

QY 993 ATTTACTTCAAAATAAAGCATG 1015
Db      |||||
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Db 1598 ATTACTCTCAAAATAAAAGCATG 1620

RESULT 14

US-09-918-995-20565

Sequence 20565, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 20565

LENGTH: 491

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-20565

Query Match

Best Local Similarity 100.0%; Pred. No. 5.5e-167; Length 491;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTTCAAGTGCCATTCACTATGTGACAAAGAGAAAATGGAATTATCTC 392

Db 129 AGTTACAGAGTGTTTCAAGTGCCATTCACTATGTGACAAAGAGAAAATGGAATTATCTC 188

QY 393 TGAACATACCTGTAATCATGTCGCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 452

Db 189 TGAACATACCTGTAATCATGTCGCAAGAGGAATCATGTGATCCTCTCAGCTCCATG 248

QY 453 AATAAGTGGTCTCTCTGAAATTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 512

Db 249 AATAAGTGGTCTCTCTGAAATTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTT 308

QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAATCACA 572

Db 309 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCCTGGAATCACA 368

QY 573 GTTGGGATAGCACCATTCTCGGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 632

Db 369 GTTGGGATAGCACCATTCTCGGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC 428

QY 633 CATGCTCTTCAGCAATAATAATCACTCTCACTGAGGAACTCAGAACGTCGTGAGC 692

Db 429 CATGCTCTTCAGCAATAATAATCACTCTCACTGAGGAACTCAGAACGTCGTGAGC 488

QY 693 CTG 695

Db 489 CTG 491

LENGTH: 299

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 243

OTHER INFORMATION: n = A,T,C or G

US-09-919-580-544

Query Match

Best Local Similarity 100.0%; Pred. No. 5.9e-97; Length 299;

Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1441 TTAATTGCCCTACAAAGGGTTATTAAATTTAAAACTCCATTATTAGGATTACATTTTAAAG 1500

Db 242 TTAATTGCCCTACAAAGGGTTATTAAATTTAAAACTCCATTATTAGGATTACATTTTAAAG 183

QY 1501 TTTTATTATGAATTTCCCTTTAAAAATGATATTTCAAAGGTTAAAAACAATACATATTAAG 1560

Db 182 TTTTATTATGAATTTCCCTTTAAAAATGATATTTCAAAGGTTAAAAACAATACATATTAAG 123

QY 1561 AAAAAATAAATATATTAATACCGCTTCCTGTCCTCCCATTTTTTAACCTCAGCCTTCCCTA 1620

Db 122 AAAAAATAAATATATTAATACCGCTTCCTGTCCTCCCATTTTTTAACCTCAGCCTTCCCTA 63

QY 1621 CTGTCAACCAACCAAGCTAAATAAAGTCAACAGCCTGA 1660

Db 62 CTGTCAACCAACCAAGCTAAATAAAGTCAACAGCCTGA 23

Search completed: April 1, 2004, 10:07:48

Job time : 705 secs

RESULT 15

US-09-919-580-544/c

Sequence 544, Application US/09919580

Patent No. US20020110832A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth

APPLICANT: Xu, Jiangchun

APPLICANT: Serist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.552

CURRENT APPLICATION NUMBER: US/09/919,580

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 544



Db 1642 ACTATGAACCTTTAGTACCAAGCCTACAAGGACCTCAAAGTCAGACAATTAAGTACAGACA 1701  
Qy 873 CTACTGACATCCAGGAGAGAAATTCGCAAGATTAAGTACAAAATTCAGAGATACACA 932  
Db 1702 CTACTGACATCCAGGAGAGAAATTCGCAAGATTAAGTACAAAATTCAGAGATACACA 1761  
Qy 933 AACAAATGGGTCTTACGCTTACCGGAAATACCTGTTGTTCTAGATCACCATCTTTAA 992  
Db 1762 AACAAATGGGTCTTACGCTTACCGGAAATACCTGTTGTTCTAGATCACCATCTTTAA 1821  
Qy 993 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTCAAGAGAAATGTTTTCATAA 1052  
Db 1822 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTCAAGAGAAATGTTTTCATAA 1881  
Qy 1053 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATAAATCCGTCAGATTAAG 1112  
Db 1882 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATAAATCCGTCAGATTAAG 1941  
Qy 1113 CTTTATTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 1172  
Db 1942 CTTTATTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 2001  
Qy 1173 TTAATTAATCAAGTAAAAAGTT 1195  
Db 2002 TTAATTAATCAAGTAAAAAGTT 2024

RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-0333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-2

Query Match 48.7%; Score 812; DB 4; Length 2502;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 333 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTCGACAGAGAAATGGAATATATCTC 392  
Db 1163 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTCGACAGAGAAATGGAATATATCTC 1222  
Qy 393 TGAACATACCTGTAATCATGTCACAGAGGAAATCATGTGATCTCTCAGCTCCATG 452  
Db 1223 TGAACATACCTGTAATCATGTCACAGAGGAAATCATGTGATCTCTCAGCTCCATG 1282  
Qy 453 AAAATAGTGGTTCCTCGAAATCTTCAAGGTCCTGCGAGCTCTTCAAGACAAATGATTTT 512  
Db 1283 AAAATAGTGGTTCCTCGAAATCTTCAAGGTCCTGCGAGCTCTTCAAGACAAATGATTTT 1342  
Qy 513 TATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTGTCCTGGAATCACA 572  
Db 1343 TATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTGTCCTGGAATCACA 1402  
Qy 573 GTTGGGATAGCACCATTCTGATCTCAAGGGCTGATCTGTGATCACAAGACCACTC 632  
Db 1403 GTTGGGATAGCACCATTCTGATCTCAAGGGCTGATCTGTGATCACAAGACCACTC 1462

Qy 633 CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGACAGAACTCAGAACGTCCTCAGC 692  
Db 1463 CATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGACAGAACTCAGAACGTCCTCAGC 1522  
Qy 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAG 752  
Db 1523 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAG 1582  
Qy 753 AAGCCTGCTTAACTACAGTGCCTTCTGTCAGGAGCTTGTATCATCAAAAGAGG 812  
Db 1583 AAGCCTGCTTAACTACAGTGCCTTCTGTCAGGAGCTTGTATCATCAAAAGAGG 1642  
Qy 813 ACTATGAACCTTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTAAGTACACA 872  
Db 1643 ACTATGAACCTTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTAAGTACACA 1702  
Qy 873 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
Db 1703 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1762  
Qy 933 AACAAATGGGTCTTTCAGCCTTACCGGAAATACCTGTTGTTTCTAGATCACCATCTTTAA 992  
Db 1763 AACAAATGGGTCTTTCAGCCTTACCGGAAATACCTGTTGTTTCTAGATCACCATCTTTAA 1822  
Qy 993 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGAGAAATGTTTTCATAA 1052  
Db 1823 ATTACTTCAAAATAAAGCATGTAAGTGAAGTCTGTTTTCAGAGAAATGTTTTCATAA 1882  
Qy 1053 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATAAATCCGTCAGTATTAAG 1112  
Db 1883 AAGGATATTTATATCTCTGTTGCTTTCAGCTTTTATATAAATCCGTCAGTATTAAG 1942  
Qy 1113 CTTTATTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 1172  
Db 1943 CTTTATTGAAGGTTCTTTGGTAAATATAGTCTCCCTCCATGACACTGCAGTATTTT 2002  
Qy 1173 TTAATTAATCAAGTAAAAAGTT 1195  
Db 2003 TTAATTAATCAAGTAAAAAGTT 2025

RESULT 3  
US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1931 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-019-942-2

Query Match 40.9%; Score 682; DB 3; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
Matches 732; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTTATCTC 392  
DB 1151 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTTATCTC 1210

QY 393 TGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCCATG 452  
DB 1211 TGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCCATG 1270

QY 453 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGTCCCTCAAGACAATGATTTT 512  
DB 1271 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGTCCCTCAAGACAATGATTTT 1330

QY 513 TATCTAGAAAGAGCTCAAGAGCTGTTATTTATGAAGCTGCATCCTCAAGACAATGATTTT 572  
DB 1331 TATCTAGAAAGAGCTCAAGAGCTGTTATTTATGAAGCTGCATCCTCAAGACAATGATTTT 1390

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGAGGCTGCAATTTCTGTGATCAAGACAATGATTTT 632  
DB 1391 GTTGGATAGCACCATTCTCGATCTCAAGAGGCTGCAATTTCTGTGATCAAGACAATGATTTT 1450

QY 633 CATGCTCTTCAAGACAATTAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 692  
DB 1451 CATGCTCTTCAAGACAATTAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 1510

QY 693 CTGGTATAGCCAGAGTGGATCCAGACAAAGAGGAGACATTTGTAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGAGTGGATCCAGACAAAGAGGAGACATTTGTAACCAATGACAG 1570

QY 753 AAGCTGCTTAAACAGTCCGTAGATGCTTCTGTCCAGGAACTTGATCAATGAAGAGG 812  
DB 1571 AAGCTGCTTAAACAGTCCGTAGATGCTTCTGTCCAGGAACTTGATCAATGAAGAGG 1630

QY 813 ACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAAGACAATTTACTAGACA 872  
DB 1631 ACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAAGACAATTTACTAGACA 1690

QY 873 CTACTGACATCAAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932  
DB 1691 CTACTGACATCAAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1750

QY 933 AACAAATGGGCTTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAA 992  
DB 1751 AACAAATGGGCTTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAA 1810

QY 993 ATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTGTTTCATAA 1052  
DB 1811 ATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTGTTTCATAA 1870

QY 1053 AAGGATATTTATA 1065  
DB 1871 AAGGATATTTATA 1883

RESULT 4  
US-09-099-041A-1  
; Sequence 1, Application US/09099041A  
; Patent No. 6340576

GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-099-041A-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTTATCTC 392  
DB 1151 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTTATCTC 1210

QY 393 TGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCCATG 452  
DB 1211 TGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCCATG 1270

QY 453 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGTCCCTCAAGACAATGATTTT 512  
DB 1271 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGTCCCTCAAGACAATGATTTT 1330

QY 513 TATCTAGAAAGAGCTCAAGAGCTGTTATTTATGAAGCTGCATCCTCAAGACAATGATTTT 572  
DB 1331 TATCTAGAAAGAGCTCAAGAGCTGTTATTTATGAAGCTGCATCCTCAAGACAATGATTTT 1390

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGAGGCTGCAATTTCTGTGATCAAGACAATGATTTT 632  
DB 1391 GTTGGATAGCACCATTCTCGATCTCAAGAGGCTGCAATTTCTGTGATCAAGACAATGATTTT 1450

QY 633 CATGCTCTTCAAGACAATTAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 692  
DB 1451 CATGCTCTTCAAGACAATTAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGC 1510

QY 693 CTGGTATAGCCAGAGTGGATCCAGACAAAGAGGAGACATTTGTAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGAGTGGATCCAGACAAAGAGGAGACATTTGTAACCAATGACAG 1570

QY 753 AAGCTGCTTAAACAGTCCGTAGATGCTTCTGTCCAGGAACTTGATCAATGAAGAGG 812  
DB 1571 AAGCTGCTTAAACAGTCCGTAGATGCTTCTGTCCAGGAACTTGATCAATGAAGAGG 1630

QY 813 ACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAAGACAATTTACTAGACA 872  
DB 1631 ACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAAGACAATTTACTAGACA 1690

QY 873 CTACTGACATCAAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932  
DB 1691 CTACTGACATCAAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1750

QY 933 AACAAATGGGCTTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAA 992  
DB 1751 AACAAATGGGCTTTCAGCCTTACCCGGAAATACCTTGTGTTTCTAGATCACCATCTTTAA 1810

QY 993 ATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTGTTTCATAA 1052  
DB 1811 ATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGAAATGTTGTTTCATAA 1870

QY 1053 AAGGATATTTATA 1065

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Db      1871 AAGGATATTATA 1883
|||||
Db      1691 CTACTGACATCCAAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 1750
|||||
QY      933 AACAAATGGTCTTTCAGCCTTACCCGGAATATCTTGGTTTCTAGATCACCATCTTTAA 992
|||||
Db      1751 AACAAATGGTCTTTCAGCCTTACCCGGAATATCTTGGTTTCTAGATCACCATCTTTAA 1810
|||||
QY      993 ATTTACTTCAAAATAAAAGCATGTAAGTGACTCTTTTCAAGAGAAATGTGTTTCATAA 1052
|||||
Db      1811 ATTACTTCAAAATAAAAGCAATGTAAGTGACTCTTTTCAAGAGAAATGTGTTTCATAA 1870
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QY      1053 AAGGATATTATA 1065
|||||
Db      1871 AAGGATATTATA 1883
|||||

RESULT 6
US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Query Match      40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No: 1.2e-309;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      333 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTTATCTC 392
|||||
Db      1151 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTTATCTC 1210
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QY      393 TGAACATACCTGTAAATCAATGTTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
|||||
Db      1211 TGAACATACCTGTAAATCAATGTTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270
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QY      453 AANAATAGTGGTTCTCTCTGAAACTTTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 512
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Query Match      40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No: 1.2e-309;
Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      333 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTTATCTC 392
|||||
Db      1151 AGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTTATCTC 1210
|||||
QY      393 TGAACATACCTGTAAATCAATGTTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
|||||
Db      1211 TGAACATACCTGTAAATCAATGTTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270
|||||
QY      453 AANAATAGTGGTTCTCTCTGAAACTTTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 512
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Db      1271 AANAATAGTGGTTCTCTCTGAAACTTTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 1330
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QY      513 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 572
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Db      1331 TATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTCGGAAATCAACA 1390
|||||
QY      573 GTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 632
|||||
Db      1391 GTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 1450
|||||
QY      633 CATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACGTCGTGAGC 692
|||||
Db      1451 CATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACGTCGTGAGC 1510
|||||
QY      693 CTGGTATAGCCAGCAGTGTGATCCAGAGCAAAAGGGAACATTTGGAACCAATGACAG 752
|||||
Db      1511 CTGGTATAGCCAGCAGTGTGATCCAGAGCAAAAGGGAACATTTGGAACCAATGACAG 1570
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QY      753 AAGCTGCTTAACTACCTAGTCCCTAGTCCCTTCTGTCCAGGGACTTGATCATCAAGAGG 812
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Db      1571 AAGCTGCTTAACTACCTAGTCCCTAGTCCCTTCTGTCCAGGGACTTGATCATCAAGAGG 1630
|||||
QY      813 ACTATGAACCTTGTGTAGTACCAAGCTCAAGAGCACTCAAAAGTCAGACAAATTTACTAGACA 872
|||||
Db      1631 ACTATGAACCTTGTGTAGTACCAAGCTCAAGAGCACTCAAAAGTCAGACAAATTTACTAGACA 1690
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QY      873 CTACTGACATCCAAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACA 932
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Db 1271 AAAATAGTGGTCTCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1330  
 QY 513 TATCTAGAAAAAGCTCAAGAGCTGTTATTTATGAAGCTGCATCACTGTCTGGAATTCACA 572  
 Db 1331 TATCTAGAAAAAGCTCAAGAGCTGTTATTTATGAAGCTGCATCACTGTCTGGAATTCACA 1390  
 QY 573 GTTGGGATAGCAACATTTCTGATCTCAAGAGCTGCATTTCTGTGATCAACAAGACCACTC 632  
 Db 1391 GTTGGGATAGCAACATTTCTGATCTCAAGAGCTGCATTTCTGTGATCAACAAGACCACTC 1450  
 QY 633 CATGCTCTTCAACAATAAATCAACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 692  
 Db 1451 CATGCTCTTCAACAATAAATCAACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1510  
 QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAAAATGACAG 752  
 Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAAAATGACAG 1570  
 QY 753 AAGCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCCAGGACCTGATCAATGAAAGAGG 812  
 Db 1571 AAGCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCCAGGACCTGATCAATGAAAGAGG 1630  
 QY 813 ACTATGAATCTTGTAGTACCAAGCTTACAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 872  
 Db 1631 ACTATGAATCTTGTAGTACCAAGCTTACAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 1690  
 QY 873 CTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1691 CTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
 QY 933 AACAAATGGTCTTCAAGCTTACCGGAAATACTTGTGTTTCTAGATCAACCATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAAGCTTACCGGAAATACTTGTGTTTCTAGATCAACCATCTTTAA 1810  
 QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGCTTTTCAAGAGAAATGTTTTCATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGCTTTTCAAGAGAAATGTTTTCATAA 1870  
 QY 1053 AAGGATATTATA 1065  
 Db 1871 AAGGATATTATA 1883

RESULT 7

US-09-207-359B-1  
 ; Sequence 1, Application US/09207359B  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/207,359B  
 ; CURRENT FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)...(1833)  
 US-09-207-359B-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
 Best Local Similarity 99.9%; Pred. No. 1.2e-309;  
 Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTCTTCAAGTGCATTTCACTATGTGCAAGAGAAAAATGGAATTTATCTC 392  
 Db 1151 AGTTACAGAGTGTCTTCAAGTGCATTTCACTATGTGCAAGAGAAAAATGGAATTTATCTC 1210  
 QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
 Db 1211 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
 QY 453 AAAATAGTGGTCTCTCAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 512  
 Db 1271 AAAATAGTGGTCTCTCAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 1330  
 QY 513 TATCTAGAAAAAGCTCAAGACATGTTATTTTATGAAGCTGCATCACTGTCTCGAAATTCACA 572  
 Db 1331 TATCTAGAAAAAGCTCAAGACATGTTATTTTATGAAGCTGCATCACTGTCTCGAAATTCACA 1390  
 QY 573 GTTGGGATAGCAACATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAACAAGACCACTC 632  
 Db 1391 GTTGGGATAGCAACATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAACAAGACCACTC 1450  
 QY 633 CATGCTCTTCAAGCAATAAATCCACTCTCAACTGCAAGGAACTCAGAACCTCTGCAGC 692  
 Db 1451 CATGCTCTTCAAGCAATAAATCCACTCTCAACTGCAAGGAACTCAGAACCTCTGCAGC 1510  
 QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAAAATGACAG 752  
 Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAAAATGACAG 1570  
 QY 753 AAGCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCCAGGACCTGATCAATGAAAGAGG 812  
 Db 1571 AAGCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCCAGGACCTGATCAATGAAAGAGG 1630  
 QY 813 ACTATGAATCTTGTAGTACCAAGCTTACAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 872  
 Db 1631 ACTATGAATCTTGTAGTACCAAGCTTACAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 1690  
 QY 873 CTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1691 CTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
 QY 933 AACAAATGGTCTTCAAGCTTACCGGAAATACTTGTGTTTCTAGATCAACCATCTTTAA 992  
 Db 1751 AACAAATGGTCTTCAAGCTTACCGGAAATACTTGTGTTTCTAGATCAACCATCTTTAA 1810  
 QY 993 ATTACTTCAAAATAAAGCATGTAAGTACGCTTTTCAAGAGAAATGTTTTCATAA 1052  
 Db 1811 ATTACTTCAAAATAAAGCATGTAAGTACGCTTTTCAAGAGAAATGTTTTCATAA 1870  
 QY 1053 AAGGATATTATA 1065  
 Db 1871 AAGGATATTATA 1883

RESULT 8

US-09-340-620A-1  
 ; Sequence 1, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1  
LENGTH: 1931  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (214)...(1833)  
US-09-340-620A-1

Query Match 40.9%; Score 682; DB 4; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 1.2e-309; Indels 0; Gaps 0;  
Matches 732; Conservative 0; Mismatches 1;

QY	333	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGCAAGAGAAATGGAATATATCTC	392
DB	1151	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGCAAGAGAAATGGAATATATCTC	1210
QY	393	TGAACATACCTGTA	ATAATCATGGTCC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCATG	452
DB	1211	TGAACATACCTGTA	ATAATCATGGTCC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCATG	1270
QY	453	AAATAGTGTTC	CTGAACTCAAGTCC	CGCAGCTCCTCAAGACAATGATTTT	512
DB	1271	AAATAGTGTTC	CTGAACTCAAGTCC	CGCAGCTCCTCAAGACAATGATTTT	1330
QY	513	TATCTAGAAAGCT	CAAGACTGTATTTAT	GAAGCTGCATCACTGTCTCGGAAATCACA	572
DB	1331	TATCTAGAAAGCT	CAAGACTGTATTTAT	GAAGCTGCATCACTGTCTCGGAAATCACA	1390
QY	573	GTGGGATAGCAC	CAATTTCTGGATCT	CAAGGGCTGCATCTCTGTGATCAAGACCACTC	632
DB	1391	GTGGGATAGCAC	CAATTTCTGGATCT	CAAGGGCTGCATCTCTGTGATCAAGACCACTC	1450
QY	633	CATGCTCTT	CAGCAATAAATCC	ACTCAACTCGAGAACTCAGAACGCTCGCAGC	692
DB	1451	CATGCTCTT	CAGCAATAAATCC	ACTCAACTCGAGAACTCAGAACGCTCGCAGC	1510
QY	693	CTGTATAGCC	CAGCAGTGGATCC	AGCAAGAGGAGACATTTGTAACCAATGACAG	752
DB	1511	CTGTATAGCC	CAGCAGTGGATCC	AGCAAGAGGAGACATTTGTAACCAATGACAG	1570
QY	753	AAGCTGCTT	TAACAGTGC	TAGATGCCCTTCTGTCCAGGACTTGTATCAAGAGAGG	812
DB	1571	AAGCTGCTT	TAACAGTGC	TAGATGCCCTTCTGTCCAGGACTTGTATCAAGAGAGG	1630
QY	813	ACTATGA	ACTTGTAGTAC	CAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA	872
DB	1631	ACTATGA	ACTTGTAGTAC	CAAGGCTCAAAAGTCAGACAATTTACTAGACA	1690
QY	873	CTACTG	CATCCAGGAGAGAAATTTG	CCAAAGTTATAGTACAAAATTTGAAAGATAACA	932
DB	1691	CTACTG	CATCCAGGAGAGAAATTTG	CCAAAGTTATAGTACAAAATTTGAAAGATAACA	1750
QY	933	ACAATAG	GGTCTTACGCTTAC	CCGGAATATCTGTGGTTCTAGATCAACATCTTTAA	992
DB	1751	ACAATAG	GGTCTTACGCTTAC	CCGGAATATCTGTGGTTCTAGATCAACATCTTTAA	1810
QY	993	ATTACTT	CAAAATAAAGCATG	TAAAGTGTGTTTCAAGAGAAATGTTTTCATAA	1052
DB	1811	ATTACTT	CAAAATAAAGCATG	TAAAGTGTGTTTCAAGAGAAATGTTTTCATAA	1870
QY	1053	AAGGATATTTATA	1065		
DB	1871	AAGGATATTTATA	1883		

RESULT 9  
US-09-865-364-1  
Sequence 1, Application US/09865364  
Patent No. 6613521  
GENERAL INFORMATION:  
APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-112001  
CURRENT APPLICATION NUMBER: US/09/865,364  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1931  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (214)...(1833)  
US-09-865-364-1

Query Match 40.9%; Score 682; DB 4; Length 1931;

Best Local Similarity 99.9%; Pred. No. 1.2e-309; Indels 0; Gaps 0;  
Matches 732; Conservative 0; Mismatches 1;

QY	333	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGCAAGAGAAATGGAATATATCTC	392
DB	1151	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGCAAGAGAAATGGAATATATCTC	1210
QY	393	TGAACATACCTGTA	ATAATCATGGTCC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCATG	452
DB	1211	TGAACATACCTGTA	ATAATCATGGTCC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCATG	1270
QY	453	AAATAGTGTTC	CTGAACTCAAGTCC	CGCAGCTCCTCAAGACAATGATTTT	512
DB	1271	AAATAGTGTTC	CTGAACTCAAGTCC	CGCAGCTCCTCAAGACAATGATTTT	1330
QY	513	TATCTAGAAAGCT	CAAGACTGTATTTAT	GAAGCTGCATCACTGTCTCGGAAATCACA	572
DB	1331	TATCTAGAAAGCT	CAAGACTGTATTTAT	GAAGCTGCATCACTGTCTCGGAAATCACA	1390
QY	573	GTGGGATAGCAC	CAATTTCTGGATCT	CAAGGGCTGCATCTCTGTGATCAAGACCACTC	632
DB	1391	GTGGGATAGCAC	CAATTTCTGGATCT	CAAGGGCTGCATCTCTGTGATCAAGACCACTC	1450
QY	633	CATGCTCTT	CAGCAATAAATCC	ACTCAACTCGAGAACTCAGAACGCTCGCAGC	692
DB	1451	CATGCTCTT	CAGCAATAAATCC	ACTCAACTCGAGAACTCAGAACGCTCGCAGC	1510
QY	693	CTGTATAGCC	CAGCAGTGGATCC	AGCAAGAGGAGACATTTGTAACCAATGACAG	752
DB	1511	CTGTATAGCC	CAGCAGTGGATCC	AGCAAGAGGAGACATTTGTAACCAATGACAG	1570
QY	753	AAGCTGCTT	TAACAGTGC	TAGATGCCCTTCTGTCCAGGACTTGTATCAAGAGAGG	812
DB	1571	AAGCTGCTT	TAACAGTGC	TAGATGCCCTTCTGTCCAGGACTTGTATCAAGAGAGG	1630
QY	813	ACTATGA	ACTTGTAGTAC	CAAGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA	872
DB	1631	ACTATGA	ACTTGTAGTAC	CAAGGCTCAAAAGTCAGACAATTTACTAGACA	1690
QY	873	CTACTG	CATCCAGGAGAGAAATTTG	CCAAAGTTATAGTACAAAATTTGAAAGATAACA	932
DB	1691	CTACTG	CATCCAGGAGAGAAATTTG	CCAAAGTTATAGTACAAAATTTGAAAGATAACA	1750
QY	933	ACAATAG	GGTCTTACGCTTAC	CCGGAATATCTGTGGTTCTAGATCAACATCTTTAA	992
DB	1751	ACAATAG	GGTCTTACGCTTAC	CCGGAATATCTGTGGTTCTAGATCAACATCTTTAA	1810
QY	993	ATTACTT	CAAAATAAAGCATG	TAAAGTGTGTTTCAAGAGAAATGTTTTCATAA	1052
DB	1811	ATTACTT	CAAAATAAAGCATG	TAAAGTGTGTTTCAAGAGAAATGTTTTCATAA	1870



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QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 10
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2

Query Match 40.9%; Score 682; DB 4; Length 1931;
Best Local Similarity 99.9%; Pred. No. 1.2e-309; Mismatches 0; Indels 0; Gaps 0;
Matches 732; Conservative 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAGAAATGGAATATATCTC 392
Db 1151 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAGAAATGGAATATATCTC 1210

QY 393 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 452
Db 1211 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 1270

QY 453 AAAATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCATCAAGCAATGATTTTTT 512
Db 1271 AAAATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCATCAAGCAATGATTTTTT 1330

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCACA 572
Db 1331 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCACA 1390

QY 573 GTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATTC 632
Db 1391 GTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATTC 1450

QY 633 CATGCTCTTCAGCAATTAATAATCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 692
Db 1451 CATGCTCTTCAGCAATTAATAATCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 1510

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 752
Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 1570

QY 753 AAGCCTGCTTAAACCAAGTCGTAGATGCCCTTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1571 AAGCCTGCTTAAACCAAGTCGTAGATGCCCTTTCTGTCCAGGGACTTGTATCATGAAGAGG 1630

QY 813 ACTATGAACCTTTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 872
Db 1631 ACTATGAACCTTTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 1690

QY 873 CTACTGACATCAAGGAGAGGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1691 CTACTGACATCAAGGAGAGGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1750
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QY 933 AACAAATGGTCTTCAGCCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATCTTTAA 992
Db 1751 AACAAATGGTCTTCAGCCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATCTTTAA 1810

QY 993 ATTTACTTTCAAAATAAAGCATGTAAAGTGACTGTTTTTCAAGAAGAAATGCTTTTCATAA 1052
Db 1811 ATTTACTTTCAAAATAAAGCATGTAAAGTGACTGTTTTTCAAGAAGAAATGCTTTTCATAA 1870

QY 1053 AAGGATATTATA 1065
Db 1871 AAGGATATTATA 1883

RESULT 11
US-09-099-041A-3
; Sequence 3, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286; Mismatches 1; Indels 0; Gaps 0;
Matches 682; Conservative 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAGAAATGGAATATATCTC 392
Db 938 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAGAAATGGAATATATCTC 997

QY 393 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 452
Db 998 TGAACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCCATG 1057

QY 453 AAAATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCATCAAGCAATGATTTTTT 512
Db 1058 AAAATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCATCAAGCAATGATTTTTT 1117

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCACA 572
Db 1118 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCACA 1177

QY 573 GTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATTC 632
Db 1178 GTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCATTC 1237

QY 633 CATGCTCTTCAGCAATTAATAATCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 692
Db 1238 CATGCTCTTCAGCAATTAATAATCACTCTCACTGCAGGAACTCAGAACCTCTGCAGC 1297

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 752
Db 1298 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 1357

QY 753 AAGCCTGCTTAAACCAAGTCGTAGATGCCCTTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1358 AAGCCTGCTTAAACCAAGTCGTAGATGCCCTTTCTGTCCAGGGACTTGTATCATGAAGAGG 1417

QY 813 ACTATGAACCTTTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 872
Db 1418 ACTATGAACCTTTAGTACCAAGCCCTCAAGACCTCAAAAGTCAGACAAATTTACTAGACA 1477
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QY 753 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGG 812
DB 1358 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGG 1417
QY 813 ACTATGAACCTCTTAGTACCAAGCTTACCAAGGACCTCAAAAGTCAGACAAATTTACTAGACA 872
DB 1418 ACTATGAACCTCTTAGTACCAAGCTTACCAAGGACCTCAAAAGTCAGACAAATTTACTAGACA 1477
QY 873 CTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
DB 1478 CTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1537
QY 933 AACAAATGGCTCTTACGCTTACCCGGAATATCTTGCTGTTCTAGATCACCATCTTTAA 992
DB 1538 AACAAATGGCTCTTACGCTTACCCGGAATATCTTGCTGTTCTAGATCACCATCTTTAA 1597
QY 993 ATTTACTTCAAAATAAAGCATG 1015
DB 1598 ATTTACTTCAAAATAAAGCATG 1620

RESULT 14
US-09-340-620A-3
; Sequence 3, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-340-620A-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATATCTC 392
DB 938 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATATCTC 997
QY 393 TGAACATACCTGTAAATCATGGTCCACAAAGAGAAATCATGTGGATCCTCTCAGCTCCATG 452
DB 998 TGAACATACCTGTAAATCATGGTCCACAAAGAGAAATCATGTGGATCCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTCGAAATTCAGGTCCTCCAGCTCCTCAAGACAATGATTTTTT 512
DB 1058 AAAATAGTGGTTCCTCGAAATTCAGGTCCTCCAGCTCCTCAAGACAATGATTTTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTCGAAATCACA 572
DB 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTCGAAATCACA 1177
QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAAGGCTCATTTCTGTGATCAAGACCATCTC 632
DB 1178 GTTGGATAGCACCATTTCTGGATCTCAAAAGGCTCATTTCTGTGATCAAGACCATCTC 1237
QY 633 CATGCTCTTACGAATAAATAATCCACTCTCAACTGACGAAACTCAGAAACGTCTGCAGC 692

RESULT 15
US-09-865-364-3
; Sequence 3, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-865-364-3

Query Match 37.9%; Score 632; DB 4; Length 1620;
Best Local Similarity 99.9%; Pred. No. 3e-286;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATATCTC 392
DB 938 AGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATATCTC 997
QY 393 TGAACATACCTGTAAATCATGGTCCACAAAGAGAAATCATGTGGATCCTCTCAGCTCCATG 452
DB 998 TGAACATACCTGTAAATCATGGTCCACAAAGAGAAATCATGTGGATCCTCTCAGCTCCATG 1057
QY 453 AAAATAGTGGTTCCTCGAAATTCAGGTCCTCCAGCTCCTCAAGACAATGATTTTTT 512
DB 1058 AAAATAGTGGTTCCTCGAAATTCAGGTCCTCCAGCTCCTCAAGACAATGATTTTTT 1117
QY 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTCGAAATCACA 572
DB 1118 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTCGAAATCACA 1177
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Qy	573	GTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC	632
Db	1178	GTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTC	1237
Qy	633	CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGAGC	692
Db	1238	CATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGAGC	1297
Qy	693	CTGGTATAGCCCGACGAGTGGATCCAGAGCAAGGGAAGACATTGTGAACCAATGACAG	752
Db	1298	CTGGTATAGCCCGACGAGTGGATCCAGAGCAAGGGAAGACATTGTGAACCAATGACAG	1357
Qy	753	AAGCCTGCTTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGCATGAAAGAGG	812
Db	1358	AAGCCTGCTTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGCATGAAAGAGG	1417
Qy	813	ACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACA	872
Db	1418	ACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACA	1477
Qy	873	CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACRAAAATTCGAAGATAACA	932
Db	1478	CTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACRAAAATTCGAAGATAACA	1537
Qy	933	AACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATCTTTAA	992
Db	1538	AACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATCTTTAA	1597
Qy	993	ATTACTTCAAAATAAAGCATG	1015
Db	1598	ATTACTTCAAAATAAAGCATG	1620

Search completed: April 1, 2004, 09:56:00  
Job time : 162 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 06:17:41 ; Search time 4639 Seconds  
(without alignments)  
10743.690 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 1669

Sequence: 1 acctagttatcacagata.....caacagcctgagtgtataaa 1669

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 20

Total number of hits satisfying chosen parameters: 465

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba:\*

2: em\_estba:\*

3: em\_estin:\*

4: em\_estin:\*

5: em\_estov:\*

6: em\_estov:\*

7: em\_estro:\*

8: em\_estro:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_nus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rtd:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	835	50.0	1201	13	BX401255
C 2	692	41.5	709	14	CA413941
C 3	677	40.6	738	9	AI824070
C 4	665	39.8	734	12	BQ008463

5	650	38.9	883	12	BG393551
6	636	38.1	1081	12	BM557041
C 7	613	36.7	667	13	BQ773811
C 8	609	36.2	656	12	BM973770
C 9	604	36.5	715	14	CB851847
C 10	599	35.9	721	13	BQ774940
C 11	599	35.9	744	14	CD365404
C 12	592	35.5	592	9	AI745575
C 13	591	35.4	624	14	CD368863
C 14	571	34.2	628	12	BQ000991
C 15	556	33.3	938	13	BQ670832
C 16	554	33.2	636	10	BE551615
C 17	554	33.2	660	12	BM840808
C 18	548	32.8	683	14	CB852764
C 19	538	32.2	852	12	BG757422
C 20	534	32.0	672	14	CA314123
C 21	532	31.9	647	10	AW960501
C 22	528	31.6	811	12	BG170405
C 23	520	31.2	615	9	AI801150
C 24	518	31.0	546	12	BQ013098
C 25	511	30.6	738	10	AW978568
C 26	510	30.6	641	10	AW150819
C 27	505	30.3	505	13	EX280487
C 28	500	30.0	1623	29	AY415527
C 29	486	29.1	834	12	BM014010
C 30	478	28.6	499	12	BQ011550
C 31	476	28.5	600	10	BF793767
C 32	475	28.5	496	12	BQ011702
C 33	470	28.2	610	13	BQ623654
C 34	465	27.9	606	9	AW085560
C 35	464	27.8	1623	29	AY415528
C 36	461	27.6	812	12	B1257472
C 37	461	27.6	870	10	BE877822
C 38	457	27.4	476	14	CF528565
C 39	455	27.3	526	9	AI769177
C 40	451	27.0	616	9	AI307810
C 41	449	26.9	455	9	AI343850
C 42	445	26.7	445	10	AW820715
C 43	445	26.7	448	9	AI499817
C 44	445	26.7	828	10	BE875947
C 45	444	26.6	518	10	AW593657

#### ALIGNMENTS

RESULT 1  
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LOCUS BX401255 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA clone CS0DK011Y11 3-PRIME, mRNA sequence.  
ACCESSION BX401255  
VERSION BX401255.1 GI:30610587  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4797.f For more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DK011AE09NP1&cluster=4797.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DK011AB09NP1.

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FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK011Y117"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 50.08; Score 835; DB 13; Length 1201;
Best Local Similarity 99.78; Pred. No. 0;
Matches 985; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 594 GATCTCAAGGGCTGCAATTCGTGATCAAGACCACTCCATGCTCTTCAGCAATATAA 653
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QY 654 ATCCACTCTCACTGCAAGAACTCAGAACGTCGTGCAAGCTGGTATAGCCCGACAGTGA 713
DB 992 ATCCACTCTCACTGCAAGAACTCAGAACGTCGTGCAAGCTGGTATAGCCCGACAGTGA 933

QY 714 TCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAGCTGCTTAAACAGTCGC 773
DB 932 TCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGAGCTGCTTAAACAGTCGC 873

QY 774 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTAGTACCA 833
DB 872 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTAGTACCA 813

QY 834 AGCTTCAAGGACTCAAAAGTCAGACAAATCTAGACACTCTGACATCAAGAGGAAG 893
DB 812 AGCTTCAAGGACTCAAAAGTCAGACAAATCTAGACACTCTGACATCAAGAGGAAG 753

QY 894 AATTGCAAGTATAGTACAAATTTGAAGATCAACAAATGGGCTTCAGCCCT 953
DB 752 AATTGCAAGTATAGTACAAATTTGAAGATCAACAAATGGGCTTCAGCCCT 693

QY 954 ACCCGGAATACCTTGCTGTCTAGATCACCATCTTTAAATTTACTTTCAAAATAAAGCA 1013
DB 692 ACCCGGAATACCTTGCTGTCTAGATCACCATCTTTAAATTTACTTTCAAAATAAAGCA 633

QY 1014 TGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATATAAGGATATTTATCTCTGTT 1073
DB 632 TGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATATAAGGATATTTATCTCTGTT 573

QY 1074 GCTTTGACTTTTTTATATAAATCCGTGAGTATTAAGCTTTATTGAAGGTTCTTTGG 1133
DB 572 GCTTTGACTTTTTTATATAAATCCGTGAGTATTAAGCTTTATTGAAGGTTCTTTGG 513

QY 1134 TAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTTTAAATTAATACAAGTAAAG 1193
DB 512 TAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTTTAAATTAATACAAGTAAAG 453

QY 1194 TTTGAATTTGCTACATAGTTCAATTTTATGCTCTTTTGTGTTAAACAGAACCACTTTA 1253
DB 452 TTTGAATTTGCTACATAGTTCAATTTTATGCTCTTTTGTGTTAAACAGAACCACTTTA 393

QY 1254 AAGGATAGTAATTTCTGTTTATACAGTGCCTTAAGGTATGATGTTTCTGATGGA 1313
DB 392 AAGGATAGTAATTTCTGTTTATACAGTGCCTTAAGGTATGATGTTTCTGATGGA 333

QY 1314 AGCCATTTTCAATTCATGTTCTTCATGGAATTTTGTACTTGTCTTAAGATCAATTTG 1373
DB 332 AGCCATTTTCAATTCATGTTCTTCATGGAATTTTGTACTTGTCTTAAGATCAATTTG 273

QY 1374 ATTTTATGAGTATATACCTTTTACCACACAGACAGTACAGAAATCCCTGCCCTAAAT 1433
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Db 272 ATTTTATGAGTATATACCTTTTACCACACAGACAGTACAGAAATCCCTGCCCTAAAT 213
QY 1434 CCAGGCTTAATTCGCTACAGAGGCTTATTAATTTAAACTCCATATAGGATTACAT 1493
DB 212 CCAGGCTTAATTCGCTACAGAGGCTTATTAATTTAAACTCCATATAGGATTACAT 153
QY 1494 TTTAAAGTTTATTTATGAAATCCCTTTAAAGATGATTTTCAAGGTAAACAAATACAA 1553
DB 152 TTTAAAGTTTATTTATGAAATCCCTTTAAAGATGATTTTCAAGGTAAACAAATACAA 93
QY 1554 TATAAGAAAAAATAAATATAATATAA 1581
DB 92 TATAAGAAAAAATAAATATAATATAA 65

RESULT 2
CA413941/c
LOCUS
DEFINITION
709 bp mRNA linear EST 07-NOV-2002
UI-H-EZO-bau-f-07-0-UI.s1 NCI CGAP Ch1 Homo sapiens cDNA clone
UI-H-EZO-bau-f-07-0-UI 3', mRNA sequence.
ACCESSION
CA413941
VERSION
CA413941.1 GI:24776592
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 709)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-64, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1. .709
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZO-bau-f-07-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/notes="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(AT)18 tail. The sequence tag for this library is
TCATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma.
TAG_LIB=UI-H-EZO
TAG_SEQ=ATCTAATATG"
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ORIGIN		COMMENT	
Query Match		Contact: Robert Strausberg, Ph.D.	
Best Local Similarity		Email: cgapbs-remail.nih.gov	
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.	
		Emmert-Buck, M.D., Ph.D.	
		cDNA Library Preparation: M. Bento Soares, Ph.D.	
		cDNA Library Arrayed by: Greg Lennon, Ph.D.	
		DNA Sequencing by: Washington University Genome Sequencing Center	
		Clone distribution: NCI-CGAP clone distribution information can be	
		found through the I.M.A.G.E. Consortium/LLNL at:	
		www-bio.llnl.gov/bbrp/image/image.html	
		Insert Length: 432 Std Error: 0.00	
		Seq primer: -40UP from Gibco	
		High quality sequence stop: 460.	
FEATURES		Location/Qualifiers	
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		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:2404860"	
		/tissue_type="2 pooled tumors (clear cell type)"	
		/lab_host="DH10B"	
		/clone_lib="NCI CGAP Kid12"	
		/note="Toregan: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."	
ORIGIN		Query Match	
		40.6%; Score 677; DB 9; Length 738;	
		Best Local Similarity 99.9%; Pred. No. 0;	
		Matches 727; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
		QY 942 GTCCTCAGCCTTACCGGAAATCTGTGGTTCTTAGATCACCATCTTTAAATTTACTTC 1001	
		DB 728 GTCCTCAGCCTTACCGGAAATCTGTGGTTCTTAGATCACCATCTTTAAATTTACTTC 669	
		QY 1002 AAAATAAAGCATGTAGTACTGTCTTCAAGAGAAATGTCTTCAATAAGGATATT 1061	
		DB 668 AAAATAAAGCATGTAGTACTGTCTTCAAGAGAAATGTCTTCAATAAGGATATT 609	
		QY 1062 TATATCTCTGTCTTGCACCTTTTATATAAAATCCGTGAGTATTAAAGCTTTATGCA 1121	
		DB 608 TATATCTCTGTCTTGCACCTTTTATATAAAATCCGTGAGTATTAAAGCTTTATGCA 549	
		QY 1122 AGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTTTAAATTAAT 1181	
		DB 548 AGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTTTAAATTAAT 489	
		QY 1182 ACAAGTAAAAAGTTGAATTTTGCTACATGTTCAATTTTTTATGTCCTCTTTTGTGTAACAG 1241	
		DB 488 ACAAGTAAAAAGTTGAATTTTGCTACATGTTCAATTTTTTATGTCCTCTTTTGTGTAACAG 429	
		QY 1242 AAACCACTTTTAAAGGATAGTAAATTTCTGTTTATTAACAGTGCCTTAAAGTATGATGT 1301	
		DB 428 AAACCACTTTTAAAGGATAGTAAATTTCTGTTTATTAACAGTGCCTTAAAGTATGATGT 369	
		QY 1302 ATTTCTGATGAAGCCATTTTCAATCTTCATGATTTATGTTGTTACTTGTCTTA 1361	
		DB 368 ATTTCTGATGAAGCCATTTTCAATCTTCATGATTTATGTTGTTACTTGTCTTA 309	
		QY 1362 AGATGCAATTTGATTTTATGAAGTATATACCTTTTACCACAGACAGTACAGATCC 1421	
		DB 308 AGATGCAATTTGATTTTATGAAGTATATACCTTTTACCACAGACAGTACAGATCC 249	
		QY 1422 CTGCCCTAAATCCAGGCTTAATTCCTCAAGAGGTTATTAATTTAAACTCCATTA 1481	
		DB 248 CTGCCCTAAATCCAGGCTTAATTCCTCAAGAGGTTATTAATTTAAACTCCATTA 189	

RESULT 3  
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 Locus  
 DEFINITION wj3507.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404860 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ; mRNA sequence.  
 ACCESSION AI824070  
 VERSION AI824070.1 GI:5444741  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 738)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)

QY 1482 TTAGGATTACATTTTAAAGTTTATTTATGAAATTCCTTTTAAATAATGATATTTCAAAGGT 1541  
Db 188 TTAGGATTACATTTTAAAGTTTATTTATGAAATTCCTTTTAAATAATGATATTTCAAAGGT 129  
QY 1542 AAAACAATACAAATATAAAGAAAAAATAAATAATATTAATTAATACCGGCTTCCTGTCCCCCATTT 1601  
Db 128 AAAACAATACAAATATAAAGAAAAAATAAATAATATTAATTAATACCGGCTTCCTGTCCCCCATTT 69  
QY 1602 TTAACCTCAGCCTTCCTACTGTCCACCAACCAAGCTTAATAATAAGTCAACGCTGTAT 1661  
Db 68 TTAACCTCAGCCTTCCTACTGTCCACCAACCAAGCTTAATAATAAGTCAACGCTGTAT 9  
QY 1662 GTGTAAAA 1669  
Db 8 GTGTAAAA 1

RESULT 4  
BO008463/c 734 bp mRNA linear EST 26-MAR-2002  
LOCUS UI-H-ED1-ayk-k-19-0-UI.sl NCI\_CGAP\_ED1 Homo sapiens cDNA clone  
DEFINITION IMAGE:5840010 3', mRNA sequence.  
ACCESSION BO008463  
VERSION BQ008463.1 GI:19733364  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 734)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1. 734  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IWAGE:5840010"  
/tissue\_type="Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP ED1"  
/notes="Organ: Left Pubic Bone; Vector: pTV73-Pac  
(Pharmacia) with a modified polylinker; Site 1: EcoR I;  
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library  
containing the following tissue(s): Chondrosarcoma cell  
line C85. The library was constructed according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pTV73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is GCTCAGGCT.  
TAG\_TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-ED1  
TAG\_SEQ=CGTCAGGCT"

ORIGIN

Query Match 39.8%; Score 665; DB 12; Length 734;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTCAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAA 521  
Db 683 GTTCTCTCAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAA 624  
QY 522 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCAAGTTGGATA 581  
Db 623 AGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCAAGTTGGATA 564  
QY 582 GCACCAATTTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGTCTTT 641  
Db 563 GCACCAATTTCTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCATGTCTTT 504  
QY 642 CAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTTGCGAGCCCTGTATAG 701  
Db 503 CAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTTGCGAGCCCTGTATAG 444  
QY 702 CCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAAAATGACAGAGCCTGCC 761  
Db 443 CCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAAAATGACAGAGCCTGCC 384  
QY 762 TTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGGACTATGAAC 821  
Db 383 TTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGGACTATGAAC 324  
QY 822 TTGTTAGTACCAAGCCTCAAGACCTCAAAAGTTCAGACAAATCTAGACACTACTGACA 881  
Db 323 TTGTTAGTACCAAGCCTCAAGACCTCAAAAGTTCAGACAAATCTACTAGACACTACTGACA 264  
QY 882 TCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAACAATGG 941  
Db 263 TCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAACAATGG 204  
QY 942 GTCTTCAGCCTTACCCGGAAATCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTC 1001  
Db 203 GTCTTCAGCCTTACCCGGAAATCTTGTGTTTCTAGATCACCATCTTTAAATTTACTTC 144  
QY 1002 AAATAAAGCATGTAAGTGCATGTTTTTCAGAAGAAATGTGTTTCATAAAGGATATT 1061  
Db 143 AAATAAAGCATGTAAGTGCATGTTTTTCAGAAGAAATGTGTTTCATAAAGGATATT 84  
QY 1062 TATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 1121  
Db 83 TATATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGTGAGTATTAAGCTTTATTGA 24  
QY 1122 AGGTT 1126  
Db 23 AGGTT 19

RESULT 5  
BG393551  
LOCUS BG393551  
DEFINITION 602411943F1 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:4540787 5',  
mRNA sequence.  
ACCESSION BG393551  
VERSION BG393551.1 GI:13286999  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 883)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: ATCC



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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10471 row: e column: 12
High quality sequence stop: 767.

FEATURES
    source
        1..883
            /organism="Homo sapiens"
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            /db_xref="taxon:9606"
            /clone="IMAGE:4540787"
            /tissue_type="embryonal carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 92"
            /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
            Average insert size 2.5 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."

ORIGIN
Query Match      38.9%; Score 650; DB 12; Length 883;
Best Local Similarity 100.0%; Pred. No. 8e-308;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 TGTAAATCATGCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAATAAGTGG 462
DB 1 TGTAAATCATGCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAATAAGTGG 60
QY 463 TTCTCTCTGAAACTTCAAGTCCCTGCAGCTCCTCTCAAGCAATGATTTTATCTAGAAA 522
DB 61 TTCTCTCTGAAACTTCAAGTCCCTGCAGCTCCTCTCAAGCAATGATTTTATCTAGAAA 120
QY 523 AGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTCGGAATCAAGTTGGGATAG 582
DB 121 AGCTCAAGACTGTATTTATGAAGCTGCATCACTCTCTCGGAATCAAGTTGGGATAG 180
QY 583 CACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACACCTCCATGCTCTTC 642
DB 181 CACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACACCTCCATGCTCTTC 240
QY 643 AGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCTGGTATAGC 702
DB 241 AGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCTGGTATAGC 300
QY 703 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 762
DB 301 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 360
QY 763 TAACCAAGTCTAGATGCGCTTCTGTCCAGGAGCTTGTATCATGAAGAGGACTATGAAC 822
DB 361 TAACCAAGTCTAGATGCGCTTCTGTCCAGGAGCTTGTATCATGAAGAGGACTATGAAC 420
QY 823 TGTAGTACCAAGCTTACAGAGACCTCAAAAGTTCAGACAAATCTAGACACTACTGCACAT 882
DB 421 TGTAGTACCAAGCTTACAGAGACCTCAAAAGTTCAGACAAATCTAGACACTACTGCACAT 480
QY 883 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAAATTTGAAAGATAACAAACAAATGGG 942
DB 481 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAAATTTGAAAGATAACAAACAAATGGG 540
QY 943 TCTTACGCTTACCGGAAATCTTGTGGTTCTAGATCACCATCTTTAAATTTACTTCA 1002
DB 541 TCTTACGCTTACCGGAAATCTTGTGGTTCTAGATCACCATCTTTAAATTTACTTCA 600
QY 1003 AATAAAGCATCTAAGTGCATCTTTTCAAGAGAAATGTGTTTCATAA 1052
DB 601 AATAAAGCATCTAAGTGCATCTTTTCAAGAGAAATGTGTTTCATAA 650

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RESULT 6
BM557041
LOCUS
DEFINITION
    BM557041
    AGENCOURT 6561869 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547645
    5' mRNA sequence.
ACCESSION
    BM557041
    BM557041.1 GI:18798748
VERSION
    EST.
KEYWORDS
    SOURCE
    Homo sapiens (human)
    ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 1081)
    NIH-MGC http://mgs.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: ATCC/DCTD/DTP
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM12255 row: e column: 22
    High quality sequence stop: 662.

FEATURES
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            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_72"
            /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2 kb. Library constructed by Life
            Technologies."

ORIGIN
Query Match      38.1%; Score 636; DB 12; Length 1081;
Best Local Similarity 100.0%; Pred. No. 5.8e-301;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1031 CAAGAAGAAATGCTTTTCATAAAGGATATTTATCTCTGTTGCTTTCACATTTTAT 1090
DB 1 CAAGAAGAAATGCTTTTCATAAAGGATATTTATCTCTGTTGCTTTCACATTTTAT 60
QY 1091 ATAAATCCGTCAGTATTAAAGCTTTTATTGAAGGTTCTTTGGGTAATAATTAGTCTCCCT 1150
DB 61 ATAAATCCGTCAGTATTAAAGCTTTTATTGAAGGTTCTTTGGGTAATAATTAGTCTCCCT 120
QY 1151 CCATGACACTGTCAGTATTTTTTTAAATTAATCAAGTAAAAAGTTTGAATTTTGTCACAT 1210
DB 121 CCATGACACTGTCAGTATTTTTTTAAATTAATCAAGTAAAAAGTTTGAATTTTGTCACAT 180
QY 1211 AGTTCAATTTTATGTCCTTTTGTGTAAAGGATAGTAATTTATTC 1270
DB 181 AGTTCAATTTTATGTCCTTTTGTGTAAAGGATAGTAATTTATTC 240
QY 1271 TTGTTTATAACAGTCCCTTAAAGTATGATTTCTGTATGAAGGATTTTTCACATTCA 1330
DB 241 TTGTTTATAACAGTCCCTTAAAGTATGATTTCTGTATGAAGGATTTTTCACATTCA 300
QY 1331 TGTCTCTCATGGAATTTTGTGTTAATGCTAAGATGCAATTTGATTTTATGAAGTATATA 1390
DB 301 TGTCTCTCATGGAATTTTGTGTTAATGCTAAGATGCAATTTGATTTTATGAAGTATATA 360
QY 1391 CCCTTTACCCACAGACAGTACAGATCCCTGCGCTTAAATCCAGAGCTTAATTTGCC 1450
DB 361 CCCTTTACCCACAGACAGTACAGATCCCTGCGCTTAAATCCAGAGCTTAATTTGCC 420

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QY 1451 TACAAAGGGTATTAAATTTAAACCTCCATTATTAGGATTACATTTTAAAGCTTTTATTAT 1510
Db 421 TACAAAGGGTATTAAATTTAAACCTCCATTATTAGGATTACATTTTAAAGCTTTTATTAT 480
QY 1511 GAATTCCTCTTAAATATGATTTTCAAGGTAAACCAATACATTAATAAGAAAAATAAA 1570
Db 481 GAATTCCTCTTAAATATGATTTTCAAGGTAAACCAATACATTAATAAGAAAAATAAA 540
QY 1571 ATATATTAATACCGGCTTCCTGCTCCCATTTTAACTCAGCTTCCCTACTGTCACCAA 1630
Db 541 ATATATTAATACCGGCTTCCTGCTCCCATTTTAACTCAGCTTCCCTACTGTCACCAA 600
QY 1631 CAACCAAGCTTAATAAGTCAACAGCCTGATGTGA 1666
Db 601 CAACCAAGCTTAATAAGTCAACAGCCTGATGTGA 636

RESULT 7
BQ773811/c
LOCUS
DEFINITION
UI-H-EZ1-bbz-f-10-0-UI.s1 NCI CGAP_Ch2 Homo sapiens cDNA clone
UI-H-EZ1-bbz-f-10-0-UI 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 667)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..667
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="NCI CGAP Ch2"
/clone_lib="NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"

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ORIGIN
Query Match 36.7%; Score 613; DB 13; Length 667;
Best Local Similarity 100.0%; Pred. No. 1.3e-289;
Matches 613; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 514 ATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTACTGCTCGTGAATACAG 573
Db 631 ATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTACTGCTCGTGAATACAG 572
QY 574 TTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCCTCC 633
Db 571 TTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCCTCC 512
QY 634 ATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACTGTCAGGCC 693
Db 511 ATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACTGTCAGGCC 452
QY 694 TGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGCAATTTGTGAACCAATGACAGA 753
Db 451 TGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGCAATTTGTGAACCAATGACAGA 392
QY 754 AGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGGA 813
Db 391 AGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAGAGGA 332
QY 814 CTATGAACCTTGTAGTACCAAGCCTTACAAGGACTCAAAAGTCAAGCAATTTACTAGAC 873
Db 331 CTATGAACCTTGTAGTACCAAGCCTTACAAGGACTCAAAAGTCAAGCAATTTACTAGAC 272
QY 874 TACTGATCCAAAGGAGAAAGATTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 933
Db 271 TACTGATCCAAAGGAGAAAGATTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 212
QY 934 AGAATGGGCTTTCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTAA 993
Db 211 AGAATGGGCTTTCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTAA 152
QY 994 TTTACTTTCAAAATPAAAGCATGTAAGTGAATGTTTTTCAAGAGAAGAAATGTTTCATAA 1053
Db 151 TTTACTTTCAAAATPAAAGCATGTAAGTGAATGTTTTTCAAGAGAAGAAATGTTTCATAA 92
QY 1054 AGGATATTATATCTCTGTTGCTTTGACCTTTTATATAAAATCCGTGAGTATTAAAGC 1113
Db 91 AGGATATTATATCTCTGTTGCTTTGACCTTTTATATAAAATCCGTGAGTATTAAAGC 32
QY 1114 TTTATTGAAGGTT 1126
Db 31 TTTATTGAAGGTT 19

RESULT 8
BQ773770/c
LOCUS
DEFINITION
UI-CF-EC1-ach-1-07-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-ach-1-07-0-UI 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 656)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
8889548
COMMENT
Contact: McCray, PB
University of Iowa

```

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source  
1. .656  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/dev\_stage="Adult and Fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTCTTAC.  
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383  
TAG LIB=UI-CF-EC1  
TAG\_SEQ=AAGTCTTAC"

ORIGIN  
Query Match 36.5%; Score 609; DB 12; Length 656;  
Best Local Similarity 100.0%; Pred. No. 1.2e-287;  
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAGGTCCTCCAGCTCTCTCAGACAAATGATTTTATCTAGAA 521  
DB 627 GTTCTCTGAACTTCAGGTCCTCCAGCTCTCTCAGACAAATGATTTTATCTAGAA 568  
QY 522 AAGCTCAGACTGTTATTTATGAAGTGCATCTGCTGATCACAAGCACTCCATCTCTT 581  
DB 567 AAGCTCAGACTGTTATTTATGAAGTGCATCTGCTGATCACAAGCACTCCATCTCTT 508  
QY 582 GCACCATTTCTGGATCTCAAGGGTGGCATTTCTGATCACAAGCACTCCATCTCTT 641  
DB 507 GCACCATTTCTGGATCTCAAGGGTGGCATTTCTGATCACAAGCACTCCATCTCTT 448  
QY 642 CAGCAATAATAATCACTCTCACTGCAAGGAACTCAGAACGCTGCGAGCTGTATAG 701  
DB 447 CAGCAATAATAATCACTCTCACTGCAAGGAACTCAGAACGCTGCGAGCTGTATAG 388  
QY 702 CCCAGCTGGATCAGAGCAAAAGGGAGACATTTGTGAACCAATGACAGAGCTGCC 761  
DB 387 CCCAGCTGGATCAGAGCAAAAGGGAGACATTTGTGAACCAATGACAGAGCTGCC 328  
QY 762 TTAACCACTGCTAGATGCTCTTCTGTCAGGGACTTGTATCATGAAGAGGACTATGAAC 821  
DB 327 TTAACCACTGCTAGATGCTCTTCTGTCAGGGACTTGTATCATGAAGAGGACTATGAAC 268  
QY 822 TTGTTAGTACCAGGCTACAGGACCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACTACTGACA 881

DB 267 TTGTTAGTACCAGGCTACAAAGGACCTCAAAAGTCAGACAAATTACTAGACACTACTGACA 208  
QY 882 TCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAACAATGG 941  
DB 207 TCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAACAATGG 148  
QY 942 GTCTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCACCACCTCTTTAAATTTACTTC 1001  
DB 147 GTCTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCACCACCTCTTTAAATTTACTTC 88  
QY 1002 AAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTTTCATAAAGGATATT 1061  
DB 87 AAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTTTCATAAAGGATATT 28  
QY 1062 TATATCTCT 1070  
DB 27 TATATCTCT 19

RESULT 9  
CB851847/c  
LOCUS  
DEFINITION  
UI-CF-FNO-aem-o-20-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
ACCESSION  
CB851847  
VERSION  
CB851847.1 GI:30046667  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 715)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
AUTHORS  
Normalization and subtraction: two approaches to facilitate gene  
TITLE  
discovery  
JOURNAL  
Genome Res. 6 (9), 791-806 (1996)  
MEDLINE  
97044477  
PUBMED  
8889548  
COMMENT  
Contact: McCray, PB  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-24, >AT-rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=yes.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-FNO-aem-o-20-0-UI"  
/tissue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-FNO"  
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DUI1). The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:

bento-soares@uiowa.edu  
TAG\_SEQ=None found"

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ORIGIN
Query Match      36.2%; Score 604; DB 14; Length 715;
Best Local Similarity 100.0%; Pred. No. 3.3e-285;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 521
DB 619 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 560

QY 522 AAGCTCAAGCTGTATTTATGAAGCTGCATCACTCTCTGGAATACACAGTTGGGATA 581
DB 559 AAGCTCAAGCTGTATTTATGAAGCTGCATCACTCTCTGGAATACACAGTTGGGATA 500

QY 582 GCACCATTTCTGATCTCAAGGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTT 641
DB 499 GCACCATTTCTGATCTCAAGGGCTGATTTCTGTGATCAAGACCACTCCATGCTCTT 440

QY 642 CAGCAATAATAAATCCACTCTCAACTGCAGAACTCAGAACTGCTGAGCTGGTATAG 701
DB 439 CAGCAATAATAAATCCACTCTCAACTGCAGAACTCAGAACTGCTGAGCTGGTATAG 380

QY 702 CCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 761
DB 379 CCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 320

QY 762 TTAACCAAGCTCGTAGATGCTCTCTGTCAGGAGCTTGATCATGAAGAGGACTATGAAC 821
DB 319 TTAACCAAGCTCGTAGATGCTCTCTGTCAGGAGCTTGATCATGAAGAGGACTATGAAC 260

QY 822 TTGTTAGTACCAAGCTTACAGGAGCTCAAAAGTCAGACAAATTTACTAGACACTACTGACA 881
DB 259 TTGTTAGTACCAAGCTTACAGGAGCTCAAAAGTCAGACAAATTTACTAGACACTACTGACA 200

QY 882 TCCAGAGAGAAGATTTGGCCAAAGTTATAGTACAAAATTTGAAGATAACAAATGG 941
DB 199 TCCAGAGAGAAGATTTGGCCAAAGTTATAGTACAAAATTTGAAGATAACAAATGG 140

QY 942 GTCTTCAGCTTACCCGGAAATCTGTGTTCTAGATCACCATCTTTAAATTTACTTC 1001
DB 139 GTCTTCAGCTTACCCGGAAATCTGTGTTCTAGATCACCATCTTTAAATTTACTTC 80

QY 1002 AAAATAAAGCATGTAGTACACTGTTTTCAGAGAAATGTTTTCATAAAGAGTATT 1061
DB 79 AAAATAAAGCATGTAGTACACTGTTTTCAGAGAAATGTTTTCATAAAGAGTATT 20

QY 1062 TATA 1065
DB 19 TATA 16
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```
RESULT 10
BO774940/c
LOCUS
DEFINITION
BO774940
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 721)
NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: James Martin
```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-22, >AT rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

#### FEATURES

Location/Qualifiers  
1..721  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FHO-bcd-1-20-0-UI"  
/tissue\_type="Human Chondrosarcoma Cell Line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FHO"  
/note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP\_FHO is a cDNA library containing the following  
tissue(s): Human Grade 1 Chondrosarcoma Cell Line The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into p773-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is AGAATCCGGC. The cell line was provided by Dr  
James Martin from University of Iowa  
TAG\_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG\_LIB=UI-H-FHO  
TAG\_SEQ=AGAATCCGGC"

#### ORIGIN

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Query Match      35.9%; Score 599; DB 13; Length 721;
Best Local Similarity 99.8%; Pred. No. 9.4e-283;
Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 462 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 521
DB 665 GTTCTCTGAACTTCAAGGTCCTCGCAGCTCTCAAGCAATGATTTTATCTAGAA 606

QY 522 AAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTGGAATACACAGTTGGGATA 581
DB 605 AAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTGGAATACACAGTTGGGATA 546

QY 582 GCACCATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCAAGACCACTCCATGCTCTT 641
DB 545 GCACCATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCAAGACCACTCCATGCTCTT 486

QY 642 CAGCAATAATAAATCCACTCTCACTGAGGAACTCAGAGCTCTGAGCTGCTATAG 701
DB 485 CAGCAATAATAAATCCACTCTCACTGAGGAACTCAGAGCTCTGAGCTGCTATAG 426

QY 702 CCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 761
DB 425 CCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCCTGCC 366

QY 762 TTAACCAAGCTCGTAGATGCTCTCTGTCAGGAGCTTGATCATGAAGAGGACTATGAAC 821
DB 365 TTAACCAAGCTCGTAGATGCTCTCTGTCAGGAGCTTGATCATGAAGAGGACTATGAAC 306

QY 822 TTGTTAGTACCAAGCTTACAGGAGCTCAAAAGTCAGACAAATTTACTAGACACTACTGACA 881
DB 305 TTGTTAGTACCAAGCTTACAGGAGCTCAAAAGTCAGACAAATTTACTAGACACTACTGACA 246

QY 882 TCCAGAGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAATGG 941
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Db      245  TCAAAGGAGAAGAAATTTGCCAAGTATATAGTACAAAATTTGAAGATACAAACCAATGG 186
QY      942  GTCTTCAGCCTTACCCGGAATACTTGTTCTTCTAGATCACCATCTTTAAATTTACTTTC 1001
Db      185  GTCTTCAGCCTTACCCGGAATACTTGTTCTTCTAGATCACCATCTTTAAATTTACTTTC 126
QY      1002 AAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAAAGGATATT 1061
Db      125  AAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAAAGGATATT 66
QY      1062 TATATCTCTGCTTGTGCTTTTATATATAAATCCGTGAGTATATA 1111
Db      65  TATATCTCTGCTTGTGCTTTTATATATAAATCCGTGAGTATATA 16

RESULT 11
LOCUS   CD365404/c
DEFINITION UI-H-FT2-bj1-h-03-0-UI.81 NCI CGAP FT2 Homo sapiens cDNA clone
ACCESSION CD365404
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1. (bases 1 to 744)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Dr. Gary W. Hunninghake, U of I
          cDNA library preparation: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Distribution information can be found at
          http://genome.uiowa.edu/distribution/cgap.html
          Seq primer: M13 FORWARD
          POLYA=yes.

FEATURES             Location/Qualifiers
     source            1..744
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="UI-H-FT2-bj1-h-03-0-UI"
     tissue_type="Aveolar Macrophage"
     dev_stage="Adult"
     lab_host="DH10B (Life Technologies)"
     clone_lib="NCI CGAP FT2"
     note="Organ: lung; Vector: p7713-Pac (Pharmacia) with a
modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Ronaldo, Lennon and Soares' Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Aveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATCGCG"

ORIGIN
Query Match      35.9%; Score 599; DB 14; Length 744;
Best Local Similarity 99.8%; Pred. No. 9.3e-283;
Matches 649; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      387  TATCTCTGAACATACCTGTAATATCATGTGTCACAGAGCAATCATGTGGATCCTCTCAGC 446
Db      664  TATCTCTGAACATACCTGTAATATCATGTGTCACAGAGCAATCATGTGGATCCTCTCAGC 605
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QY      447  TCATGAAAAATAGTGGTTCTCTCTGAAACTTTCAAGTCCCTGCCAGCTCCTCAAGCAATG 506
Db      604  TCCATGAAAAATAGTGGTTCTCTCTGAAACTTTCAAGTCCCTGCCAGCTCCTCAAGCAATG 545
QY      507  ATTTTTCATCTAGAAAAAGCTCAAGACTCTTATTTTATGAAGTGCATCACTGCTCTGGAA 566
Db      544  ATTTTTCATCTAGAAAAAGCTCAAGACTCTTATTTTATGAAGTGCATCACTGCTCTGGAA 485
QY      567  ATCAGAGTTGGGATAGCACCATTCTTGGATCTCAAAAGGCTGCATTTCTGTGATCAACA 626
Db      484  ATCAGAGTTGGGATAGCACCATTCTTGGATCTCAAAAGGCTGCATTTCTGTGATCAACA 425
QY      627  CCATCTCATGCTCTTTCAGCAATAATAATCAACTCTCAACTCTCAACTCTCAAGTGCAG 686
Db      424  CCATCTCATGCTCTTTCAGCAATAATAATCAACTCTCAACTCTCAAGTGCAGTGCAGTGC 365
QY      687  TGCAGCCTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAA 746
Db      364  TGCAGCCTGGTATAGCCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAA 305
QY      747  TGACAGAAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGGACTTTGATCATGA 806
Db      304  TGACAGAAAGCCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGGACTTTGATCATGA 245
QY      807  AAGAGGACTATGAATCTTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTTCAGACAATTAC 866
Db      244  AAGAGGACTATGAATCTTGTAGTACCAAGCCTTCAAGGACCTCAAAAGTTCAGACAATTAC 185
QY      867  TAGACACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAG 926
Db      184  TAGACACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAG 125
QY      927  ATAACAAAATAATGGTCTTTCAGCCTTACCCGGAATTAAGTGTGTTCTAGATCACCAT 986
Db      124  ATAACAAAATAATGGTCTTTCAGCCTTACCCGGAATTAAGTGTGTTCTAGATCACCAT 65
QY      987  CTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGAAGTGTGTTTCAAGAA 1036
Db      64  CTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGAAGTGTGTTTCAAGAA 15

RESULT 12
LOCUS   AI745575/c
DEFINITION AI745575.1 Homo sapiens cDNA clone IMAGE:2317103.3, similar to TR_043353 O43353 SERINE/THREONINE KINASE RICK. ;, mRNA sequence.
ACCESSION AI745575
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Insert Length: 673 Std Error: 0.00
          Seq primer: -40UP from Gibco
          High quality sequence stop: 459.
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FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2317103"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 35.5%; Score 592; DB 9; Length 592;  
Best Local Similarity 100.0%; Pred. No. 2.7e-279; Mismatches 0; Indels 0; Gaps 0;  
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 473 ACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGAC 532  
DB 592 ACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGAC 533  
QY 533 TGTATTATTAGAGTCGCATCATCTGCTCGGAATCACAGTGGGATAGACCATTTCT 592  
DB 532 TGTATTATTAGAGTCGCATCATCTGCTCGGAATCACAGTGGGATAGACCATTTCT 473  
QY 593 GGATCTCAAGGGCTGCACTTCTGTGATCAAGACCACTCATCTCTTCAGCAATAATA 652  
DB 472 GGATCTCAAGGGCTGCACTTCTGTGATCAAGACCACTCATCTCTTCAGCAATAATA 413  
QY 653 AATCCACTCTCACTGAGGAACTCAGAACTCAGAACTGCTGAGCTGGTATAGCCAGTGG 712  
DB 412 AATCCACTCTCACTGAGGAACTCAGAACTCAGAACTGCTGAGCTGGTATAGCCAGTGG 353  
QY 713 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGACCTGCTTACCAGTCG 772  
DB 352 ATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAGACCTGCTTACCAGTCG 293  
QY 773 CTAGATGCCCTTCTGTGCCAGGACTTGATCATGAAGAGCACTATGAACCTTTGTAGTACC 832  
DB 292 CTAGATGCCCTTCTGTGCCAGGACTTGATCATGAAGAGCACTATGAACCTTTGTAGTACC 233  
QY 833 AAGCTACAGGACCTCAAAAGTCAGACAATTTACTAGACACTACTGACATCCAGGAGAA 892  
DB 232 AAGCTACAGGACCTCAAAAGTCAGACAATTTACTAGACACTACTGACATCCAGGAGAA 173  
QY 893 GAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCT 952  
DB 172 GAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCT 113  
QY 953 TACCCGAAATACCTGTGGTTTCTAGATCAACCTCTTTAAATTTACTTCAAAATAAAGC 1012  
DB 112 TACCCGAAATACCTGTGGTTTCTAGATCAACCTCTTTAAATTTACTTCAAAATAAAGC 53  
QY 1013 ATGTAAGTGAAGTCTTTTCAAGAGAAATGTTTTCATAAAGGATTTAT 1064  
DB 52 ATGTAAGTGAAGTCTTTTCAAGAGAAATGTTTTCATAAAGGATTTAT 1

## RESULT 13

CD368863/c  
LOCUS 624 bp mRNA linear EST 29-MAY-2003  
DEFINITION UI-H-Ftl1-bjx-o-04-0-UI.s1 NCI\_CGAP\_Ftl1 Homo sapiens cDNA clone  
UI-H-Ftl1-bjx-o-04-0-UI 3', mRNA sequence.  
ACCESSION CD368863  
VERSION CD368863.1 GI:31152953

KEYWORDS  
SOURCE  
ORGANISM

EST.  
Homo sapiens (human)  
Homo sapiens

## REFERENCE

1 (bases 1 to 624)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Tumor Gene Index

## COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..624

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-H-Ftl1-bjx-o-04-0-UI"

/tissue\_type="Aveolar Macrophage"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP\_Ftl1"

/note="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP\_Ftl1 is a normalized cDNA library constructed from

a pool of 81 RNA samples from Alveolar Macrophages

challenged with different treatments. The library was

normalized according to Bonaldo, Lennon and Soares, Genome

Research, 6:791-806, 1996. First strand cDNA synthesis was

primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor,

digested with Not I, and cloned directionally into

p7T3-Pac vector. The oligonucleotide used to prime the

synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

GGCCATGCGG. The tissue was provided by Dr. Gary W.

Hunninghake of the University of Iowa.

TAG\_TISSUE=Human Lung Aveolar Macrophage

TAG\_LIB=UI-H-Ftl1

TAG\_SEQ=GGCCATGCGG"

## ORIGIN

Query Match 35.4%; Score 591; DB 14; Length 624;  
Best Local Similarity 100.0%; Pred. No. 8.2e-279; Mismatches 0; Indels 0; Gaps 0;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 603 GGGCTGCACTTCTGTGATCAACAAGACCTCCATGCTCTTCAGCAATAATAATCCACTCT 662  
DB 624 GGGCTGCACTTCTGTGATCAACAAGACCTCCATGCTCTTCAGCAATAATAATCCACTCT 565  
QY 663 CAACTGCGAGAACTCAGAACTCTGCGAGCTGGTATAGCCAGAGTGGATCCAGAGCA 722  
DB 564 CAACTGCGAGAACTCAGAACTCTGCGAGCTGGTATAGCCAGAGTGGATCCAGAGCA 505  
QY 723 AAAGGGAAGACATTGTGAACCAATGACAGAAGCTGCTTAAACAGTCGCTAGATGCC 782  
DB 504 AAAGGGAAGACATTGTGAACCAATGACAGAAGCTGCTTAAACAGTCGCTAGATGCC 445  
QY 783 TTCTGTCCAGGACCTTGATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCCTACAA 842  
DB 444 TTCTGTCCAGGACCTTGATCATGAAGAGGACTATGAACCTTGTAGTACCAAGCCTACAA 385  
QY 843 GGACCTCAAAAGCTCAGACAATTACTAGACACTTACTGACATCCCAAGGAGAAGATTGGCA 902

Db 384 GGACCTCAAAAGTCAGACAAATTACTAGACACTACTGACATCCAGAGAGAAATTTGCCA 325  
 QY 903 AAGTTATAGTACAAAATTTAAAGATAACAACAAATGGGTCTTCCAGCCTTACCCGGAAA 962  
 Db 324 AAGTTATAGTACAAAATTTAAAGATAACAACAAATGGGTCTTCCAGCCTTACCCGGAAA 265  
 QY 963 TACTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATTAAGATGTAAGTGA 1022  
 Db 264 TACTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATTAAGATGTAAGTGA 205  
 QY 1023 CTGTTTTTCAAGAGAAATGTGTTTCATAAAGGATATTTATATCTCTGTTCTTGACT 1082  
 Db 204 CTGTTTTTCAAGAGAAATGTGTTTCATAAAGGATATTTATATCTCTGTTCTTGACT 145  
 QY 1083 TTTTATATAAAATCCCGTGTGTTTAAAGCTTTTAAAGGTTCTTTGGGTAATATATTA 1142  
 Db 144 TTTTATATAAAATCCCGTGTGTTTAAAGCTTTTAAAGGTTCTTTGGGTAATATATTA 85  
 QY 1143 GTCTCCCTCCATGACACTGACGATATTTTAAATTAATTAAGTAAGTAAGTAAG 1193  
 Db 84 GTCTCCCTCCATGACACTGACGATATTTTAAATTAATTAAGTAAGTAAGTAAG 34

RESULT 14  
 BQ000991/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 628)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 The following repetitive elements were found in this cDNA  
 sequence: 1-60, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5823297"  
 /tissue\_type="Metastatic Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP DH1"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 NCI CGAP DH1 is a normalized cDNA library containing the  
 following tissue(s): VS-8 Cell line from Metastatic  
 Chondrosarcoma in Lung. The library was constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT7T3-Pac  
 vector. The oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is AGATCATTCG.  
 TAG\_TISSUE=lung  
 TAG\_LIB=UI-H-DH1  
 TAG\_SEQ=AGATCATTCG

ORIGIN

Query Match 34.2%; Score 571; DB 12; Length 628;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-269;  
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 CTCCTTACGCAATATAAATCCACTCTCAACTCCAGAGAAATCTCAGAACGCTCTGACGCTGG 696  
 Db 588 CTCCTTACGCAATATAAATCCACTCTCAACTCCAGAGAAATCTCAGAACGCTCTGACGCTGG 529  
 QY 697 TATAGCCAGAGAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAAGC 756  
 Db 528 TATAGCCAGAGAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAAGC 469  
 QY 757 CTGCTTTAACCAAGTCTGATGCTCTCTGCTCCAGGACCTTGTATGATGATGATGATGATGAT 816  
 Db 468 CTGCTTTAACCAAGTCTGATGCTCTCTGCTCCAGGACCTTGTATGATGATGATGATGATGAT 409  
 QY 817 TGAATCTGTTAGTACCAAGCCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGACACTAC 876  
 Db 408 TGAATCTGTTAGTACCAAGCCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGACACTAC 349  
 QY 877 TGACATCCAGAGAGAAATTTGCCAAAGTATATAGTACAAATTTGAAGATTAACAACA 936  
 Db 348 TGACATCCAGAGAGAAATTTGCCAAAGTATATAGTACAAATTTGAAGATTAACAACA 289  
 QY 937 AATGGGTCTTACGCTTACCCGGAAATATCTGTGTTCTAGATCACCATCTTTAAATTT 996  
 Db 288 AATGGGTCTTACGCTTACCCGGAAATATCTGTGTTCTAGATCACCATCTTTAAATTT 229  
 QY 997 ACTTCAAAATAAAGCATGTAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAATAAAGG 1056  
 Db 228 ACTTCAAAATAAAGCATGTAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAATAAAGG 169  
 QY 1057 ATATTATATCTCTGTTGTTGTTGTTTATATAAATCCGTGAGTATTAAAGCTTT 1116  
 Db 168 ATATTATATCTCTGTTGTTGTTGTTTATATAAATCCGTGAGTATTAAAGCTTT 109  
 QY 1117 ATTGAAGTCTTCTTGGTAAATATTTAGTCTCCCTCCATGACACTGAGTATTATTTTAA 1176  
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 Db 48 TTAATACAGTAAAGTTTGAATTTTGTCTA 18

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 DEFINITION  
 ACCESSION  
 VERSION  
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 SOURCE  
 ORGANISM  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 938)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCW2410 row: k column: 04  
High quality sequence stop: 659.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6257019"  
/tissue\_type="epidermoid carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_102"  
/notes="Organ: salivary gland; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed  
by Ling Hong in the laboratory of Gerald M. Rubin  
(University of California, Berkeley) using ZAP-cDNA  
synthesis kit (Stratagene) and Superscript II RT (Life  
Technologies). Note: this is a NIH\_MGC Library."

FEATURES  
SOURCE

## ORIGIN

Query Match 33.3%; Score 556; DB 13; Length 938;  
Best Local Similarity 100.0%; Pred. No. 1.2e-261; Mismatches 0; Indels 0; Gaps 0;  
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QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTGGAAATCACA 572  
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QY 573 GTTGGGATAGACCAATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCAAGACCCTC 632  
DB 377 GTTGGGATAGACCAATTTCTGGATCTCAAGGGCTGCAATTTCTGTGATCAAGACCCTC 436  
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QY 693 CTGSTATAGCCAGCAGTGGATCCAGAGCAAAAGGGGAAGACATTGTGAACCAATGACAG 752  
DB 497 CTGSTATAGCCAGCAGTGGATCCAGAGCAAAAGGGGAAGACATTGTGAACCAATGACAG 556  
QY 753 AAGCCTGCCTTAACCACTCGTAGATGCCCTTCTGTCCAGGACTTGCATGTAAGAGG 812  
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DB 677 CTACTGACATCCAAAGG 692

Search completed: April 1, 2004, 09:53:35  
Job time : 4665 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:28:33 ; Search time 24 Seconds  
(without alignments)  
7180.312 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0  
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Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 20

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	227	42.7	478	4	US-09-069-023-4
3	227	42.7	530	4	US-09-069-023-3
4	227	42.7	531	4	US-09-069-023-1
5	227	42.7	540	4	US-09-069-023-27
6	227	42.7	540	4	US-09-345-473E-28
7	167	31.5	167	4	US-09-069-023-6
8	128	24.1	540	3	US-09-019-942-1
9	128	24.1	540	4	US-09-099-041A-2
10	128	24.1	540	4	US-09-245-281-2
11	128	24.1	540	4	US-09-470-271-1
12	128	24.1	540	4	US-09-207-359B-2

ALIGNMENTS

RESULT 1  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

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Best Local Similarity: 100.00%  
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Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-5 (1-284)

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DB	98	AsnSerGlySerProGluThrSerArg	SerLeuProAlaProGlnAspAsnAsp	PheLeu	117		
QY	515	TCTAGAAAAGCTCAAGACTGTAT	TTATGAAGCTGCATCAGTCTCTGGA	ATCACAGT	574		
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QY	575	TGGGATAGCACCATTTCTGGATCT	CAAGGGCTGCATTCCTGTGATCACA	AGACCACTCA	634		
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QY 995 TTACTTCAAAATAAAAGCATG 1015  
Db 278 LeuLeuGlnAsnLysSerMet 284

## RESULT 2

US-09-069-023-4  
; Sequence 4, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-4

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DB: 4 Gaps: 0

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QY 455 AATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 514  
Db 292 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 311  
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Db 472 LeuLeuGlnAsnLysSerMet 478

## RESULT 3

US-09-069-023-3  
; Sequence 3, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-3

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Pred. No.: 5,26e-232 Length: 530  
Score: 227.00 Matches: 227  
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Query Match: 42.75% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-3 (1-530)

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QY 395 AACATACCTGTAATCATGTGCACAGAGCAATCATGTGATCTCTCAGCTCCATGAA 454  
Db 324 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 343  
QY 455 AATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 514  
Db 344 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 363  
QY 515 TCTAGAAAAGCTCAAGACTGTATTATTATGAGCTGCATCTGCTGGAATACACT 574

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Db 364 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 383
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Db 384 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 403
Qy 635 TGCTCTTACGCAATATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCCT 694
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Qy 695 GGTATAGCCACAGTCAGTCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACAGAA 754
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Db 464 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 483
Qy 875 ACTGACATCCAAAGGAGAAGATTGCAAAAGTTATAGTACAAAAATGAAAGATAACAAA 934
Db 484 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 503
Qy 935 CAAATGGGTCTTACGCTTACCCGGAATACCTGTGTTTCTAGATCACCATCTTTAAAT 994
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Qy 995 TTACTTCAAAATAAAGCATG 1015
Db 524 LeuLeuGlnAsnLysSerMet 530

RESULT 4
US-09-069-023-1
; Sequence 1, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-1

Alignment Scores:
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Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 4 Gaps: 0

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Qy 395 ACATACCTGTAATCATGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454
Db 325 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 344
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Qy 455 AATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCAGCTCCTCAAGACAAATGATTTT 514
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Qy 515 TCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCACACT 574
Db 365 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 384
Qy 575 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCACAAAGACCACTCCA 634
Db 385 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 404
Qy 635 TGCTCTTACGCAATATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCCT 694
Db 405 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 424
Qy 695 GGTATAGCCACAGTCAGTCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACAGAA 754
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Qy 755 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 814
Db 445 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 464
Qy 815 TATGAACCTTGTAGTACCAAGCTCAAGGACTCAAAAGTCAAGCAATTAAGTACACT 874
Db 465 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 484
Qy 875 ACTGACATCCAAAGGAGAAGATTGCAAAAGTTATAGTACAAAAATGAAAGATAACAAA 934
Db 485 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 504
Qy 935 CAAATGGGTCTTACGCTTACCCGGAATACCTGTGTTTCTAGATCACCATCTTTAAAT 994
Db 505 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 524
Qy 995 TTACTTCAAAATAAAGCATG 1015
Db 525 LeuLeuGlnAsnLysSerMet 531

RESULT 5
US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-27

Alignment Scores:
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Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.75% Indels: 0
DB: 4 Gaps: 0

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 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
 455 AATAGTGGTCTCTCCTGAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 514  
 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
 515 TCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCCTCTCGGAAATCAACAGT 574  
 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
 575 TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGTGATCACAAGACCATCCA 634  
 394 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 413  
 635 TGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACTCTGCAGCCT 694  
 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 695 GGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAGAA 754  
 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
 755 GCCTGCTTAAACAGTCCGTAGTGCCTCTCTGTCAGGAGCTTGATCATGAAGAGGAC 814  
 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 815 TATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGACAATTAAGACACT 874  
 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 875 ACTGACATCCAGAGAAATTTGCCAAAGTTATAGTACAAAAATGGAAGATAACAAA 934  
 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
 935 CAAATGGGTCTTACGCTTACCCGGAATCTGTGGTCTTGTAGTCAACCATCTTTAAAT 994  
 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
 995 TTACTTCAAAATAAAGCATG 1015  
 534 LeuLeuGlnAsnLysSerMet 540

RESULT 6  
 US-09-345-473E-28  
 ; Sequence 28, Application US/09345473E  
 ; Patent No. 6558903  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hodge, Martin  
 ; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
 ; FILE REFERENCE: 3580/163781  
 ; CURRENT APPLICATION NUMBER: US/09/345,473E  
 ; CURRENT FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 62  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-345-473E-28

Alignment Scores:  
 Pred. No.: 5,26e-232 Length: 540  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-345-473E-28 (1-540)  
 QY 335 TTACAGAGTGTTCAGTGGCCATTCACTTATGTGACAGAGAAATGGAATTTATCTCTG 394  
 Db 314 LeuGlnSerValSerSerAlaileHisLeuCysAspLysLysMetGluLeuSerLeu 333  
 QY 395 AACATACCTGTAATCATGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 454  
 Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
 QY 455 AATAGTGGTCTCTCCTGAACTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTAA 514  
 Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
 QY 515 TCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCCTCTCGGAAATCAACAGT 574  
 Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
 QY 575 TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGTGATCACAAGACCATCCA 634  
 Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 413  
 QY 635 TGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACTCTGCAGCCT 694  
 Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 QY 695 GGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGACAGAA 754  
 Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
 QY 755 GCCTGCTTAAACAGTCCGTAGTGCCTCTCTGTCAGGAGCTTGATCATGAAGAGGAC 814  
 Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 QY 815 TATGAACCTTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGACAATTAAGACACT 874  
 Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 QY 875 ACTGACATCCAGAGAAATTTGCCAAAGTTATAGTACAAAAATGGAAGATAACAAA 934  
 Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
 QY 935 CAAATGGGTCTTACGCTTACCCGGAATCTGTGGTCTTGTAGTCAACCATCTTTAAAT 994  
 Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
 QY 995 TTACTTCAAAATAAAGCATG 1015  
 Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 7  
 US-09-069-023-6  
 ; Sequence 6, Application US/09069023A  
 ; Patent No. 6348573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nunez, Gabriel  
 ; APPLICANT: Inohara, Naohiro  
 ; APPLICANT: Koseki, Takeyoshi  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
 ; FILE REFERENCE: UM-03333  
 ; CURRENT APPLICATION NUMBER: US/09/069,023A  
 ; CURRENT FILING DATE: 1998-04-27  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 167  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-069-023-6

Alignment Scores:  
 Pred. No.: 2.6e-168 Length: 167  
 Score: 227.00 Matches: 167  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 4 Gaps: 0

Score: 167.00 Matches: 167  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 31.45% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-6 (1-167)

QY 515 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAATCACAGT 574  
Db 1 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 20  
QY 575 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCTCTCTGTGATCACAAGACCACTCA 634  
Db 21 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 40  
QY 635 TCCTCTTCAGCAATATAATCACTCTCACTGAGGAACTCAGAACTGCTGAGCT 694  
Db 41 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLysGlnPro 60  
QY 695 GGTATAGCCAGCAGCTGATCCAGACCAAAAGGAGACATTGTGAACCAATGACAGAA 754  
Db 61 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 80  
QY 755 GCCTGCTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGCATGATGAAGAGGAC 814  
Db 81 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 100  
QY 815 TATGAACTGTTAGTACCAAGCCTACAGGACTCAAAAGTCCAGAACTTAAAGATACAAA 934  
Db 121 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 140  
QY 935 CAAATGGGTCTTACAGCTTACCCGAAATACTTGTGGTTTCTAGATCACCATTCTTAAT 994  
Db 141 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 160  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 161 LeuLeuGlnAsnLysSerMet 167

RESULT 8  
US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-019-942-1

Alignment Scores:  
Pred. No.: 5,696-127 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-019-942-1 (1-540)

QY 632 CCATGCTCTTCCAGCAATATAATCCACTCTCACTGAGGAACTCAGAACTGCTGAC 691  
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CCTGTATAGCCAGCAGCTGATCCAGACCAAAAGGAGACATTGTGAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCTTAAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGCATGATGAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAAGCCTACAGGACTCAAAAGTCCAGCAATCTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGCATCCAGGAGAGAAATTCGCAAGTTATAGTACAAATTTGAAAGATAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGTCTTCCAGCTTACCCGAAATACTTGTGGTTTCTAGATCACCATTCTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9  
US-09-099-041A-2  
; Sequence 2, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-099-041A-2

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-099-041A-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691  
 |||||  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 |||||  
 QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACA 751  
 |||||  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 |||||  
 QY 752 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGACCTTGTATCATGAAAGAG 811  
 |||||  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 |||||  
 QY 812 GACTATGAACCTTTAGTACCAAGCCTCAAGACCTCAAAAGTATAGTACAAATTTACTAGAC 871  
 |||||  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 |||||  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAAGATAAC 931  
 |||||  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 |||||  
 QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991  
 |||||  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532  
 |||||  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 |||||  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
 |||||

RESULT 10

US-09-245-281-2  
 ; Sequence 2, Application US/09245281  
 ; Patent No. 6369196  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/09/245,281  
 ; CURRENT FILING DATE: 1999-02-05  
 ; EARLIER APPLICATION NUMBER: US 09/207,359  
 ; EARLIER FILING DATE: 1998-12-08  
 ; EARLIER APPLICATION NUMBER: US 09/099,041  
 ; EARLIER FILING DATE: 1998-06-17  
 ; EARLIER APPLICATION NUMBER: US 09/019,942  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-245-281-2

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540  
 Score: 128.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 24.11% Indels: 0  
 DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-245-281-2 (1-540)

QY 632 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691  
 |||||  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 |||||  
 QY 692 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAAAATGACA 751  
 |||||  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 |||||  
 QY 752 GAAGCCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGACCTTGTATCATGAAAGAG 811  
 |||||  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
 |||||  
 QY 812 GACTATGAACCTTTAGTACCAAGCCTCAAGACCTCAAAAGTATAGTACAAATTTACTAGAC 871  
 |||||  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 |||||  
 QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAAGATAAC 931  
 |||||  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 |||||  
 QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991  
 |||||  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532  
 |||||  
 QY 992 AATTACTTCAAAATAAAAGCATG 1015  
 |||||  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
 |||||

RESULT 11

US-09-470-271-1  
 ; Sequence 1, Application US/09470271  
 ; Patent No. 6410689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
 ; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/470,271  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/019,942  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.  
 ; REGISTRATION NUMBER: 35,283  
 ; REFERENCE/DOCKET NUMBER: 07334/068001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 540 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-09-470-271-1

Alignment Scores:  
 Pred. No.: 5.69e-127 Length: 540

Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-470-271-1 (1-540)

QY 632 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGCATCCAGACCAAAAGGAGAGACATTGTGCAACCAATGACA 751  
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 811  
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871  
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAC 931  
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGCTTCAGCCTTACCAGGAACTTGTGTTCTAGATCACCACCTTTTA 991  
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAAGCATG 1015  
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12

US-09-207-359B-2  
; Sequence 2, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-207-359B-2

Alignment Scores:  
Pred. No.: 5,69e-127 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-207-359B-2 (1-540)

QY 632 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CCTGTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGAGACATTGTGCAACCAATGACA 751  
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 811  
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871  
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAC 931  
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGCTTCAGCCTTACCAGGAACTTGTGTTCTAGATCACCACCTTTTA 991  
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAAGCATG 1015  
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13

US-09-340-620A-2  
; Sequence 2, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-620A-2

Alignment Scores:  
Pred. No.: 5,69e-127 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-340-620A-2 (1-540)

QY 632 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CCTGTATAGCCAGCAGTGCATCCAGACCAAAAGGAGAGACATTGTGCAACCAATGACA 751  
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 811  
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAGCCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871

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Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGATTTGCCAAGTTATAGTACAAAATTGGAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 14
US-09-865-364-2
; Sequence 2, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-2

Alignment Scores:
Pred. No.: 5.69e-127 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-865-364-2 (1-540)
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACGCTGTCAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGATAGCCCAAGAGATTTGCCAAGTTATAGTACAAAATTGGAACCAAGATAAC 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTACCAAGTCGTAGATGCCCTTCTGTCAGGACTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGATTTGCCAAGTTATAGTACAAAATTGGAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532

Search completed: March 29, 2004, 14:37:45
Job time : 35 secs

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QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 15
US-09-748-537-1
; Sequence 1, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Alignment Scores:
Pred. No.: 5.69e-127 Length: 540
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.11% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)
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Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGATAGCCCAAGAGATTTGCCAAGTTATAGTACAAAATTGGAACCAAGATAAC 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTACCAAGTCGTAGATGCCCTTCTGTCAGGACTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCCAAGAGAGATTTGCCAAGTTATAGTACAAAATTGGAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

Search completed: March 29, 2004, 14:37:45
Job time : 35 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:20:43 ; Search time 81.5 Seconds  
(without alignments)  
11572.314 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 531

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Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Word size: 20

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=20  
-ALIGN=15 -MODE=LOCAL -OUTFMT=ext -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09711161 @CGN 1.1.81 @runat.29032004.124856.14304  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

A\_Geneseq.29Jan04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	227	42.7	284	3	AAV59406	AAV59406 Human RIC
2	227	42.7	478	3	AAV59405	AAV59405 Human RIC
3	227	42.7	531	3	AAV59404	AAV59404 Human RIC
4	227	42.7	540	2	AAW92795	AAW92795 Human B1
5	227	42.7	540	3	AAV68774	AAV68774 Amino aci
6	227	42.7	540	4	AAW93621	AAW93621 Human pol
7	227	42.7	540	5	AAU80369	AAU80369 Human cel
8	227	42.7	540	5	AAE27882	AAE27882 Human rec
9	227	42.7	544	3	AAW43570	AAW43570 Human can
10	197	37.1	510	7	ADC99079	ADC99079 Human KPP

11 167 31.5 167 3 AAY59407  
12 128 24.1 540 2 AAY31140  
13 128 24.1 540 4 AAB20079  
14 128 24.1 540 5 ABG31075  
15 128 24.1 540 5 AAO22107  
16 128 24.1 540 6 ABUS6269  
17 128 24.1 540 7 ADB81362  
18 110 20.7 110 6 ABUS6272  
19 109 20.5 109 5 AAO22110  
20 98 18.5 131 5 AAO22109  
21 98 18.5 131 6 ABUS6271  
22 92 17.3 92 5 ABJ04754

#### ALIGNMENTS

RESULT 1  
AAV59406  
ID AAY59406 standard; protein; 284 AA.  
XX  
AC AAY59406;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK protein sequence residues 248-531.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO955134-A2.  
XX  
PD 04-NOV-1999.  
XX  
XX 27-APR-1999; 99WO-US009183.  
XX 27-APR-1998; 98US-00069023.  
XX (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
XX WPI; 2000-072163/06.  
XX  
XX Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.  
XX  
XX Claim 6; Page; 93pp; English.

CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography



QY 395 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 454  
DB |||||  
DB 272 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 291  
QY 455 AATAGTGGTTCCTCTGAACTCAAGCTCCCTGCGAGCTCCTCAAGACAATGATTTTAA 514  
DB |||||  
DB 292 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 311  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGTCTGGAATCACAGT 574  
DB |||||  
DB 312 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 331  
QY 575 TGGGTAGCACCATTTCTGGATCTCAAGGGCTGCTTCTGTGATCACAAGACCACTCCA 634  
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DB 332 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 351  
QY 635 TGCTCTTACGCAATTAATCACTCTCAACTGCAGGAACTCAGAAGCTGTGAGCT 694  
DB |||||  
DB 352 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 371  
QY 695 GGTATAGCCACAGCTGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 754  
DB |||||  
DB 372 GlyIleAlaGlnIleThrIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 391  
QY 755 GCCTGCTTAAACCACTGCTAGATCCCTTCTGTCCAGGACTTGATCATGAAGAGGAC 814  
DB |||||  
DB 392 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 411  
QY 815 TATGAACCTGTTAGTACAGCTACAGGACTCAAGGCTCAAAAGTCAGACAATTAAGACT 874  
DB |||||  
DB 412 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 431  
QY 875 ACTGACATCCAGGAGAGAATTTGCCAAAGTTATAGTACAAATTTGAAAGATACAAA 934  
DB |||||  
DB 432 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 451  
QY 935 CAAATGGGTCTTACGCTTACCCGGAATACCTTGTGTTTCTAGATCACCATTCTTAAAT 994  
DB |||||  
DB 452 GlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAsn 471  
QY 995 TTACTTCAAAATAAAGCATG 1015  
DB |||||  
DB 472 LeuLeuGlnAsnLysSerMet 478

## RESULT 3

AA59404  
ID AA59404 standard; protein; 531 AA.  
AC AA59404;  
XX  
XX 21-MAR-2000 (first entry)  
DE Human RICK protein sequence.  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
OS Homo sapiens.  
PN WO955134-A2.  
XX  
XX 04-NOV-1999.  
PD  
XX  
PF 27-APR-1999; 99WO-US009183.  
PR 27-APR-1998; 98US-00069023.  
XX  
XX (UNMI ) UNIV MICHIGAN.

PI Nunez G, Inohara N, Koseki T;  
XX WPI; 2000-072163/06.  
DR N-PSDB; AAZ48762.  
XX  
XX Compositions for identifying apoptosis signaling pathway inhibitors  
XX useful for treating diseases.  
PS Claim 1; Fig 7a; 93pp; English.  
XX  
XX This sequence is the human RICK (RIP-like interacting CLARP kinase)  
XX protein of the invention. The RICK protein acts as a positive regulator  
XX of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
XX during CD95 signalling. The invention provides methods for identifying  
XX apoptosis signalling pathway inhibitors and activators, and methods and  
XX compositions for screening compounds which will modulate the interactions  
XX of the various compositions identified: ARC, RICK, and the CIDE family of  
XX activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening of  
XX assays for agents, useful in the diagnosis, prognosis or treatment of  
XX disease associated with excess cell growth and dysregulation of  
XX apoptosis. Complexes containing RICK and CLARP can be used in drug  
XX screening assays to identify inhibitor molecules blocking CD95-mediated  
XX apoptosis. Overexpression of ARC in an in vitro cell system can be used  
XX to identify inhibitors of the enzymatic activity of caspase-8.  
XX Identification of ARC-like inhibitory compounds may be useful for gene  
XX therapy treatment of disease with increased cell death in muscle tissue  
XX and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
XX treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
XX ischaemic injury, and toxin-induced liver disease. Anti-RICK antibodies  
XX can be used as reagents for the preparation or affinity chromatography  
XX media, and for diagnostically measuring RICK levels. A specific inhibitor  
XX of an essential step in the biochemistry of apoptosis is needed. RICK  
XX interaction with intracellular factors such as CLARP and FADD appears to  
XX be essential for apoptosis, inhibitors of RICK binding to intracellular  
XX apoptosis factors are potential drug candidates  
SQ Sequence' 531 AA;

## Alignment Scores:

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US-09-771-161A-2 (1-1669) x AAY59404 (1-531)

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QY 455 AATAGTGGTTCCTCTGAACTTCAAGGCTCCCTGCGAGCTCCTCAAGACAATGATTTTAA 514  
DB |||||  
DB 345 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 364  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGTCTGGAATCACAGT 574  
DB |||||  
DB 365 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 384  
QY 575 TGGGTAGCACCATTTCTGGATCTCAAGGGCTGATCTCTGTGATCACAAGACCACTCCA 634  
DB |||||  
DB 385 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 404  
QY 635 TGCTCTTACGCAATTAATCACTCTCAACTGCAGGAACTCAGAAGCTGTGAGCT 694  
DB |||||  
DB 405 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 424  
QY 695 GGTATAGCCACAGCTGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 754

Db 425 GlyileAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 444  
QY 755 GCCTGCCTTACCAAGTGGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGGAC 814  
Db 445 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 464  
QY 815 TATGAACCTTGTAGTACCAAGCTTACCAAGGACCTCAAAAGTCACACAATTTACTAGACACT 874  
Db 465 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 484  
QY 875 ACTGACATCCCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
Db 485 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 504  
QY 935 CAAATGGGTCTTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 994  
Db 505 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 524  
QY 995 TTACTTCAAAATAAAAGCATG 1015  
Db 525 LeuLeuGlnAsnLysSerMet 531

RESULT 4  
AAW92795

ID AAW92795 standard; protein; 540 AA.

AC AAW92795;

DT 07-MAY-1999 (first entry)

DE Human B1 protein.

KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
cell survival pathway; intracellular signalling; AIDS; cancer; human.

OS Homo sapiens.

PN W09855507-A2.

PD 10-DEC-1998.

PF 01-JUN-1998; 98WO-IL000255.

PR 05-JUN-1997; 97IL-00121011.

PR 30-JUN-1997; 97IL-00121199.

PR 11-SEP-1997; 97IL-00121746.

PA (YEDA ) YEDA RES & DEV CO LTD.

XX Wallach D, Boldin M, Malinin N;

XX WPI; 1999-070258/06.

XX N-PSDB; AAX02558.

PT New B1 protein regulates cell death and cell survival pathways -  
derivatives, DNA and antibodies, also regulate intracellular inflammation  
; for treating AIDS, cancer.

PS Claim 4; Fig 3A; 90pp; English.

CC This invention describes the isolation of a novel human B1 protein which  
can interact with, intracellular mediators or modulators of inflammation,  
cell death and/or cell survival pathways, directly or indirectly. Cells  
can be modulated or mediated in inflammation, cell death or cell survival  
pathways or another intracellular signalling activity using B1.  
Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
oligonucleotides and ribozymes can also be used to regulate the above  
pathways

XX Sequence 540 AA;

Alignment Scores:

Pred. No.: 2,86e-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 2 Gaps: 0

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Db 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333

QY 395 AACATACCTCTTAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454

Db 334 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHisGlu 353

QY 455 AATAGTGGTTCCTCTCAAACTTCAAGTCCCTGCCAGCTCCCTCAAGACAAATGATTTTTTA 514

Db 354 AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnLeuPheLeu 373

QY 515 TCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCTGTCTCGAAATCAGT 574

Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393

QY 575 TGGGATAGCACCATTCTCGATCTCAAGGGCTGCTTCTGTGATCACAAGACCCTCCA 634

Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThrPro 413

QY 635 TGCTCTTCAGCAATATATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAGCCT 694

Db 414 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433

QY 695 GGTATAGCCAGCAGTGGATCCAGACCAAGGAGAGACATTGTGAACCAATGACAGAA 754

Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453

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Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493

QY 875 ACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGTACACAA 934

Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513

QY 935 CAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATCTTTAAAT 994

Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533

QY 995 TTACTTCAAAATAAAAGCATG 1015

Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 5  
AAW68774

ID AAW68774 standard; protein; 540 AA.

AC AAW68774;

DT 16-MAY-2000 (first entry)

XX Amino acid sequence of a human phosphorylation effector PHSP-6.  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
immune disorder; neuronal disorder.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

FT Region 18..287  
FT /note= "protein kinase family signature sequence"  
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FT /note= "potential phosphorylation site"  
FT 34  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 58  
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FT /note= "potential phosphorylation site"  
FT 100  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 102  
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FT /note= "potential phosphorylation site"  
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FT /note= "potential phosphorylation site"  
FT 360  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 374  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 391  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 401  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 428  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 442  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 457  
FT Modified-site  
FT /note= "potential glycosylation site"  
FT 478  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 478  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 484  
FT Modified-site  
FT /note= "potential phosphorylation site"  
FT 537  
FT Modified-site  
FT /note= "potential glycosylation site"  
XX  
PN W0200006728-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 28-JUL-1999; 99WO-US017132.  
XX  
PR 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155196P.  
PR 14-OCT-1998; 98US-0155239P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX  
PA (INCYTE) INCYTE PHARM INC.  
XX  
PI Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX  
XX WPI: 2000-183125/16.  
DR N-PSDB; AA246143.  
DR  
XX New human phosphorylation effectors useful for the diagnosis, treatment

PT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 1; Page 84-85; 142pp; English.  
XX  
CC AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
CC given in the specification). The sequences were isolated from cDNA  
CC libraries prepared from various human tissues. The PHSP proteins are  
CC useful for the diagnosis, treatment and prevention of proliferative  
CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
CC form pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity  
XX  
SQ Sequence 540 AA;  
  
Alignment Scores:  
Pred. No.: 2,86e-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-771-161A-2 (1-1669) x AAY68774 (1-540)  
QY 335 TTACAGAGTGTTCCTCAAGTGCCATTCACCTATGTGACAAAGAAATGGAATTATCTCTG 394  
DB 314 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAAATCATGTCCTCAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
DB 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 353  
QY 455 AATAGTGTTCTCTGAACCTCAAGTCCCTCCAGCTCCCTCAAGACATCATTTTTTA 514  
DB 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTATTATTTATGAAGTGCATCTCTCTGGAATCACACT 574  
DB 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 393  
QY 575 TGGATACACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTCCA 634  
DB 394 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 413  
QY 635 TGCTCTTCAGCAATATAATCCACTCTCAACTGAGGAACTCAGAACTCTGAGCTGAGCCT 694  
DB 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTGTGAACCAAAATGACAGAA 754  
DB 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTCCCTTAACCACTCCCTAGATGCCCTTCTGTCCAGGACTTCATCATGAAAGAGGAC 814  
DB 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
QY 815 TATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874  
DB 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATACAA 934  
DB 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAAATGGGTCTTCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATTCTTAAT 994  
DB 514 GlnMetGlyLeuGlnProIleProGluIleLeuValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAGCATG 1015  
|||||



PS Disclosure; Page 23-24; 49pp; English.

XX The present invention relates to a new method for identifying compounds  
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
CC related diseases. The method of the invention comprises contacting a test  
CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
CC activity. The method of the invention can be used to treat and/or prevent  
CC CMV infections and related diseases. Oligonucleotides that can detect the  
CC specified kinases can also be used for diagnosis of infection. The  
CC present amino acid sequence represents the human cellular kinase RICK  
CC protein of the invention, as described above

XX SQ Sequence 540 AA;

Alignment Scores:  
Pred. No.: 2,866-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x AAU80369 (1-540)

QY 335 TTACAGAGTGTTTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCTCTG 394  
Db 314 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCCTGAACTTCAAGTCCCTGAGCTCTCAAGACAAATGATTTTGA 514  
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTGGAATACACAGT 574  
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCTATGTGATCACAAGACCACTCCA 634  
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 413  
QY 635 TGCTCTTCAGCAATTAATAATCACTCTCAACTGCAGGAACTCAGAACTCTGAGCT 694  
Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
QY 695 GGTATAGCCACAGCTGGATCCAGACCAAAAGGAGACATTTGCAACCAATGACAGAA 754  
Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
QY 755 GCCTGCTTAACAGCTCGTAGATGCCCTTCTGTCAGGAGCTTATCATGATGAAAGAGAC 814  
Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
QY 815 TATGAACCTGTTAGTACCAAGCTTCAAGGACTCAAGAGCTCAAAAGTCAAGCAATTA 874  
Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
QY 875 ACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
Db 494 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
QY 935 CAATGGGTCTTCAGCTTACCGGGAATACTTGGTTTCTAGATCACCATTCTTAAT 994  
Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 533  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 534 LeuLeuGlnAsnLysSerMet 540

RESULT 8

AAE27882  
ID AAE27882 standard; protein; 540 AA.  
XX AC AAE27882;  
XX DT 27-DEC-2002 (first entry)  
XX DE Human receptor interacting protein (RIP)2.  
XX KW Human; receptor interacting protein; RIP2; antisense; gene therapy.  
XX OS Homo sapiens.  
XX PN US6426221-B1.  
XX PD 30-JUL-2002.  
XX PF 01-AUG-2001; 2001US-00920663.  
XX PR 01-AUG-2001; 2001US-00920663.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Ward DT, Cowseert LM;  
XX DR WPI; 2002-673017/72.  
XX DR N-PSDB; AAD45172.  
XX PT New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP)2, for treating diseases  
PT associated with RIP2 expression.  
XX PS Example 15; Col 49-54; 35pp; English.  
XX CC The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding human receptor interacting protein (RIP)2 to inhibit its  
CC expression. Antisense compounds are used for treating diseases associated  
CC with RIP2 expression. They are also useful in antisense gene therapy. The  
CC present sequence is human RIP2 protein  
XX SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 2,866-237 Length: 540  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 42.75% Indels: 0  
DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x AAE27882 (1-540)

QY 335 TTACAGAGTGTTTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCTCTG 394  
Db 314 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 333  
QY 395 AACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 454  
Db 334 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 353  
QY 455 AATAGTGGTTCCTGAACTTCAAGGCTCCCTGAGCTCTCAAGACAAATGATTTTGA 514  
Db 354 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 373  
QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGCTGGAATACACAGT 574  
Db 374 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 393  
QY 575 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCTATGTGATCACAAGACCACTCCA 634  
Db 394 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 413

QY 635 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACGCTCGAGCCT 694  
 Db 414 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433  
 QY 695 GGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTTGAAACCAATGACAGAA 754  
 Db 434 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 453  
 QY 755 GCCTGCCTTACCAAGTGCCTAGATGCCCTCTGCTCCAGGACCTTGATCATGAAAGAGAC 814  
 Db 454 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 473  
 QY 815 TATGAACCTTGTACTCAAGCCTTACAGGACCTCAAAAGTTCAGACAAATTAAGACACT 874  
 Db 474 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493  
 QY 875 ACTGACATCCAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
 Db 494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 513  
 QY 935 CAAATGGGTCTTACAGCCTTACCCGGAAATCTTGTGGTTTCTAGATCACCACATCTTTAAAT 994  
 Db 514 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 533  
 QY 995 TTACTTCAAAATAAAGCATG 1015  
 Db 534 LeuLeuGlnAsnLysSerMet 540  
 RESULT 9  
 AAB43570  
 ID AAB43570 standard; protein; 544 AA.  
 XX  
 AC AAB43570;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human cancer associated protein sequence SEQ ID NO:1015.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
 KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antidiabetic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005882.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587533/55.  
 XX  
 DR N-PSDB; AAC77779.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 XX useful for treating or diagnosing e.g. cancer.  
 XX  
 PS Claim 11; Page 1595-1597; 2352pp; English.  
 XX  
 CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44239. The proteins can have activities based on the

CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnery; immunomodulator;  
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 544 AA;  
 Alignment Scores:  
 Pred. No.: 2,856-237 Length: 544  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 42.75% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAB43570 (1-544)  
 QY 335 TTACAGAGTGTTCAGTGCCTTACCTTACCTATGTGACAGAGAAATGGAATATCTCTG 394  
 Db 318 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 337  
 QY 395 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCTCTCAGCTCATGAA 454  
 Db 338 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 357  
 QY 455 ATATGTGGTTCCTCGAACTTCAAGTCCCTGCGCAGCTCTCTCAAGACATGATTTTAA 514  
 Db 358 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 377  
 QY 515 TCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTGCTGGAATCAGACT 574  
 Db 378 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 397  
 QY 575 TGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACTCCA 634  
 Db 398 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 417  
 QY 635 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACGCTCGAGCCT 694  
 Db 418 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 437  
 QY 695 GGTATAGCCAGCAGTGGATCCAGCAAAAGGGAAGACATTTGAAACCAATGACAGAA 754  
 Db 438 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 457  
 QY 755 GCCTGCCTTACCAAGTGCCTAGATGCCCTCTGCTCCAGGACCTTGATCATGAAAGAGAC 814  
 Db 458 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 477  
 QY 815 TATGAACCTTGTACTCAAGCCTTACAGGACCTCAAAAGTTCAGACAAATTAAGACACT 874  
 Db 478 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 497  
 QY 875 ACTGACATCCAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACAAA 934  
 Db 498 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 517  
 QY 935 CAAATGGGTCTTACAGCCTTACCCGGAAATCTTGTGGTTTCTAGATCACCACATCTTTAAAT 994



Db 518 GlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeuAsn 537  
QY 995 TTACTTCAAAATAAAGCATG 1015  
Db 538 LeuLeuGlnAsnLysSerMet 544  
RESULT 10  
ID ADC99079 standard; protein; 510 AA.  
XX AC ADC99079;  
XX DT 01-JAN-2004 (first entry)  
XX DE .Human KPP protein - SEQ ID 32.  
XX anti-HIV; anti-allergic; anti-inflammatory; antianaemic; anti-parkinsonian;  
KW neurotropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
KW immunosuppressive; antichyroid; cytostatic; hepatotropic; dermatological;  
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
KW cancer; developmental; mental retardation; neurological;  
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
KW helminthic infection; transgenic; gene therapy; human; enzyme.  
XX Homo sapiens.  
OS  
XX WO2003033680-A2.  
PN  
PD 24-APR-2003.  
XX  
PF 17-OCT-2002; 2002WO-US033723.  
XX  
PR 19-OCT-2001; 2001US-0345474P.  
PR 02-NOV-2001; 2001US-0343910P.  
PR 13-NOV-2001; 2001US-0333098P.  
PR 16-NOV-2001; 2001US-0332424P.  
PR 30-NOV-2001; 2001US-0334289P.  
XX  
(INCY-) INCYTE GENOMICS INC.  
PA  
XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
PI Emerling BM, Forsythe JJ, Gandhi AR, Gorvad AE, Griffin JA;  
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
PI Zebarjadian Y;  
XX WPI; 2003-403214/38.  
DR N-PSDB; ADC99131.  
XX  
PT New human kinases and phosphatases and polynucleotides, useful for  
PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
PT cancer or hepatitis.  
XX  
PS Claim 1; SEQ ID NO 32; 424pp; English.  
XX  
CC The invention relates to a novel isolated polypeptide which is a human  
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
CC agonists and antagonists are useful for diagnosing, treating or  
CC preventing cell proliferative disorders such as atherosclerosis,  
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
CC retardation, neurological disorders including Alzheimer's disease and  
CC Parkinson's disease, autoimmune and inflammatory disorders such as  
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the

CC polynucleotides encoding KPP may be useful for creating transgenic  
CC animals to model human disease, as well as during gene therapy  
CC procedures. The current sequence is that of the human KPP protein of the  
XX invention.  
XX SQ Sequence 510 AA;  
Alignment Scores:  
Pred. No.: 1.25e-204 Length: 510  
Score: 197.00 Matches: 197  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 37.10% Indels: 0  
DB: 7 Gaps: 0  
US-09-771-161A-2 (1-1669) x ADC99079 (1-510)  
QY 425 GAATCATGTCGATCCTCTCAGCTCCATCAAAATAGTGGTCTCTCTGAACCTCAAGGTCC 484  
Db 314 GluSerCysGlySerSerGlnLeuHisGlnAsnSerGlySerProGluThrSerArgSer 333  
QY 485 CTGCCAGCTCTCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTATG 544  
Db 334 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 353  
QY 545 AAGCTGCATCATCTGCTCGAAATCACAGTGGGATAGACCATTTCTGGATCTCAAAGG 604  
Db 354 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 373  
QY 605 GCTGCATTTCTGATCACAAGACCACTCCATGCTCTTCAGCAATTAATTAATCACTCTCA 664  
Db 374 AlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleAlaAsnProLeuSer 393  
QY 665 ACTGCAGGAAACTCAGAACTCTGAGCTGTGTATAGCCAGCAGTGGATCCAGAGCAA 724  
Db 394 ThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnTrpIleGlnSerLys 413  
QY 725 AGGGAAGACATTGTGAACCAATGACAGAGCTCCCTTAACCACTCGCTAGATGCCCTT 784  
Db 414 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 433  
QY 785 CTGTCCAGGACTTGTATCATCAAGAGGACTATGACTTGTGTAGTACCAAGCCTCAAGG 844  
Db 434 LeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 453  
QY 845 ACCTCAAAAGTCAGACAAATTTACTAGACACTACTGATCCCAAGAGAGAAATTTGCCAA 904  
Db 454 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLys 473  
QY 905 GTTATAGTACAAAATTCAAGATACAAACAAATGGGTCTTTCAGCCTTTACCCGAAATA 964  
Db 474 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIle 493  
QY 965 CTGTGGTCTTCTAGATCACCCTTTAAATTTACTTCAAAATAAAGCATG 1015  
Db 494 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 510  
RESULT 11  
ID AAY59407 standard; protein; 167 AA.  
XX AC AAY59407;  
XX DT 21-MAR-2000 (first entry)  
XX DE Human RICK protein sequence residues 365-531.  
XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX



PT regulation of cellular proliferation and differentiation and cell survival.

XX PS

XX Example 2; Fig 2; 181pp; English.

CC This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial murine CARD-4L protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the TNF receptor complex, or abnormal activity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4L, a short transcript that encodes CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence represents the human CARD-3 protein described in the method of the invention

XX SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 1.47e-129 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 2 Gaps: 0

US-09-771-161A-2 (1-1669) x ANY31140 (1-540)

QY 632 CCATGCTCTTTCAGCAATAATAATCACTCTCACTCGAGGAACCTCAGACGCTCTGCAG 691  
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTGTGAAACCAATGACA 751  
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCTGCCTTAACAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811  
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAACCTTGTAGTACCAAGCCTACAAGACCTCAAAAGTCAGACAAATTACTAGAC 871  
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGAGAGAATTTGCCAAGTTATAGTCAAAAATGGAAGATAC 931  
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAATGGGCTTCAGCCTTACCGGAATACTTGTTGTTCTAGATCACCATTCTTA 991  
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValIleSerArgSerProSerLeu 532  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13

AAB20079  
ID AAB20079 standard; protein; 540 AA.

XX AC AAB20079;

XX DT 23-APR-2001 (first entry)

XX DE Human CARD-3 protein.

XX KW CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antiinflammatory; apoptosis; diagnosis; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT Domain 1..400  
FT /note= "kinase domain"  
FT Domain 401..431  
FT /note= "linker domain"  
FT Domain 432..540  
FT /note= "CARD"

XX WO200100826-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US017691.

XX 28-JUN-1999; 99US-00340620.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2001-061973/07.

XX N-PSDB; AAF30001.

XX Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of e.g. cancer, viral infections, autoimmune diseases, neurological diseases and hematological disorders.

XX Claim 9; Fig 2; 208pp; English.

XX The present sequence is that of human caspase recruitment domain 3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, -4, -5 or -6 protein, or production of an aberrant protein

XX SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 1.47e-129 Length: 540  
Score: 128.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.11% Indels: 0  
DB: 4 Gaps: 0

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US-09-771-161A-2 (1-1669) x AAB20079 (1-540)
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DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACCAAGGAGGACACATTTGTGAACCAATGACA 751
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAGAG 811
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAAGACATTTACTAGAC 871
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCATTCTTA 991
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 14
ABG31075
ID ABG31075 standard; protein; 540 AA.
XX AC ABG31075;
XX DT 21-OCT-2002 (first entry)
XX DE Human caspase recruitment domain protein CARD-3.
XX KW Human; caspase recruitment domain; CARD-3; CARD-4; LRR;
XX KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;
XX KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;
XX KW systemic lupus erythematosus; immune-mediated glomerulonephritis;
XX KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;
XX KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;
XX KW gastrointestinal allergy; insulin-dependent diabetes;
XX KW bacterial infection; tuberculosis; lepromatous leprosy;
XX KW cell signalling disorder; tissue disorder.
XX OS Homo sapiens.
XX PN W0200253765-A1.
XX XX 11-JUL-2002.
XX XX 20-DEC-2001; 2001WO-US049798.
XX XX 29-DEC-2000; 2000US-0258724P.
XX XX (MILL-) MILLENNIUM PHARM INC.
XX XX Bertin J, Philpott D, Sansonetti P, Girardin S;
XX XX WPI; 2002-583627/62.
XX XX DR N-ESDB; ABK89280.
XX XX Identifying modulators of long form of caspase recruitment domain, CARD-
XX XX 4L useful for treating cancer, infections, and immune disorders, by
XX XX contacting test compound with CARD-4L and determining effect of the
XX XX compound.
```

Example 2; Fig 2; 139pp; English.

The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein

Sequence 540 AA;

Alignment Scores:

Pred. No.:	1,47e-129	Length:	540
Score:	128.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	24.11%	Indels:	0
DB:	5	Gaps:	0

US-09-771-161A-2 (1-1669) x ABG31075 (1-540)

```
QY 632 CCATGCTCTTCACCAATAAATCACTCACTCACTGCGAGAACTCAGAACGTCGTGCAG 691
DB 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGACCAAGGAGGACACATTTGTGAACCAATGACA 751
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAGAG 811
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAAGACATTTACTAGAC 871
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
DB 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCATTCTTA 991
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
DB 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 15
AAO22107
ID AAO22107 standard; protein; 540 AA.
XX XX
```

AC	AAO22107;
XX	
XX	27-SEP-2002 (first entry)
XX	
DE	Protein of human CARD-3 SEQ ID No 2.
XX	
XX	Cytostatic; virucide; immunomodulatory; neuroprotective; anti-alzheimers;
KW	cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;
KW	nootropic; anti-anemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;
KW	cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;
KW	hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;
KW	systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;
KW	anaemia; neutropenia; myelodysplastic syndrome; human.
XX	
OS	Homo sapiens.
PX	
NN	US6369196-B1.
XX	
PD	09-APR-2002.
XX	
PF	05-FEB-1999; 99US-00245281.
XX	
PR	06-FEB-1998; 98US-00019942.
PR	17-JUN-1998; 98US-00039041.
PR	08-DEC-1998; 98US-00207359.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
PI	Bertin J;
XX	
DR	WPI; 2002-391988/42.
DR	N-PSDB; AAL40752, AAL40753.
PT	
PT	Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD
PT	-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's
PT	disease, cancers and viral infections.
XX	
PS	Example 2; Fig 2; 116pp; English.
XX	
CC	The invention relates to novel isolated Caspase Recruitment Domain (CARD)
CC	polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may
CC	be used to treat disorders associated with decreased CARD expression by
CC	supplementing the patient's own production of CARD. Disorders associated
CC	with the expression and activity of CARD include cancers (particularly
CC	follicular lymphomas, carcinomas associated with mutations in p53, and
CC	hormone-dependent tumours such as breast cancer, prostate cancer, and
CC	ovarian cancer), autoimmune disorders (such as systemic lupus
CC	erythematosus, immune-mediated glomerulonephritis), viral infections
CC	(such as those caused by herpes viruses, poxviruses, and adenoviruses),
CC	neurological diseases (such as Alzheimer's disease, parkinson's disease,
CC	amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal
CC	muscular atrophy, and various forms of cerebellar degeneration), anaemia
CC	associated with chronic disease, aplastic anaemia, chronic neutropenia,
CC	and the myelodysplastic syndromes. This sequence represents a human CARD
CC	protein relating to the invention
XX	
SQ	Sequence 540 AA;
	Alignment Scores:
	Pred. No.: 1,47e-129 Length: 540
	Score: 128.00 Matches: 128
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 24.11% Indels: 0
	DB: 5 Gaps: 0
US-09-771-161A-2 (1-1669) x RAO22107 (1-540)	
Qy	632 CCATGCTCTTTCAGCAATAATAATCCACTCTCACTGCAGGAAGAACTCAGAACGTCTGCAG 691
Db	413 ProCyseSerAlaAlaIleAsnProLeuSerThrAlaGliYasSerGliUa'gLeuGln 432
Qy	692 CCTGGTATGCCCGACGAGTGGAATCAGAGCAAAAAGGGGAAGAACATTGTGAACCAAATGACA 751

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: April 1, 2004, 10:15:17 ; Search time 471 Seconds  
(without alignments)  
2092.531 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 20

Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=quality -THR MIN=20  
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-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N\_Geneseq.29Jan04:\*  
1: Geneseqn1980s:\*  
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3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	2024	3	Aaz46143 CDNA sequ
2	227	97.8	2033	4	Aak94554 Human ful
3	227	97.8	2098	2	Aax02558 Human B1
4	227	97.8	2501	6	Abk51169 cDNA enco
5	227	97.8	2501	6	Aad45172 Human rec
6	227	97.8	2502	3	Aaz48762 Human RIC
7	227	97.8	2709	3	Aac77779 Human can
8	197	84.9	1959	9	Adc99131 Human KPP

9	128	55.2	1620	7	ABX75870	Abx75870 Human Cas
10	128	55.2	1931	2	Aaz09246	Aaz09246 Human CAR
11	128	55.2	1931	4	Aaf30001	Aaf30001 Human CAR
12	128	55.2	1931	6	ABK89280	Abk89280 Human CDN
13	128	55.2	1931	6	AA140752	AA140752 CDNA of h
14	128	55.2	1931	7	ABX75869	Abx75869 Human cas
15	128	55.2	1931	9	ADB81363	Adb81363 Human cDN
16	120	51.7	491	8	ACH33353	Ach33353 Human end
17	110	47.4	1619	6	AA140753	AA140753 DNA of hu
18	44	19.0	762	7	ACD96414	Ac96414 Human col
c 19	40	17.2	575	4	AAK93010	Aak93010 Human CDN

ALIGNMENTS

RESULT 1  
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ID AAZ46143 standard; cDNA; 2024 BP.  
XX AAZ46143;  
AC AAZ46143;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA sequence encoding a human phosphorylation effector PHSP-6.  
XX  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 203..1825  
FT /\*tag= a  
FT /product= "phosphorylation effector"  
XX  
PN WO200006728-A2.  
XX  
PD 10-FEB-2000.  
XX  
XX 28-JUL-1999; 99WO-US017132.  
PR 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155198P.  
PR 14-OCT-1998; 98US-0155233P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX  
DR WPI; 2000-183125/16.  
DR P-PSDB; AAY68774.  
XX  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
XX  
PS Claim 9; Page 121-122; 142pp; English.  
XX  
CC AAZ46138-246168 encode human phosphorylation effectors (PHSP), designated  
CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the  
CC specification). The sequences were isolated from cDNA libraries prepared  
CC from various human tissues. The PHSP proteins are useful for the  
CC diagnosis, treatment and prevention of proliferative disorders, immune  
CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical  
CC compositions which useful for treating or preventing disorders associated  
CC with decreased PHSP expression/activity. PHSP antagonists are useful for  
CC treating or preventing disorders associated with increased PHSP  
CC expression/activity

XX SQ Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.13e-218 Length: 2024  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 97.84% Indels: 0  
 DB: 3 Gaps: 0  
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 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1202 AACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1261  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1262 AATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1321  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1322 TCTAGAAAGCTCAAGACTGTATTATGAGCTGCATCTCTGGAATCAGT 1381  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
 DB 1382 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1441  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
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 QY 126 GlyIleAlaGlnIntrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1502 GGTATAGCCCGAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 1561  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGluAsp 165  
 DB 1562 GCCTGCCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1621  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1622 TATGAACCTTGTGTAGTCAAGCCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1681  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1682 ACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATACAAA 1741  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeuAsn 225  
 DB 1742 CAAATGGGTCTTCCAGCTTACCAGGAATATCTGTGGTTCTAGATCACCATCTTTAAAT 1801  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1802 TTACTTCAAAATAAAGCATG 1822

RESULT 2  
 AAK94554  
 ID AAK94554 standard; cDNA; 2033 BP.  
 XX AC AAK94554;  
 XX 06-NOV-2001 (first entry)  
 XX Human full-length cDNA, SEQ ID NO: 3453.  
 XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.  
 PN EF1130094-A2.  
 XX 05-SEP-2001.  
 PD 07-JUL-2000; 2000BP-00114089.  
 XX 08-JUL-1999; 99JP-00194486.  
 XX 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR P-PSDB; AAM93621.  
 XX 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
 PS The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a full length human cDNA of the  
 CC invention. Note: the sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in CD-ROM format directly  
 CC from EPO  
 XX SQ Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.13e-218 Length: 2033  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 97.84% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-771-161a-93 (1-232) x AAK94554 (1-2033)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1158 TTACAGAGTGTTCACAGTCCATTCACCTATGTGACAAAGAAATGGAATATCTCTG 1217  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1218 AACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1277  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1278 AATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1337  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1338 TCTAGAAAGCTCAAGACTGTATTATGAGCTGCATCTCTCTGGAATACACT 1397  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
 DB 1398 TGGGATAGCACCATTCTGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 1457  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1458 TGTCTTTCAGCAATAATAATCCACTCTCACTGCGAGAACTCAGAACTGTGCGACCT 1517



QY 126 GlylleAlaGlnGlnTrrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 Db 1518 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACAGAA 1577  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 Db 1578 GCCTGCCCTTAACCAAGTGGTATGATCCCTTCTGTCAGGAGCTTGTATGATGAAGAGGAC 1637  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 Db 1638 TATGAACCTGTGTAGTACCAAGCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1697  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 Db 1698 ACTGACATCCAGGAGAGAAATTTGCTAAAGTTATAGTACAAAAATTTGAAAGATAACAAA 1757  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 Db 1758 CAAATGGGTCCTTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCCTTTAAAT 1817  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 Db 1818 TTACTTCAAAATAAAGCATG 1838  
 RESULT 3  
 AAX02558  
 ID AAX02558 standard; cDNA; 2098 BP.  
 AC AAX02558;  
 XX  
 DT 07-MAY-1999 (first entry)  
 DE Human B1 cDNA.  
 KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
 KW cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.  
 OS Homo sapiens.  
 PN W09855507-A2.  
 XX  
 PD 10-DEC-1998..  
 XX  
 PF 01-JUN-1998; 98WO-IL000255.  
 PR 05-JUN-1997; 97IL-00121011.  
 PR 30-JUN-1997; 97IL-00121199.  
 PR 11-SEP-1997; 97IL-00121746.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Wallach D, Boldin M, Malinin N;  
 XX  
 DR WPI; 1999-070258/06.  
 DR P-PSDB; AAW92795.  
 PT New B1 protein regulates cell death and cell survival pathways -  
 PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
 PT ; for treating AIDS, cancer.  
 XX  
 PS Claim 4; Fig 3B; 90pp; English.  
 XX  
 CC This invention describes the isolation of a novel human B1 protein which  
 CC can interact with, intracellular mediators or modulators of inflammation,  
 CC cell death and/or cell survival pathways, directly or indirectly. Cells  
 CC can be modulated or mediated in inflammation, cell death or cell survival  
 CC pathways or another intracellular signalling activity using B1.  
 CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
 CC oligonucleotides and ribozymes can also be used to regulate the above  
 CC pathways  
 XX  
 SQ Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;

Alignment Scores:  
 Pred. No.: 1.17e-218 Length: 2098  
 Score: 227.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 97.84% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAX02558 (1-2098)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 Db 1199 TTACAGAGTGTTCAGTGCCCATTCACCTATGTGCAAGAGAAATGAAATTTACTCTG 1258  
 QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1259 AACATACCTGTAAATCATGTGTCACACAGGAATCATGTGGATCTCTCAGCTCCATGAA 1318  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1319 AATAGTGGTCTCTCTGAAACCTCAAGGTCCCTGCCAGCTCTCTCAAGACAATGATTTTAA 1378  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 1379 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGTCATCTGCTCTGGAAATCACAGT 1438  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 Db 1439 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAAGACCCTCCA 1498  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 Db 1499 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAGCCT 1558  
 QY 126 GlylleAlaGlnGlnTrrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 Db 1559 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACAGAA 1618  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 Db 1619 GCCTGCCCTTAACCAAGTGGTATGATCCCTTCTGTCAGGAGCTTGTATGATGAAGAGGAC 1678  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 Db 1679 TATGAACCTGTGTAGTACCAAGCTCACAAGGAGCTCAAAAGTCAGACAATTACTAGACACT 1738  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 Db 1739 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAA 1798  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 Db 1799 CAAATGGGCTTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCCTTTAAAT 1858  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 Db 1859 TTACTTCAAAATAAAGCATG 1879  
 RESULT 4  
 ABK51169  
 ID ABK51169 standard; cDNA; 2501 BP.  
 XX  
 AC ABK51169;  
 XX  
 DT 30-JUL-2002 (first entry)  
 DE cDNA encoding human cellular kinase RICK protein.  
 XX  
 KW Human; viricide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.  
 XX  
 OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT 225..1847  
XX FT /\*tag= a  
XX FT /product= "Human cellular kinase RICK"  
XX EP1201765-A2.  
XX PN  
XX PD 02-MAY-2002.  
XX PF 15-OCT-2001; 2001EP-00124604.  
XX PR 16-OCT-2000; 2000US-0240750P.  
XX PA (AXXI-) AXIXIMA PHARM AG.  
XX PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
XX DR WPI; 2002-373930/41.  
XX DR P-PSDB; AAU80369.  
XX PT Identifying agents for treatment or prevention of cytomegalovirus  
XX PT infection, comprises contacting test compound with cellular kinase and  
XX PT detecting change in cellular kinase activity.  
XX PS Disclosure; Page 20-23; 49pp; English.  
XX CC The present invention relates to a new method for identifying compounds  
XX CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
XX CC related diseases. The method of the invention comprises contacting a test  
XX CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
XX CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
XX CC activity. The method of the invention can be used to treat and/or prevent  
XX CC CMV infections and related diseases. Oligonucleotides that can detect the  
XX CC specified kinases can also be used for diagnosis of infection. The  
XX CC present nucleic acid sequence encodes the human cellular kinase RICK  
XX CC protein of the invention, as described above  
XX SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.38e-218 Length: 2501  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 6 Gaps: 0  
US-09-771-161A-93 (1-232) x ABK51169 (1-2501)  
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
DB 1164 TTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGATATCTCTG 1223  
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1224 AACATACCTGTAATCATGGTCCACAGAGAGAAATCATGTGCATCTCTCAGCTCCATGAA 1283  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1284 AATAGTGGTCTCTCGAAACTTCAAGGTCCCTCGCAGCTCCTCAAGACAAATGATTTTAA 1343  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
DB 1344 TCTAGAAAGCTCAAGACTGTATTATTATGAGCTGCATCCTCTCGAATCAGT 1403  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
DB 1404 TGGGATAGCACCATTCTGGTCTCTCAAGGGCTGCAATCTCTGATCACAGACCACTCCA 1463  
QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
DB 1464 TGCTCTTCAGCAATATATAATCCACTCTCACTGCAGGAAACTCAGAACGCTCTGCACCT 1523

QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
DB 1524 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAACCAATGACAGAA 1583  
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
DB 1584 GCGTGCCTTAACGAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAGGAC 1643  
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
DB 1644 TATGAACCTTGTGTAGTACCAGGCTCAAGAGCTCAAAAGTCAGACAAATTACTAGACACT 1703  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
DB 1704 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1763  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
DB 1764 CAAATGGGTCTTCAGCCTTACCCTGGGAAATACCTTGTTGTCTAGATCACCATCTTTAAAT 1823  
QY 226 LeuLeuGlnAsnLysSerMet 232  
DB 1824 TTACTTCAAAATAAAAGCATG 1844  
RESULT 5  
AAD45172  
ID AAD45172 standard; DNA; 2501 BP.  
XX AC AAD45172;  
XX DT 27-DEC-2002 (first entry)  
XX DE Human receptor interacting protein (RIP) 2 DNA.  
XX KW Human; receptor interacting protein; RIP2; antisense; gene therapy; gene  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 225..1847  
XX FT /\*tag= a  
XX FT /product= "Human RIP2 protein"  
XX PN US6426221-B1.  
XX PD 30-JUL-2002.  
XX PF 01-AUG-2001; 2001US-00920663.  
XX PR 01-AUG-2001; 2001US-00920663.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Ward DT, Cowser LM;  
XX DR WPI; 2002-673017/72.  
XX DR P-PSDB; AA27882.  
XX PT New antisense oligonucleotide that targets regions of a nucleic acid  
XX PT encoding human receptor interacting protein (RIP)2, for treating diseases  
XX PS associated with RIP2 expression.  
XX PS Claim 1; Col 49-54; 35pp; English.  
XX CC The invention relates to antisense compounds targetted to a nucleic acid  
XX CC encoding human receptor interacting protein (RIP)2 to inhibit its  
XX CC expression. Antisense compounds are used for treating diseases associated  
XX CC with RIP2 expression. They are also useful in antisense gene therapy. The  
XX CC present sequence is human RIP2 DNA  
XX SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

XX	OS	Homo sapiens.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</
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aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.

Homo sapiens.

WO9955134-A2.

04-NOV-1999.

27-APR-1999; 99WO-US009183.

27-APR-1998; 98US-00069023.

(UNMI ) UNIV MICHIGAN.

Nunez G, Inohara N, Koseki T;

WPI; 2000-072163/06.

P-PSDB; AAY59404.

Compositions for identifying apoptosis signaling pathway inhibitors useful for treating diseases.

Claim 8; Fig 7b; 93pp; English.

This sequence encodes the human RICK (RIP-like interacting CLARP kinase) protein of the invention. The RICK protein acts as a positive regulator of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation of affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates

Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-218 Length: 2502

Score: 227.00 Matches: 227

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 97.84% Indels: 0

DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x AAZ48762 (1-2502)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25

DB 1165 TTACAGAGTGTTCACGATGCCATTACCTATGTGACAAAGAAATGGAATTAATCTCTG 1224

QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45

DB 1225 AACATACCTGTAAATCATGTGTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1284

QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65

DB 1285 AATAGTGGTTCCTCGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTGA 1344

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1345 TCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTCTGGAAATCAGCT 1404  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 1405 TGGGATAGCAGCAATTCCTGGTCTCAAGAGGCTGCATCTGTGATCAAGACCACTCCA 1464  
 QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1465 TGCTCTTCAGCAATAAATCCACTCTCACTGCAGGAACCTCAGAACGCTGCGAGCCT 1524  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1525 GGTATAGCCCGAGCAGTGGATCCAGAGCAAGAGGAGACATTTGACCAATGACAGAA 1584  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 1585 GCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1644  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1645 TATGAATCTGTAGTACCAAGCTTACAGGACCTCAAAAGTTCAGACAAATCTAGACACT 1704  
 QY 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1705 ACTGACATCCCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATGAAAGATACAAA 1764  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 DB 1765 CAATGGGTCTTACAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 1824  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1825 TTACTTCAAAATAAAGCAATG 1845

RESULT 7  
 AAC77779  
 ID AAC77779 standard; cDNA; 2709 BP.  
 AC AAC77779;  
 AC AAC77779;  
 DT 08-FEB-2001 (first entry)  
 XX Human cancer associated gene sequence SEQ ID NO:173.  
 XX Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
 KW antidiabetic; antisthmatic; antirheumatic; antithyroid; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; neutropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX W0200055350-A1.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 08-MAR-2000; 2000WO-US005882.  
 XX  
 XX 12-MAR-1999; 99US-0124270P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX PI  
 XX Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2000-587533/55.

DR P-PSDB; AAB43570.

XX Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.

XX Claim 1; Page 751-752; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC ABA43398 to ABA44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnary; immunomodulator;  
 CC antidiabetic; antisthmatic; antirheumatic; antithyroid; antiviral;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC neutropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease, and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and ABA44240 represent sequences used in the exemplification of  
 CC the present invention

SQ Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Alignment Scores:

Pred. No.:	1.49e-218	Length:	2709
Score:	227.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.84%	Indels:	0
DB:	3	Gaps:	0

US-09-771-161A-93 (1-232) x AAC77779 (1-2709)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 DB 1206 TTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATATCTCTG 1265  
 QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHisGlu 45  
 DB 1266 ACATACCTGTAAATCATGTGTCCACAGAGGAAATCATGTGGATCTCTCAGCTCCATGAA 1325  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1326 AATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 1385  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1386 TCTAGAAAAGCTCAAGACTGTTATTTATGCAAGCTGCATCTGCTCTCGAATACAGT 1445  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 1446 TGGGAYAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAGACCACTCCA 1505  
 QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 1506 TGCTCTTCAGCAATAAATAATCCACTCTCACTGCAGGAAACTCAGACGCTCTGCAGCCT 1565  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 1566 GGTATAGCCCGAGTGGATCCAGAGCAAGAGGAGACATTTGTGAACCAATGACAGAA 1625  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 1626 GCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1685

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1686 TATGAACCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGACACT 1745  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1746 ACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATTAACAAA 1805  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 DB 1806 CAATGGGTCTTTCAGCTTACCCGGAATACCTGTGTGTTCTAGATCACCCTCTTTAAAT 1865  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1866 TTACTTCAAAATAAAAGCATG 1886

## RESULT 8

ADC99131

ID ADC99131 standard; cDNA; 1959 BP.

XX AC ADC99131;

XX DT 01-JAN-2004 (first entry)

XX DE Human KPP cDNA - SEQ ID 84.

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CC The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP cDNA of the  
 CC invention.

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## Alignment Scores:

Pred. No.: 1,92e-188 Length: 1959  
 Score: 197.00 Matches: 197  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 84.91% Indels: 0  
 DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x ADC99131 (1-1959)

QY 36 GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer 55  
 DB 1160 GAATCATCTGGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAACTTCAAGGTCC 1219  
 QY 56 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 75  
 DB 1220 CTGCCAGCTCTCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACTGTTTATTTATG 1279  
 QY 76 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 95  
 DB 1280 AAGTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTCTGGATCTCAAGG 1339  
 QY 96 AlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleAsnProLeuSer 115  
 DB 1340 GCTGCATTTCTGTGATCACAGACCACTCATGCTCTTCAGCAATAATAATCCACTCTCA 1399  
 QY 116 ThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys 135  
 DB 1400 ACTGCAGGAAACTCAGAACTGTCAGGCTGCTGTATAGCCAGCAGCTGGATCCAGAGCAA 1459  
 QY 136 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 155  
 DB 1460 AGGGAAGACATTGTGAACCAATGACAGAGCTCGCTTAACCACTGGTAGATGCCCTT 1519  
 QY 156 LeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 175  
 DB 1520 CTGTCAGGAGCTTGATCATGAAAGAGGACTATGAATTTGTTAGTACCAAGCTCAAGG 1579  
 QY 176 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLys 195  
 DB 1580 ACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCTCCAGAGAGAAATTTGCCAAA 1639  
 QY 196 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIle 215  
 DB 1640 GTTATAGTACAAAATTGAAGATTAACAAACAAATGGGTCTTCAGCCTTTACCCGGAAATA 1699  
 QY 216 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232  
 DB 1700 CTTGTGGTTTCTAGATCACCATCTTTAAATTACTTTCAAAATAAAAGCATG 1750

## RESULT 9

ABX75870

ID ABX75870 standard; cDNA; 1620 BP.

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QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 1686 TATGAACCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGACACT 1745  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1746 ACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGATTAACAAA 1805  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 DB 1806 CAATGGGTCTTTCAGCTTACCCGGAATACCTGTGTGTTCTAGATCACCCTCTTTAAAT 1865  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 DB 1866 TTACTTCAAAATAAAAGCATG 1886

anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;  
 nootropic; anticonvulsant; antiarteriosclerotic; antidiabetic;  
 immunosuppressive; anticholesteric; cytotatic; hepatotropic; dermatological;  
 antidiabetic; nephrotropic; antitumor; thyromimetic; neuroprotective;  
 osteoprotic; antiallergic; antiparasitic; antihelminthic; antiparasitic;  
 uterine; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
 cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 cancer; developmental; mental retardation; neurological;  
 Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 helminthic infection; transgenic; gene therapy; human; ss; gene.

Homo sapiens.  
 WO2003033680-A2.  
 24-APR-2003.  
 17-OCT-2002; 2002WO-US033723.  
 19-OCT-2001; 2001US-0345474P.  
 02-NOV-2001; 2001US-0343910P.  
 13-NOV-2001; 2001US-0330988P.  
 16-NOV-2001; 2001US-0332424P.  
 30-NOV-2001; 2001US-0334288P.  
 (INCY-) INCYTE GENOMICS INC.

Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 Emerling BN, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;  
 Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
 Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 Zebajadian Y;  
 WPI: 2003-403214/38.  
 P-PSDB; ADC99079.

New human kinases and phosphatases and polynucleotides, useful for  
 diagnosing, treating or preventing autoimmune or inflammatory disorders  
 (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 cancer or hepatitis.

Claim 5; SEQ ID NO 84; 424pp; English.



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FT FT      /*tag= a
PN PN      /product= "CARD-3"
XX XX
XX XX
XX XX
PD PD      WO9940102-A1.
XX XX      12-AUG-1999.
XX XX
XX XX      05-FEB-1999; 99WO-US002544.
XX XX      06-FEB-1998; 98US-00019942.
PR PR      17-JUN-1998; 98US-00099041.
PR PR      08-DEC-1998; 98US-00207359.
XX XX      (MILL-) MILLENNIUM PHARM INC.
PA PA
XX XX      Bertin J;
PI PI
XX XX      WPI: 1999-494269/41.
DR DR      P-PSDB; AAY31140.
XX XX
XX XX      Novel CARD-3 and CARD-4 genes and polypeptides used or treating
PT PT      regulation of cellular proliferation and differentiation and cell
PT PT      survival.
XX XX
XX XX      Example 2; Fig 1; 181pp; English.
XX XX
XX XX      This invention describes the isolation of novel human caspase recruitment
CC CC      domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial
CC CC      murine CARD-4L protein and genes. The genes and proteins of the invention
CC CC      are involved in the regulation of caspase activation. The caspase
CC CC      recruitment domain (CARD) polynucleotides, polypeptides, homologues and
CC CC      antibodies can be used in screening assays, detection assays, predictive
CC CC      medicine and therapeutic and prophylactic methods of treatment. The
CC CC      methods may be used to diagnose and treat patients which are suffering
CC CC      from a disorder associated with abnormal level or rate of apoptotic cell
CC CC      death, abnormal activity of the Fas/APO-1 receptor complex, abnormal
CC CC      activity of the TNF receptor complex, or abnormal activity of a caspase.
CC CC      Diseases that may be treated include cancer (particularly follicular
CC CC      lymphoma, carcinomas associated with mutations in p53 and hormone-
CC CC      dependent tumours), autoimmune disorders (e.g. systemic lupus
CC CC      erythematosus, immune-mediated glomerulonephritis), viral infections,
CC CC      Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC CC      retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,
CC CC      anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.
CC CC      CARD-3 protein interacts with other cellular proteins, and so can be used
CC CC      for regulation of cellular proliferation and differentiation and cell
CC CC      survival. The CARD proteins may also be used to for screen drugs or
CC CC      compounds which modulate their activity. The CARD-4 gene can express a
CC CC      long transcript that encodes CARD-4L, a short transcript that encodes
CC CC      CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence
CC CC      encodes the human CARD-3 protein described in the method of the invention
XX XX
XX XX      SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      6.9e-119      Length:      1931
Score:      128.00      Matches:      226
Percent Similarity:      99.12%      Conservative:      0
Best Local Similarity:      99.12%      Mismatches:      1
Query Match:      55.17%      Indels:      2
DB:      2      Gaps:      0

US-09-771-161A-93 (1-232) x AAZ09246 (1-1931)

QY      6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysValSerMetGluLeuSerLeu 25
DB      1153 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGAATATCTCTG 1212
QY      26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45
DB      1213 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCTCATGTCATGAA 1272
QY      46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65

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DB      1273 AATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACATGATTTTAA 1332
QY      66 SerArgLysAlaGlnAspCysGlyThrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB      1333 TCTAGAAAAGCTCAAGACTGTTATTTATTAAGCTGTCATCACTGTCTCTGGAATCACAGT 1392
QY      86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPr 105
DB      1393 TGGGATAGCACCATTTCTGGATCTCAAAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451
QY      105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB      1452 ATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGAAACTCGAAACGTCTCGAGCC 1511
QY      125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
DB      1512 TGGTATAGCCCGAGCAGTGCATCCAGAGCAAAAGGAGACATTTGTGAACCAATCACAGA 1571
QY      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
DB      1572 AGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGA 1631
QY      165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
DB      1632 CTATGAACCTTGTAGTCAAGCCTTACAGGACCTCAAAAGTCAGACAAATTTACTAGACAC 1691
QY      185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
DB      1692 TACTGACATCCAAAGAGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751
QY      205 sGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeuAs 225
DB      1752 ACAATGGGTCTTACAGCCTTACCGGAAATATTGTGGTCTTTCTAGATCACCATCTTTAA 1811
QY      225 nLeuLeuGlnAsnLysSerMet 232
DB      1812 TTTACTTCAAAATAAAGCATG 1833

RESULT 11
ID AAF30001 standard; cDNA; 1931 BP.
AC AAF30001;
DT 23-APR-2001 (first entry)
DE Human CARD-3 cDNA.
KW CARD-3; caspase recruitment domain; human; cancer; infection;
KW autoimmune disease; neurological disease; haematological disease;
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;
KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 214..1826
FT /*tag= a
FT /note= "the open reading frame is also specifically
FT claimed in Claim 1(a)"
XX WO200100826-A2.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US017691.
XX
XX 28-JUN-1999; 99US-00340620.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J;

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XX WPI; 2001-061973/07.  
 DR P-PSDB; AAB20079.  
 XX  
 PT Isolated intracellular proteins predicted to be involved in regulating  
 PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
 PT viral infections, autoimmune diseases, neurological diseases and  
 PT hematological disorders.  
 XX  
 PS Claim 1(a); Fig 1; 208pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding human caspase recruitment  
 CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
 CC database search using known CARD sequences. Plasmid pXEL17A containing  
 CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
 CC protein predicted to be involved in regulating caspase activation. It is  
 CC useful as a modulating agent in regulating cellular processes include  
 CC cell growth and cell death. Methods of diagnosing and treating patients  
 CC suffering from a disorder associated with an abnormal level or rate of  
 CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
 CC complex, abnormal activity of the tumour necrosis factor receptor complex  
 CC or abnormal activity of a caspase involve administering a compound that  
 CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
 CC e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.  
 CC Such disorders include cancer, viral infection, autoimmune disorders,  
 CC neurological diseases, haematological disorders, inflammatory disorders  
 CC and immune disorders. CARD nucleic acids can be used to express CARD  
 CC proteins in a host cell e.g. for gene therapy applications, to detect a  
 CC genetic lesion and to modulate CARD activity  
 XX  
 SQ Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAF30001 (1-1931)  
 QY 6 LeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1153 TTACAGAGTGTTCACAGTGCCTACCTATGTGACAAAGAAATGGAATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1213 AACATACCTGTAATATGATGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1273 AATAGTGTTCCTGAACTTCAGGTCCCTGCCAGTCTCTCAAGCAATGATTTTAA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1333 TCTAGAAAGCTCAAGACTGTATTTATGAGTGCATCCTGCTGGAATTCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 DB 1393 TGGATAGCACCATTCTGGATCTCAAGGGCTGCTCTGTGATCACAAGACCAT -TCC 1451  
 QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGCTCGAGCC 1511  
 QY 125 oGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 DB 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 DB 1572 AGCCTGCTTACAGTCGGTAGTAGCCCTCTGTCCAGGACTTGTATCATGAAGAGGA 1631

QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 DB 1632 CTATGACTTGTAGTACCAAGCTTCAAGACCTCAAAAGTCAGACAATTACTAGACAC 1691  
 QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 DB 1692 TACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
 DB 1752 ACAATGGGTCTTACCGGAAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 DB 1812 TTTACTTCAAAATATAAAGCATG 1833  
 RESULT 12  
 ABK89280  
 ID ABK89280 standard; cDNA; 1931 BP.  
 XX  
 AC ABK89280;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human cDNA encoding caspase recruitment domain protein CARD-3.  
 XX  
 KW Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
 KW nuclear factor kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 214..1836  
 FT /\*tag= a  
 FT /product= "CARD-3"  
 XX  
 PN WO200253765-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 20-DEC-2001; 2001WO-US049798.  
 XX  
 PR 29-DEC-2000; 2000US-0258724P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Bertin J, Philpott D, Sansonetti P, Girardin S;  
 XX  
 XX WPI; 2002-583627/62.  
 XX  
 DR P-PSDB; ABG31075.  
 DR  
 XX  
 XX Identifying modulators of long form of caspase recruitment domain, CARD-  
 PT 4L useful for treating cancer, infections, and immune disorders, by  
 PT contacting test compound with CARD-4L and determining effect of the  
 PT compound.  
 XX  
 PS Example 2; Fig 1; 139pp; English.  
 XX  
 CC The invention relates to identifying (M1) a compound which modulates a  
 CC human or murine caspase recruitment domain (CARD)-4L (long form)  
 CC polypeptide with a by contacting the polypeptide with a test compound and  
 CC determining the effect of the test compound on the activity of the  
 CC polypeptide to identify a compound which modulates the polypeptide. The  
 CC method may be adapted for identifying a compound which binds to the LRR  
 CC (leucine rich repeat) domain of CARD-4. Also included is a method of



CC identifying a candidate compound for modulating LPS (lipopolysaccharide)-  
 CC mediated activation of nuclear factor-kappa B (NF-kB), by providing a  
 CC cell expressing a polypeptide comprising the LRR domain of CARD-4 and  
 CC harbouring LPS, exposing the cell to a test compound and measuring NF-kB  
 CC activation, where altered NF-kB activation polypeptide in the presence of  
 CC the test compound compared to the binding in the absence of the test  
 CC compound indicates that the test compound is a candidate compound for  
 CC modulating LPS-mediated activation of NF-kB. Modulators identified by  
 CC (M1) are useful for treating a disorder characterised by aberrant CARD-4  
 CC protein or nucleic acid. Compounds that modulate the activity of CARD-4L  
 CC are useful to treat or diagnose disorders such as cancer, viral  
 CC infections, autoimmune disorders e.g. systemic lupus erythematosus,  
 CC immune-mediated glomerulonephritis and arthritis, immune disorders, such  
 CC as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as  
 CC asthma, allergy, psoriasis, contact dermatitis, gastrointestinal  
 CC allergies, insulin-dependent diabetes, bacterial infections, including  
 CC tuberculosis, and lepromatous leprosy, disorders of cell signalling and  
 CC disorders of tissues. The present sequence is the human cDNA encoding  
 CC CARD-3  
 XX

SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x ABK89280 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 1153 TTACAGAGTGTTCAGTCCATTCACCTATGTGACAGAGAAATGGAATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 1213 AACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 1273 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCGCAGCTCCTCAAGACAAATGATTTTVA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 1333 TCTAGAAAGCTCAGACTGTTATTTATGAGCTGCATCAGTCTCTGGAATCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 DB 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451  
 QY 105 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 DB 1452 ATGCTCTTCAGCAATAATAATCCACTTCAACTGCAGGAATCTCAGACGCTCGAGCC 1511  
 QY 125 OGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 DB 1512 TGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAAGCATTTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 DB 1572 AGCTGCTTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 DB 1632 CTATGAACCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1691  
 QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 DB 1692 TACTGATCCCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATNACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225

DB 1752 ACAATGGGTCTTACGCTTACCGGAATACTTGTTGGTTCTAGATCACCATCTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 DB 1812 TTTACTTCAAAATAAAGCATG 1833  
 RESULT 13  
 AAL40752  
 ID AAL40752 standard; cDNA; 1931 BP.  
 XX AAL40752;  
 AC AAL40752;  
 XX 27-SEP-2002 (first entry)  
 DE CDNA of human CARD-3 SEQ ID No 1.  
 KW Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's;  
 KW cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;  
 KW nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;  
 KW cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;  
 KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
 KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
 KW anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.  
 XX Homo sapiens.  
 OS US6369196-B1.  
 PN 09-APR-2002.  
 PD 05-FEB-1999; 98US-00245281.  
 PF 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA Bertin J;  
 PI WPI: 2002-391988/42.  
 DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.  
 XX Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's disease, cancers and viral infections.  
 PS Example 2; Fig 1; 116pp; English.  
 XX The invention relates to novel isolated Caspase Recruitment Domain (CARD) polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This polynucleotide sequence represents the cDNA of a human CARD relating to the invention  
 SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.9e-119 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0

XX	OS	Homo sapiens.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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```

Db      1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTGCTCTGGAATCACAGT 1392
QY      86  TTPASerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrPr 105
Db      1393 TGGGATAGACCACTTCTGGATCTCAAGGGGTGCATTTCTGTGATCACAGACCAT-TCC 1451
QY      105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db      1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAAGCTCTGCAGCC 1511
QY      125 oGlyIleAlaGlnGlnTrpIleGlnSerIlySargGluAspIleValAsnGlnMetThrGl 145
Db      1512 TGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571
QY      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db      1572 AGCCTGCTTACCAAGCTCGTAGATGCCCTCTGTCAGGAGCTTGATCATGAAGAGA 1631
QY      165 pTyrGluLeuValSerThrIlyProThrArgThrSerIlySargValArgGlnLeuLeuAspTh 185
Db      1632 CTATGAACCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691
QY      185 rThrAspIleGlnGlyGluGluPheAlaIlyValIleValGlnIlyLeuLysAspAsnly 205
Db      1692 TACTGACATCCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1751
QY      205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225
Db      1752 ACNATGGGCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1811
QY      225 nLeuLeuGlnAsnLysSerMet 232
Db      1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 15
ADB81363
ID      ADB81363 standard; cDNA; 1931 BP.
XX
AC      ADB81363;
XX
DT      04-DEC-2003 (first entry)
XX
DE      Human caspase recruitment domain 3 (CARD-3) cDNA.
XX
KW      human; ss; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;
KW      p75; tumour necrosis factor; TNF; neutrophin receptor; cancer;
KW      autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;
KW      viral infection; neurological; retinitis pigmentosa; haematologic;
KW      chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAX.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      CDS 214..1836
FT      /*tag= a
FT      /product= "CARD-3 protein"
XX
US2002061833-A1.
XX
PD      23-MAY-2002.
XX
XX      26-DEC-2000; 2000US-00748537.
XX
PR      06-FEB-1998; 98US-00019942.
PR      17-JUN-1998; 98US-00099041.
XX
XX      (BERT/) BERTIN J.
XX      (CHAO/) CHAO M V.
PI      Bertin J, Chao MV;
XX
XX      WPI; 2003-657125/62.
DR

```

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DR      P-PSDB; ADB81362.
XX
PT      Detecting compounds which alter binding of the caspase recruitment domain
PT      (CARD)-3 polypeptide to the neutrophin receptor p75 is useful
PT      to provide compounds for treating CARD-3 mediated disorders.
XX
PS      Disclosure; Fig 2; 40pp; English.
XX
XX      This invention relates to two novel genes CARD-3 and CARD-4 (caspase
CC      recruitment domains), which are mediators of apoptosis and are useful in
CC      the identification of compounds that modulate apoptosis. Specifically,
CC      CARD-3 (also known as RLP2, RICK and CARDIAX) is known to be a mediator
CC      of p75 (a member of the tumour necrosis factor (TNF) family), and is
CC      believed to provide the switch for cell survival and cell death decisions
CC      mediated by this p75 neutrophin receptor. Accordingly these genes, and
CC      the proteins encoded thereof, are linked to certain disorders associated
CC      with an increased number of cells surviving and proliferating when
CC      apoptosis is inhibited. These include cancer, autoimmune disorders e.g.
CC      systemic lupus and immune mediated glomerulonephritis, viral infections
CC      such as those caused by the herpesvirus, neurological disorders such as
CC      retinitis pigmentosa, haematologic diseases including chronic
CC      neutropenia, as well as myocardial infarction and strokes. The present
CC      invention further describes a novel method for determining whether a test
CC      compound alters the binding of CARD-3 to p75, which comprises measuring
CC      the binding of a polypeptide containing the CARD domain of CARD-3 to a
CC      polypeptide comprising the death domain of p75 in the presence and
CC      absence of the test compound, and determining if binding is altered. This
CC      polynucleotide is the human CARD-3 cDNA sequence of the invention.
XX
SQ      Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      6.9e-119      Length:      1931
Score:          128.00      Matches:      226
Percent Similarity: 99.12%      Conservative: 0
Best Local Similarity: 99.12%      Mismatches: 1
Query Match:      55.17%      Indels:      2
DB:              9          Gaps:      0

US-09-771-161A-93 (1-232) x ADB81363 (1-1931)
QY      6  LeuGlnSerValSerSerAlaIleHisIleCysAspLysLysMetGluLeuSerLeu 25
Db      1153 TTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTTATCTCTG 1212
QY      26  AnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHisGlu 45
Db      1213 AACATCTCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY      46  AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      1273 AATAGTGGTTCTCTGAAACTTCAAGGTCCTGCCAGCTCTCTCAAGACAATGATTTTTA 1332
QY      66  SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db      1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTGCTCTGGAATCACAGT 1392
QY      86  TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrPr 105
Db      1393 TGGGATAGACCACTTCTGGATCTCAAGGGGTGCATTTCTGTGATCACAGACCAT-TCC 1451
QY      105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db      1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAAGCTCTGCAGCC 1511
QY      125 oGlyIleAlaGlnGlnTrpIleGlnSerIlySargGluAspIleValAsnGlnMetThrGl 145
Db      1512 TGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571
QY      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db      1572 AGCCTGCTTACCAAGCTCGTAGATGCCCTCTGTCAGGAGCTTGATCATGAAGAGA 1631

```

QY	165	pTyrGluLeuValSerThrIysProThrArgThrSerLysValArgGlnLeuLeuAsp	185
Db	1632	CTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTACTAGACAC	1691
QY	185	rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp	205
Db	1692	TACTGACATCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAACAA	1751
QY	205	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225
Db	1752	ACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCACTTTTAA	1811
QY	225	nLeuLeuGlnAsnLysSerMet	232
Db	1812	TTTACTTCAAAATAAAAGCATG	1833

Search completed: April 1, 2004, 12:58:53  
Job time : 485 secs



CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies, and  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Query Match 64.6%; Score 1079; DB 3; Length 2709;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCAGAGGCCATTCCACCTATGTGACAGAGAGAAAATGGAATTAATCTC 392  
DB 1204 AGTTACAGAGTGTTCAGAGGCCATTCCCTATGTGACAGAGAGAAAATGGAATTAATCTC 1263  
QY 393 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
DB 1264 TGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1323  
QY 453 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAAATGATTTT 512  
DB 1324 AAAATAGTGGTTCCTGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAAATGATTTT 1383  
QY 513 TATCTGAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCACTACTGTCCTGGAATCACA 572  
DB 1384 TATCTGAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCACTACTGTCCTGGAATCACA 1443  
QY 573 GTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 632  
DB 1444 GTTGGGAYAGCACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACTC 1503  
QY 633 CATGCTCTTCAGCAATTAATTAATCCACTCTCAACTGAGGAACTCAGACGCTGCGAGC 692  
DB 1504 CATGCTCTTCAGCAATTAATTAATCCACTCTCAACTGAGGAACTCAGACGCTGCGAGC 1563  
QY 693 CTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 752  
DB 1564 CTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAG 1623  
QY 753 AAGCCTCCCTTAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGCATCATGAAGAGG 812  
DB 1624 AAGCCTCCCTTAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGCATCATGAAGAGG 1683  
QY 813 ACTATGAACCTTTAGTACCAAGCTCAGAGCTCCTCAAGAGTCAAGCAATTAAGTACACA 872  
DB 1684 ACTATGAACCTTTAGTACCAAGCTCCTCAAGAGTCAAGCAATTAAGTACACA 1743  
QY 873 CTACTGACATCCAAAGGAGAGAAATTTGCAAGTATAGTACAAAATTTGAAAGATACACA 932  
DB 1744 CTACTGACATCCAAAGGAGAGAAATTTGCAAGTATAGTACAAAATTTGAAAGATACACA 1803  
QY 933 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCCTAGATCAACCATCTTTAA 992  
DB 1804 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCCTAGATCAACCATCTTTAA 1863  
QY 993 ATTTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052  
DB 1864 ATTTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1923

QY 1053 AAGGATATTTATATCTCTCTGTTGACTTTTTTTATATAAAATCCGTCAGTATTAAG 1112  
DB 1924 AAGGATATTTATATCTCTCTGTTGACTTTTTTTATATAAAATCCGTCAGTATTAAG 1983  
QY 1113 CTTTATGAGGTTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTCGCAGTATTTTT 1172  
DB 1984 CTTTATGAGGTTCTTTGGGTAATAATATAGTCTCCCTCCATGACACTCGCAGTATTTTT 2043  
QY 1173 TTAATTAATACAGTAAGTAAGTTGAAATTTGCTACATAGTTCAATTTTATGCTCTCTTT 1232  
DB 2044 TTAATTAATACAGTAAGTAAGTTGAAATTTGCTACATAGTTCAATTTTATGCTCTCTTT 2103  
QY 1233 TGTAAACAGAAACCACTTTTAAAGGATAGTAATATTTCTTTTATAACAGTCGCTTAAG 1292  
DB 2104 TGTAAACAGAAACCACTTTTAAAGGATAGTAATATTTCTTTTATAACAGTCGCTTAAG 2163  
QY 1293 GTAAGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTCATGATTAATTTGTT 1352  
DB 2164 GTATGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTCATGATTAATTTGTT 2223  
QY 1353 ACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCACGACAGACAGT 1412  
DB 2224 ACTTGTCTAARAWGCAATTTGATTTTATGAAGTATATACCTTTACCCACGACAGACAGT 2283  
QY 1413 ACAGAAATCCCTGCTTAAATCCAGGCTTAATTTGCCCTACAAAGGGTTATTAATTTAA 1472  
DB 2284 ACAGAAATCCCTGCTTAAATCCAGGCTTAATTTGCCCTACAAAGGGTTATTAATTTAA 2343  
QY 1473 ACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAATTCCTTTTAAATGATAT 1532  
DB 2344 ACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAATTCCTTTTAAATGATAT 2403  
QY 1533 TTCAAAGGTAAACCAATACAAATAAAGAAATAAATAATATATATATATACCGGCTTCCCTG 1592  
DB 2404 TTCAAAGGTAAACCAATACAAATAAAGAAATAAATAATATATATATATACCGGCTTCCCTG 2463  
QY 1593 TCCCAATTTTAACTCAGCCTTCCCTACTGTCCACCAACCAAGCTAAATAAGTCAA 1652  
DB 2464 TCCCAATTTTAACTCAGCCTTCCCTACTGTCCACCAACCAAGCTAAATAAGTCAA 2523  
QY 1653 CAGCCTGATGTGTA 1666  
DB 2524 CAGCCTGATGTGTA 2537  
RESULT 2  
AAZ46143  
ID AAZ46143 standard; cDNA; 2024 BP.  
XX  
AC AAZ46143;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA sequence encoding a human phosphorylation effector PHSP-6.  
XX  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 203..1825  
FT /\*tag= a  
FT /product= "phosphorylation effector"  
XX  
PN WO200006728-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 28-JUL-1999; 99WO-US017132.  
XX  
PR 28-JUL-1998; 98US-0155213P.  
PR 14-SEP-1998; 98US-0155196P.

PR 14-OCT-1998; 98US-01552339P.  
PR 03-NOV-1998; 98US-0106889P.  
PR 19-NOV-1998; 98US-0109093P.  
PR 22-DEC-1998; 98US-0113796P.  
PR 12-JAN-1999; 99US-0155233P.  
XX (INCY-) INCYTE PHARM INC.  
PA Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX WPI; 2000-183125/16.  
DR P-PSDB; AAY68774.  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 9; Page 121-122; 142pp; English.  
XX AA246138-246168 encode human phosphorylation effectors (PHSP), designated  
CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the  
CC specification). The sequences were isolated from cDNA libraries prepared  
CC from various human tissues. The PHSP proteins are useful for the  
CC diagnosis, treatment and prevention of proliferative disorders, immune  
CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical  
CC compositions which useful for treating or preventing disorders associated  
CC with decreased PHSP expression/activity. PHSP antagonists are useful for  
CC treating or preventing disorders associated with increased PHSP  
CC expression/activity  
XX  
SQ Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;  
Query Match 52.7%; Score 879; DB 3; Length 2024;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 879; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCAGGTGCGCATTCACCTATGTGACAGAGAAATGGAATTATCTC 392  
DB 1140 AGTTACAGAGTGTTCAGGTGCGCATTCACCTATGTGACAGAGAAATGGAATTATCTC 1199  
QY 393 TGAACATAGCTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGTCCATG 452  
DB 1200 TGAACATAGCTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGTCCATG 1259  
QY 453 AAAATAGTGTCTCTGAAATCTCAAGGTCCCTGCGAGTCTCTCAAGACAATGATTTT 512  
DB 1260 AAAATAGTGTCTCTGAAATCTCAAGGTCCCTGCGAGTCTCTCAAGACAATGATTTT 1319  
QY 513 TATCTAGAAAAGCTCAAGACTGTATTATTAAGAGTGCATCACTCTCTGGAAATCACA 572  
DB 1320 TATCTAGAAAAGCTCAAGACTGTATTATTAAGAGTGCATCACTCTCTGGAAATCACA 1379  
QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 632  
DB 1380 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 1439  
QY 633 CATGCTCTTCAGCAATAATAATCACTCTCAACTGAGAACTCAGAAAGTCTGCAGC 692  
DB 1440 CATGCTCTTCAGCAATAATAATCACTCTCAACTGAGAACTCAGAAAGTCTGCAGC 1499  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGAAACCAATGACAG 752  
DB 1500 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGAAACCAATGACAG 1559  
QY 753 AGCCTGCTTAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTGTGATCATGAAGAGG 812  
DB 1560 AGCCTGCTTAACAGTGCCTAGATGCCCTTCTGTCCAGGGACTGTGATCATGAAGAGG 1619  
QY 813 ACTATGAACTGTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCAAGCAATTAAGACA 872  
DB 1620 ACTATGAACTGTGTAGTACCAAGCCCTACAGGACCTCAAAAGTCAAGCAATTAAGACA 1679

QY 873 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
DB 1680 CTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1739  
QY 933 AACAAATGGGTCTTCAGCGCTTACCCGGAATACTTTGGTGTCTAGATCACCATCTTTAA 992  
DB 1740 AACAAATGGGTCTTCAGCGCTTACCCGGAATACTTTGGTGTCTAGATCACCATCTTTAA 1799  
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACCTTTTATATAAAATCCGTCGATATAAG 1112  
DB 1800 ATTTACTTCAAAATAAAAGCATGTAAAGTACCTTTTATATAAAATCCGTCGATATAAG 1919  
QY 1113 CTTTATGAAGTCTCTTTGGGTAATAATTTAGTCTCCCTCCATGACACTGCAGTATTTTT 1172  
DB 1920 CTTTATGAAGTCTCTTTGGGTAATAATTTAGTCTCCCTCCATGACACTGCAGTATTTTT 1979  
QY 1173 TTAATTAATACAAAGTAAAGATTTTGAATTTTGTCTACATA 1211  
DB 1980 TTAATTAATACAAAGTAAAGATTTTGAATTTTGTCTACATA 2018  
RESULT 3  
AAK94554  
ID AAK94554 standard; cDNA; 2033 BP.  
XX AAK94554;  
AC AAK94554;  
XX DT 06-NOV-2001 (first entry)  
XX Human full-length cDNA, SEQ ID NO: 3453.  
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX Homo sapiens.  
XX EP1130094-A2.  
XX PD 05-SEP-2001.  
XX PF 07-JUL-2000; 2000EP-00114089.  
XX PR 08-JUL-1999; 99JP-00194486.  
XX PR 11-JAN-2000; 2000JP-00118774.  
XX PR 02-MAY-2000; 2000JP-00183765.  
XX (HELI-) HELIX RES INST.  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
XX DR P-PSDB; AAM93621.  
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
XX Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly

CC from BPO  
 XX Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;  
 SQ  
 Query Match 49.6%; Score 827; DB 4; Length 2033;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 877; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 333 AGTTACAGAGTGTTCAGTGCCTTACCTATCTGTGACAGAGAAATGAATATATCTC 392  
 DB 1156 AGTTACAGAGTGTTCAGTGCCTTACCTATCTGTGACAGAGAAATGAATATATCTC 1215  
 QY 393 TGAACATACCTGTAAATCATGTGCCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452  
 DB 1216 TGAACATACCTGTAAATCATGTGCCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1275  
 QY 453 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGGTCCTCCAGACAAATGATTTT 512  
 DB 1276 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGGTCCTCCAGACAAATGATTTT 1335  
 QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCTATCTGTGATCACAAGACCACTC 572  
 DB 1336 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCTATCTGTGATCACAAGACCACTC 1395  
 QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACTC 632  
 DB 1396 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACTC 1455  
 QY 633 CATGCTCTTACGAAATTAATCACTCTCACTGAGGAACTCAGAGCTGCGAGC 692  
 DB 1456 CATGCTCTTACGAAATTAATCACTCTCACTGAGGAACTCAGAGCTGCGAGC 1515  
 QY 693 CTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAG 752  
 DB 1516 CTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGCAACCAATGACAG 1575  
 QY 753 AAGCTCGCTTAAACAGTGGTATGATCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 812  
 DB 1576 AAGCTCGCTTAAACAGTGGTATGATCCCTTCTGTCCAGGACTTGCATCATGAAGAGG 1635  
 QY 813 ACTATGACTGTGTAGTACCAAGCTCAGAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGAC 872  
 DB 1636 ACTATGACTGTGTAGTACCAAGCTCAGAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGAC 1695  
 QY 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATGCAAGATACCA 932  
 DB 1696 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATGCAAGATACCA 1755  
 QY 933 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 992  
 DB 1756 AACAAATGGGTCTTTCAGCTTACCCGGAATATCTGTGGTTCTAGATCAACCATCTTTAA 1815  
 QY 993 ATTTACTTCAAAATAAAGCATGTAGTGTGTTTTCAGAGAAATGTGTTTCATAA 1052  
 DB 1816 ATTTACTTCAAAATAAAGCATGTAGTGTGTTTTCAGAGAAATGTGTTTCATAA 1875  
 QY 1053 AAGGATATTTATATCTCTGTGCTTTCGACATTTTTTTATATAAAATCCGTGAGTATTAAG 1112  
 DB 1876 AAGGATATTTATATCTCTGTGCTTTCGACATTTTTTTATATAAAATCCGTGAGTATTAAG 1935  
 QY 1113 CTTTATTAAGAGTCTTTGGTAAATATAGTCTCCCTCCATGACACATGCGAGTATTTTT 1172  
 DB 1936 CTTTATTAAGAGTCTTTGGTAAATATAGTCTCCCTCCATGACACATGCGAGTATTTTT 1995  
 QY 1173 TTAATTAACAAGTAAAGTTTGAATTTTGTACAT 1210  
 DB 1996 TTAATTAACAAGTAAAGTTTGAATTTTGTACAT 2033

RESULT 4  
 ABK51169  
 ID ABK51169 standard; cDNA; 2501 BP.  
 XX

AC ABK51169;  
 XX 30-JUL-2002 (first entry)  
 DT  
 XX cDNA encoding human cellular kinase RICK protein.  
 DE  
 XX Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human cellular kinase RICK"  
 XX  
 PN EF1201765-A2.  
 XX  
 XX 02-MAY-2002.  
 XX  
 XX 15-OCT-2001; 2001EP-00124604.  
 XX  
 XX 16-OCT-2000; 2000US-0240750P.  
 PR  
 XX (AXXI-) AXIMA PHARM AG.  
 PA  
 XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
 PI  
 XX WPI; 2002-373930/41..  
 DR P-PSDB; AAU80369.  
 XX  
 XX Identifying agents for treatment or prevention of cytomegalovirus  
 PT infection, comprises contacting test compound with cellular kinase and  
 PT detecting change in cellular kinase activity.  
 XX  
 XX Disclosure; Page 20-23; 49pp; English.  
 PS  
 XX The present invention relates to a new method for identifying compounds  
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
 CC related diseases. The method of the invention comprises contacting a test  
 CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
 CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
 CC activity. The method of the invention can be used to treat and/or prevent  
 CC CMV infections and related diseases. Oligonucleotides that can detect the  
 CC specified kinases can also be used for diagnosis of infection. The  
 CC present nucleic acid sequence encodes the human cellular kinase RICK  
 CC protein of the invention, as described above  
 XX  
 SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
 Query Match 48.7%; Score 812; DB 6; Length 2501;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 333 AGTTACAGAGTGTTCAGTGCCTTACCTATCTGTGACAGAGAAATGAATATATCTC 392  
 DB 1162 AGTTACAGAGTGTTCAGTGCCTTACCTATCTGTGACAGAGAAATGAATATATCTC 1221  
 QY 393 TGAACATACCTGTAAATCATGTGCCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452  
 DB 1222 TGAACATACCTGTAAATCATGTGCCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1281  
 QY 453 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGGTCCTCCAGACAAATGATTTT 512  
 DB 1282 AAAATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGGTCCTCCAGACAAATGATTTT 1341  
 QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCTATCTGTGATCACAAGACCACTC 572  
 DB 1342 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCTATCTGTGATCACAAGACCACTC 1401  
 QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACTC 632  
 DB 1402 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCAATCTGTGATCACAAGACCACTC 1461



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QY 633 CATGCTCTTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC 692
Db 1462 CATGCTCTTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACTCTGCAGC 1521
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752
Db 1522 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1581
QY 753 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1582 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 1641
QY 813 ACTATGAACCTTGTATGATACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872
Db 1642 ACTATGAACCTTGTATGATACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 1701
QY 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1702 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1761
QY 933 AACAAATGGGCTCTCAGCCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTTAA 992
Db 1762 AACAAATGGGCTCTCAGCCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTTAA 1821
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052
Db 1822 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1881
QY 1053 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1112
Db 1882 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1941
QY 1113 CTTTATTTGAAGTCTTTCGGTAAATATTAGTCTCCCTCATGACACTGCAGTATTTTTT 1172
Db 1942 CTTTATTTGAAGTCTTTCGGTAAATATTAGTCTCCCTCATGACACTGCAGTATTTTTT 2001
QY 1173 TTAATTAATACAAGTAAAAAGTT 1195
Db 2002 TTAATTAATACAAGTAAAAAGTT 2024

RESULT 5
AAD45172
ID AAD45172 standard; DNA; 2501 BP.
XX AC AAD45172;
XX DT 27-DEC-2002 (first entry)
XX DE Human receptor interacting protein (RIP)2 DNA.
XX KW Human; receptor interacting protein; RIP2; antisense; gene therapy; gene
XX ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 225..1847
XX FT /*tag= a
XX FT /product= "Human RIP2 protein"
XX PN US6426221-B1.
XX PP 30-JUL-2002.
XX PR 01-AUG-2001; 2001US-00920663.
XX PR 01-AUG-2001; 2001US-00920663.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Ward DT, Cowsert LM;
XX PI
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XX WPI; 2002-673017/72.
DR P-PSDB; AAE27882.
XX PT New antisense oligonucleotide that targets regions of a nucleic acid
PT encoding human receptor interacting protein (RIP)2, for treating diseases
PT associated with RIP2 expression.
XX PS Claim 1; Col 49-54; 35pp; English.
XX CC The invention relates to antisense compounds targeted to a nucleic acid
CC encoding human receptor interacting protein (RIP)2 to inhibit its
CC expression. Antisense compounds are used for treating diseases associated
CC with RIP2 expression. They are also useful in antisense gene therapy. The
CC present sequence is human RIP2 DNA
XX SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Query Match 48.7%; Score 812; DB 6; Length 2501;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACACAGTGTTCCTCAAGTGCCTTCACTTATGTGACAAAGAGAAATGGAAATTTATCTC 392
Db 1162 AGTTACACAGTGTTCCTCAAGTGCCTTCACTTATGTGACAAAGAGAAATGGAAATTTATCTC 1221
QY 393 TGAACATACCTGTAAATCATGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452
Db 1222 TGAACATACCTGTAAATCATGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1281
QY 453 AAAATAGTGGTCTCTGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTTTT 512
Db 1282 AAAATAGTGGTCTCTGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTTTT 1341
QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCCTGCTGAAATCACA 572
Db 1342 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCCTGCTGAAATCACA 1401
QY 573 GTTGGATAGCACCAATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCCTC 632
Db 1402 GTTGGATAGCACCAATTTCTGGTCTCAAAGGGCTGCATTTCTGTGATCACAAGACCCTC 1461
QY 633 CATGCTCTTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAGC 692
Db 1462 CATGCTCTTTCAGCAATAAATAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCAGC 1521
QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752
Db 1522 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1581
QY 753 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 812
Db 1582 AAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGG 1641
QY 813 ACTATGAACCTTGTATGATACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 872
Db 1642 ACTATGAACCTTGTATGATACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGACA 1701
QY 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 932
Db 1702 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACA 1761
QY 933 AACAAATGGGCTCTCAGCCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTTAA 992
Db 1762 AACAAATGGGCTCTCAGCCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATTCTTTAA 1821
QY 993 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1052
Db 1822 ATTTACTTCAAAATAAAAGCATGTAAAGTACTGTTTTTCAAGAGAAATGTGTTTCATAA 1881
QY 1053 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1112
Db 1882 AAGGATATTTATATCTCTGCTTGTGACTTTTTTATATAAAATCCGAGATATAAG 1941
```

QY 1113 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 1172  
 Db 1942 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 2001  
 QY 1173 TTAATTAATCAAGTAAAGTT 1195  
 Db 2002 TTAATTAATCAAGTAAAGTT 2024

RESULT 6  
 AA248762  
 ID AA248762 standard; cDNA; 2502 BP.

XX AC AA248762;  
 XX DT 21-MAR-2000 (first entry)  
 XX DE Human RICK coding sequence.

XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.  
 XX OS Homo sapiens.

XX WO995134-A2.  
 XX PD 04-NOV-1999.  
 XX PF 27-APR-1999; 99WO-US009183.  
 XX PR 27-APR-1998; 98US-00069023.  
 XX PA (UNMI ) UNIV MICHIGAN.

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XX PI Nunez G, Inohara N, Koseki T;  
 XX WPI; 2000-072163/06.  
 XX DR P-PSDE; AAY59404.

XX PT Compositions for identifying apoptosis signaling pathway inhibitors  
 XX PT useful for treating diseases.  
 XX PS Claim 8; Fig 7b; 93pp; English.

XX This sequence encodes the human RICK (RIP-like interacting CLARP kinase)  
 CC protein of the invention. The RICK protein acts as a positive regulator  
 CC of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. Antirick antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates

XX SQ Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;.  
 Query Match 48.7%; Score 812; DB 3; Length 2502;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 862; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 333 AGTTACAGAGTGTTCACAGTGCCATTACCTATGTGACAGAGAAATGGAATATCTC 392  
 Db 1163 AGTTACAGAGTGTTCACAGTGCCATTACCTATGTGACAGAGAAATGGAATATCTC 1222  
 QY 393 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 452  
 Db 1223 TGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATG 1282  
 QY 453 AAAATAGTGGTCTCCTGAAACCTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT 512  
 Db 1283 AAAATAGTGGTCTCCTGAAACCTTCAAGGTCCCTGCAGCTCCTCAAGACAATGATTTTT 1342  
 QY 513 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTGGAAATCACA 572  
 Db 1343 TATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTGGAAATCACA 1402  
 QY 573 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCAACAGCACCCTC 632  
 Db 1403 GTTGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCAACAGCACCCTC 1462  
 QY 633 CATGCTCTCAGCAATAAATCACTCTCAACTCAGAGAACTCAGAACGTCCTGAGC 692  
 Db 1463 CATGCTCTCAGCAATAAATCACTCTCAACTCAGAGAACTCAGAACGTCCTGAGC 1522  
 QY 693 CTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 752  
 Db 1523 CTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGAAGACATTTGGAACCAATGACAG 1582  
 QY 753 AAGCCTGCCTTAAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGG 812  
 Db 1583 AAGCCTGCCTTAAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGG 1642  
 QY 813 ACTATGAACCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAACTACTAGACA 872  
 Db 1643 ACTATGAACCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAACTACTAGACA 1702  
 QY 873 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 Db 1703 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1762  
 QY 933 AACAAATGGGTCTTACAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 992  
 Db 1763 AACAAATGGGTCTTACAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1822  
 QY 993 ATTACTTCAAAATAAAGCATGTAGTCACTGTTTTTCAAGAGAAATGTGTTTCATTA 1052  
 Db 1823 ATTACTTCAAAATAAAGCATGTAGTCACTGTTTTTCAAGAGAAATGTGTTTCATTA 1882  
 QY 1053 AAGGATATTTATATCTCTGTGCTGCTTTTATATAAATCCGTGAGTATTAAG 1112  
 Db 1883 AAGGATATTTATATCTCTGTGCTGCTTTTATATAAATCCGTGAGTATTAAG 1942  
 QY 1113 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 1172  
 Db 1943 CTTTATTGAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTT 2002  
 QY 1173 TTAATTAATCAAGTAAAGTT 1195  
 Db 2003 TTAATTAATCAAGTAAAGTT 2025

RESULT 7  
 ADC99131  
 ID ADC99131 standard; cDNA; 1959 BP.  
 XX AC ADC99131;

XX	01-JAN-2004 (first entry)	1158	AGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTGAACTTCAAGGT	1217
XX	Human KPP CDNA - SEQ ID 84.	483	CCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTATTTTA	542
XX	anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;	1218	CCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTATTTTA	1277
XX	nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;	543	TGAAGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTGGATCTCAAA	602
XX	immunosuppressive; antithyroid; cytosstatic; hepatotropic; dermatological;	1278	TGAAGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTGGATCTCAAA	1337
XX	antidiabetic; nephrotropic; angiot; thyromimetic; neuroprotective;	603	GGGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTGGATCTCAAA	662
XX	osteopathic; antiarthritic; antiparasitic; antihelminthic; antiporiatic;	1338	GGGCTGCATCCTCTCTGGAAATCAAGTTGGATAGCACCATTCTGGATCTCAAA	1397
XX	uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;	663	CAACTGCAGGAACTCAGAACCTCTGCAGCTGGTATAGCCAGCAGTGGATCCAGAGCA	722
XX	virucide; protozoacide; fungicide; kinase; phosphatase; KPP;	1398	CAACTGCAGGAACTCAGAACCTCTGCAGCTGGTATAGCCAGCAGTGGATCCAGAGCA	1457
XX	cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;	723	AAAGGAAAGACATTTGTGAACCAATGACAGAGCTGGCTTAAACAGTCGCTAGATGCC	782
XX	cancer; developmental; mental retardation; neurological;	1458	AAAGGAAAGACATTTGTGAACCAATGACAGAGCTGGCTTAAACAGTCGCTAGATGCC	1517
XX	Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;	783	TTCTGTCCAGGACTTGTATGATGAAAGAGGACTATGAACTTGTAGTACCAAGCTTACAA	842
XX	diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;	1518	TTCTGTCCAGGACTTGTATGATGAAAGAGGACTATGAACTTGTAGTACCAAGCTTACAA	1577
XX	helminthic infection; transgenic; gene therapy; human; ss; gene.	843	GGACCTCAAAAGTCAAGCAATTTACTAGACACTTACTGACATCCAAAGAGAGAAATTTGCCA	902
OS	Homo sapiens.	1578	GGACCTCAAAAGTCAAGCAATTTACTAGACACTTACTGACATCCAAAGAGAGAAATTTGCCA	1637
XX	WO2003033680-A2.	903	AAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA	962
XX	24-APR-2003.	1638	AAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAAA	1697
XX	17-OCT-2002; 2002WO-US033723.	963	TACTTGTGGTTTCTAGATCACCCTTTTAAATTTACTTCAAAATAAAGCATGTAGTGA	1022
XX	19-OCT-2001; 2001US-0345474P.	1698	TACTTGTGGTTTCTAGATCACCCTTTTAAATTTACTTCAAAATAAAGCATGTAGTGA	1757
XX	02-NOV-2001; 2001US-0343910P.	1023	CTGTTTTCACAAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTCTGCTTGGCT	1082
XX	13-NOV-2001; 2001US-0333098P.	1758	CTGTTTTCACAAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTCTGCTTGGCT	1817
XX	16-NOV-2001; 2001US-0332424P.	1083	TTTTTATATAAAATCCGTGAGTATTTAAAGCTTTTATGAAGCTTTCTTTGGGTAAATATTA	1142
XX	30-NOV-2001; 2001US-0334288P.	1818	TTTTTATATAAAATCCGTGAGTATTTAAAGCTTTTATGAAGCTTTCTTTGGGTAAATATTA	1877
XX	(INCY-) INCYTE GENOMICS INC.	1143	GTCTCCCTCCATGACACTGCAGTATTTTAAATTAATACAAAGTAAAGTTTGAATTT	1202
XX	Bandnan O, Baughn MR, Becha SD, Borowsky M, Duggan BM;	1878	GTCTCCCTCCATGACACTGCAGTATTTTAAATTAATACAAAGTAAAGTTTGAATTT	1937
XX	Emerling BM, Forsythe ID, Gandhi AR, Gorvad AE, Griffin JA;	1203	TGCTA 1207	
XX	Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;	1938	TGCTA 1942	
XX	Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;			
XX	Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;			
XX	Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;			
XX	Zebarjadian Y;			
XX	WPI; 2003-403214/38.			
XX	P-PSDB; ADC99079.			
XX	New human kinases and phosphatases and polynucleotides, useful for			
XX	diagnosing, treating or preventing autoimmune or inflammatory disorders			
XX	(e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,			
XX	cancer or hepatitis.			
XX	Claim 5; SEQ ID NO 84; 424pp; English.			
XX	The invention relates to a novel isolated polypeptide which is a human			
XX	kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,			
XX	agonists and antagonists are useful for diagnosing, treating or			
XX	preventing cell proliferative disorders such as atherosclerosis,			
XX	cirrhosis, hepatitis and cancer, developmental disorders e.g. mental			
XX	retardation, neurological disorders including Alzheimer's disease and			
XX	Parkinson's disease, autoimmune and inflammatory disorders such as			
XX	Crohn's disease and diabetes mellitus and finally, viral, bacterial,			
XX	fungal, parasitic, protozoan or helminthic infections. Furthermore, the			
XX	polynucleotides encoding KPP may be useful for creating transgenic			
XX	animals to model human disease, as well as during gene therapy			
XX	procedures. The current sequence is that of the human KPP CDNA of the			
XX	invention.			
XX	Sequence 1959 BP; 597 A; 430 C; 420 G; 512 T; 0 U; 0 Other;			
XX	Query Match 47.0%; Score 785; DB 9; Length 1959;			
XX	Best Local Similarity 100.0%; Pred. No. 0;			
XX	Matches 785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
XX	423 AGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTGAACTTCAAGGT			

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CC domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
CC murine CARD-4L protein and genes. The genes and proteins of the invention  
CC are involved in the regulation of caspase activation. The caspase  
CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
CC antibodies can be used in screening assays, detection assays, predictive  
CC medicine and therapeutic and prophylactic methods of treatment. The  
CC methods may be used to diagnose and treat patients which are suffering  
CC from a disorder associated with abnormal level or rate of apoptotic cell  
CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
CC Diseases that may be treated include cancer (particularly follicular  
CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
CC CARD-3 protein interacts with other cellular proteins, and so can be used  
CC for regulation of cellular proliferation and differentiation and cell  
CC survival. The CARD proteins may also be used to for screen drugs or  
CC compounds which modulate their activity. The CARD-4 gene can express a  
CC long transcript that encodes CARD-4L, a short transcript that encodes  
CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
CC encodes the human CARD-3 protein described in the method of the invention  
XX  
SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;  
Query Match 40.9%; Score 682; DB 2; Length 1931;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 712; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 333 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 392  
DB 1151 AGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 1210  
QY 393 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTAGCTCCATG 452  
DB 1211 TGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTAGCTCCATG 1270  
QY 453 AAAATAGTGGTCTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTTT 512  
DB 1271 AAAATAGTGGTCTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTTT 1330  
QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGAAATCACA 572  
DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGAAATCACA 1390  
QY 573 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 632  
DB 1391 GTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCACTC 1450  
QY 633 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGC 692  
DB 1451 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACCTCAGAACCTCTGCAGC 1510  
QY 693 CTGGTATAGCCAGCAGTGGATCCAGACAAAGGAAGACATTTGGAACCAATGACAG 752  
DB 1511 CTGGTATAGCCAGCAGTGGATCCAGACAAAGGAAGACATTTGGAACCAATGACAG 1570  
QY 753 AAGCCTGCTTTAACCAAGTGCAGTATGCTTCTGTCCAGGACCTTGATCATCAAGAGAG 812  
DB 1571 AAGCCTGCTTTAACCAAGTGCAGTATGCTTCTGTCCAGGACCTTGATCATCAAGAGAG 1630  
QY 813 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGGACCTTACTAGACA 872  
DB 1631 ACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAGGACCTTACTAGACA 1690  
QY 873 CTACTCACATCCAAAGCAGAGAAATTTGCAAGCTTATAGTACAAAATTTGAAGATAACA 932  
DB 1691 CTACTCACATCCAAAGCAGAGAAATTTGCAAGCTTATAGTACAAAATTTGAAGATAACA 1750  
QY 933 AACAAATGGGTCTTTCAGCCTTACCCCGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 992

DB 1751 AACAAATGGGTCTTTCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTAA 1810  
QY 993 ATTTACTTTCAAAATAAAAGCATGTAAAGTCACTGTTTTTCAAGAAAGAAATGTTTCATAA 1052  
DB 1811 ATTTACTTTCAAAATAAAAGCATGTAAAGTCACTGTTTTTCAAGAAAGAAATGTTTCATAA 1870  
QY 1053 AAGGATATTATA 1065  
DB 1871 AAGGATATTATA 1883  
RESULT 10  
AAF30001  
ID AAF30001 standard; cDNA; 1931 BP.  
XX  
AC AAF30001;  
XX  
DT 23-APR-2001 (first entry)  
XX Human CARD-3 cDNA.  
DE  
XX CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antinflammatory; apoptosis; diagnosis; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 214..1826  
FT /\*tag= a  
FT /note= "the open reading frame is also specifically  
FT claimed in Claim 1(a)"  
XX  
PN WO200100826-A2.  
XX  
PD 04-JAN-2001.  
XX  
XX 28-JUN-2000; 2000WO-US017691.  
XX 28-JUN-1999; 99US-00340620.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Bertin J;  
XX WPI; 2001-061973/07.  
XX P-PSDB; AAB20079.  
XX Isolated intracellular proteins predicted to be involved in regulating  
XX caspase activation are used for diagnosis and treatment of e.g. cancer,  
XX viral infections, autoimmune diseases, neurological diseases and  
XX hematological disorders.  
XX  
PS Claim 1(a); Fig 1; 208pp; English.  
XX  
XX The present sequence is that of cDNA encoding human caspase recruitment  
XX domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
XX database search using known CARD sequences. Plasmid pXEL17A containing  
XX CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
XX protein predicted to be involved in regulating caspase activation. It is  
XX useful as a modulating agent in regulating cellular processes include  
XX cell growth and cell death. Methods of diagnosing and treating patients  
XX suffering from a disorder associated with an abnormal level or rate of  
XX apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
XX complex, abnormal activity of a caspase involve administering a compound that  
XX or abnormal activity of a caspase involve administering a compound that  
XX modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
XX e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.  
XX Such disorders include cancer, viral infection, autoimmune disorders,  
XX neurological diseases, haematological disorders, inflammatory disorders  
XX and immune disorders. CARD nucleic acids can be used to express CARD  
XX proteins in a host cell e.g. for gene therapy applications, to detect a

CC	genetic lesion and to modulate CARD activity	
XX		
SQ	Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;	
	Query Match 40.9%; Score 682; DB 4; Length 1931;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	333 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATCTC 392	
DB	1151 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATCTC 1210	
QY	393 TGAACATACCTGTAAATCAATGCTGCCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 452	
DB	1211 TGAACATACCTGTAAATCAATGCTGCCACAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270	
QY	453 AAAATAGTGTTCCTGAAACTTCAAGGTCCTGCGAGCTCTCTCAAGACAATGATTTT 512	
DB	1271 AAAATAGTGTTCCTGAAACTTCAAGGTCCTGCGAGCTCTCTCAAGACAATGATTTT 1330	
QY	513 TATCTAGAAAGCTCAAGAGCTGTATTTATGAGCTGCATCACTGTCTGGAATCACA 572	
DB	1331 TATCTAGAAAGCTCAAGAGCTGTATTTATGAGCTGCATCACTGTCTGGAATCACA 1390	
QY	573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 632	
DB	1391 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACTC 1450	
QY	633 CATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGAACTCAGAACGCTGCGAGC 692	
DB	1451 CATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGAACTCAGAACGCTGCGAGC 1510	
QY	693 CTGTATAGCCAGCAGTGTGATCCAGACCAAGAGGAGACATGTGACCAATGACAG 752	
DB	1511 CTGTATAGCCAGCAGTGTGATCCAGACCAAGAGGAGACATGTGACCAATGACAG 1570	
QY	753 AAGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 812	
DB	1571 AAGCTCGCTTAACCACTGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGG 1630	
QY	813 ACTATGAACCTTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTAAGTACAG 872	
DB	1631 ACTATGAACCTTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTAAGTACAG 1690	
QY	873 CTACTGACATCCAGGAGAGAAATTTCCAAAGTTATAGTACAAAATTTCAAGAGATAACA 932	
DB	1691 CTACTGACATCCAGGAGAGAAATTTCCAAAGTTATAGTACAAAATTTCAAGAGATAACA 1750	
QY	933 AACAAATGGGTCTTCAGCCTTACCCGAAATACCTGTGGTTCTTAGATCAACATCTTTAA 992	
DB	1751 AACAAATGGGTCTTCAGCCTTACCCGAAATACCTGTGGTTCTTAGATCAACATCTTTAA 1810	
QY	993 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTTCAAGAGAAATGTTTCAATAA 1052	
DB	1811 ATTACTTCAAAATAAAGCATGTAGTACTGTTTTTCAAGAGAAATGTTTCAATAA 1870	
QY	1053 AAGGATATTTATA 1065	
DB	1871 AAGGATATTTATA 1883	
RESULT 11		
ID	ABK89280 standard; cDNA; 1931 BP.	
AC	ABK89280;	
XX		
DT	21-OCT-2002 (first entry)	
XX		
DE	Human cDNA encoding caspase recruitment domain protein CARD-3.	
XX		
KW	Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;	
KW	leucine rich repeat; LPS; lipopolysaccharide; NF-kB;	

KW	nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;	
KW	systemic lupus erythematosus; immune-mediated glomerulonephritis;	
KW	arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;	
KW	atopic condition; asthma; allergy; psoriasis; contact dermatitis;	
KW	gastrointestinal allergy; insulin-dependent diabetes;	
KW	bacterial infection; tuberculosis; lepromatous leprosy;	
KW	cell signalling disorder; tissue disorder.	
XX		
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	CDS 214..1836	
FT	/tag= a	
FT	/product= "CARD-3"	
XX		
PN	WO200253765-A1.	
XX		
PD	11-JUL-2002.	
XX		
PF	20-DEC-2001; 2001WO-US049798.	
XX		
PR	29-DEC-2000; 2000US-0258724P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Bertin J, Philpott D, Sansonetti P, Girardin S;	
XX		
DR	WPI; 2002-583627/62.	
DR	P-PSDB; ABG31075.	
XX		
PT	Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.	
PT		
XX		
PS	Example 2; Fig 1; 139pp; English.	
XX		
CC	The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as asthma, allergy, psoriasis, contact dermatitis, atopic conditions such as allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding CARD-3	
XX		
SQ	Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;	
	Query Match 40.9%; Score 682; DB 6; Length 1931;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	333 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATCTC 392	
DB	1151 AGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAGAAATGGAATTATCTC 1210	

QY 393 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452  
 DB 1211 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270  
 QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAATGATTTT 512  
 DB 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAATGATTTT 1330  
 QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTCGAAATCACA 572  
 DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTCGAAATCACA 1390  
 QY 573 GTTGGATAGCACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 632  
 DB 1391 GTTGGATAGCACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 1450  
 QY 633 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACTCAGAACCTGTGCAGC 692  
 DB 1451 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACTCAGAACCTGTGCAGC 1510  
 QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAAAATGACAG 752  
 DB 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAAAATGACAG 1570  
 QY 753 AAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 812  
 DB 1571 AAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGG 1630  
 QY 813 ACTATGAATCTGTAGTACCAAGCTTCAAGGACCTCAAGGACCAAAATGACAG 872  
 DB 1631 ACTATGAATCTGTAGTACCAAGCTTCAAGGACCTCAAGGACCAAAATGACAG 1690  
 QY 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932  
 DB 1691 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750  
 QY 933 AACAAATGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 992  
 DB 1751 AACAAATGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAA 1810  
 QY 993 ATTACTTCAAAATTAAGCATGTAGTACCTGTTTTCAGAGAAATGTGTTTCATAA 1052  
 DB 1811 ATTACTTCAAAATTAAGCATGTAGTACCTGTTTTCAGAGAAATGTGTTTCATAA 1870  
 QY 1053 AAGGATATTTATA 1065  
 DB 1871 AAGGATATTTATA 1883

RESULT 12

AAAL40752  
 ID AAL40752 standard; cDNA; 1931 BP.  
 XX  
 AC AAL40752;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE cDNA of human CARD-3 SEQ ID No 1.  
 XX  
 KW Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;  
 KW cerebroprotective; antiparkinsonian; antischlerotic; ophthalmological;  
 KW nootropic; antianemic; Caspase Recruitment Domain; CARD; CARD-41; p53;  
 KW cancer; CARD-48; follicular lymphoma; carcinoma; autoimmune disorder;  
 KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
 KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
 KW anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6369196-B1.  
 XX  
 PD 09-APR-2002.

XX PF 05-FEB-1999; 99US-00245281.  
 XX PR 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Bertin J;  
 XX  
 DR WPI; 2002-391988/42.  
 DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.  
 XX  
 PT Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD  
 PT -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's  
 PT disease, cancers and viral infections.  
 XX  
 PS Example 2; Fig 1; 116pp; English.  
 XX  
 CC The invention relates to novel isolated Caspase Recruitment Domain (CARD)  
 CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may  
 CC be used to treat disorders associated with decreased CARD expression by  
 CC supplementing the patient's own production of CARD. Disorders associated  
 CC with the expression and activity of CARD include cancers (particularly  
 CC follicular lymphomas, carcinomas associated with mutations in p53, and  
 CC hormone-dependent tumours such as breast cancer, prostate cancer, and  
 CC ovarian cancer), autoimmune disorders (such as systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections  
 CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),  
 CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,  
 CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal  
 CC muscular atrophy, and various forms of cerebellar degeneration), anaemia  
 CC associated with chronic disease, aplastic anaemia, chronic neutropenia,  
 CC and the myelodysplastic syndromes. This polynucleotide sequence  
 CC represents the cDNA of a human CARD relating to the invention  
 XX  
 SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 6; Length 1931;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 392

DB 1151 AGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 1210

QY 393 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 452

DB 1211 TGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATG 1270

QY 453 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 512

DB 1271 AAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 1330

QY 513 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTCGAAATCACA 572

DB 1331 TATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTCGAAATCACA 1390

QY 573 GTTGGATAGCACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 632

DB 1391 GTTGGATAGCACCAATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTC 1450

QY 633 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACTCAGAACCTGTGCAGC 692

DB 1451 CATGCTCTTCAGCAATAAATAATCACTCTCACTGCAGGAACTCAGAACCTGTGCAGC 1510

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAAAATGACAG 752

DB 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAAAATGACAG 1570

QY 753 AAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGAACTTGTATCATGAAGAGG 812



Db 1571 AAGCCTGCCTTAACCAAGTCGCTAGATGCCCTCTCTGTCAGGAGCTTGTATCATCAAGAGAGG 1630

Qy 813 ACTATGAACCTGTGTAGTACCAAGCCTACAAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 872

Db 1631 ACTATGAACCTGTGTAGTACCAAGCCTACAAAGGACCTCAAAAGTCAGACAATTAAGTACAGACA 1690

Qy 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932

Db 1691 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750

Qy 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 992

Db 1751 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1810

Qy 993 ATTACTTCAAAATAAAGCATGTAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAA 1052

Db 1811 ATTACTTCAAAATAAAGCATGTAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAA 1870

Qy 1053 AAGGATATTTATA 1065

Db 1871 AAGGATATTTATA 1883

RESULT 13

ABX75869

ID ABX75869 standard; cDNA; 1931 BP.

XX

AC ABX75869;

XX

DT 30-APR-2003 (first entry)

XX

DE Human cDNA encoding Caspase recruitment domain protein, CARD-3.

XX

KW Human; ss; gene; caspase recruitment domain; CARD; CARD-3; CARD-4;

KW CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS;

KW autoimmune disorder; systemic lupus erythematosus; viral infection;

KW immune related glomerulonephritis; acquired immunodeficiency syndrome;

KW neurological disease; Alzheimer's disease; Parkinson's disease;

KW amyotrophic lateral sclerosis; retinitis pigmentosa;

KW spinal muscular atrophy; cerebellar degeneration; haematological disease;

KW anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;

KW stroke; chromosome 7.

XX

OS Homo sapiens.

XX

PN US6469140-B1.

XX

PD 22-OCT-2002.

XX

PF 08-DEC-1998; 98US-00207359.

XX

PR 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Bertin J;

XX

DR WPI; 2003-147109/14.

DR P-PSDB; ABUS6269.

XX

XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z

PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,

PT detection assays, predictive medicine, and in therapeutic applications.

XX

PS Example 2; Fig 1; 99pp; English.

XX

CC The invention relates to an isolated polypeptide, comprising at least 25

CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,

CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)

CC polypeptide. Also included is an isolated fusion protein, comprising the

CC CARD polypeptide covalently linked by a peptide bond to a heterologous

CC polypeptide. The CARD polypeptide is useful in screening assays,

CC detection assays (e.g. chromosomal mapping, tissue typing and forensic

CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in therapeutic and

CC prophylactic treatments (in diseases associated with apoptotic cell death

CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and

CC immune related glomerulonephritis), viral infections, AIDS (acquired

CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's

CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis

CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),

CC haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic

CC syndromes), myocardial infarction and stroke). The CARD polypeptide is

CC useful as bait protein in a two-hybrid assay or three hybrid assay to

CC identify other proteins, which bind to or interact with other CARD

CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for

CC human CARD-4 is located on chromosome 7. The present sequence is a human

CC CARD cDNA

XX

SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 7; Length 1931;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 333 AGTTACAGAGTGTTCAGTGCCTTACCTATGTCACAGAGAAATGGATTTATCTC 392

Db 1151 AGTTACAGAGTGTTCAGTGCCTTACCTATGTCACAGAGAAATGGATTTATCTC 1210

Qy 393 TGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATG 452

Db 1211 TGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCATG 1270

Qy 453 AAAATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTTT 512

Db 1271 AAAATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTTT 1330

Qy 513 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTGGAATACACA 572

Db 1331 TATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTCTCTGGAATACACA 1390

Qy 573 GTTGGATAGACACATTTCTGGATCTCAAGGGCTGCTTCTGTGATCAACAGCACCTC 632

Db 1391 GTTGGATAGACACATTTCTGGATCTCAAGGGCTGCTTCTGTGATCAACAGCACCTC 1450

Qy 633 CATGCTTTTCAGCAATAAATCAATCTCACTCAAGTCCAGGAACTCAGAACGTCTGCAGC 692

Db 1451 CATGCTTTTCAGCAATAAATCAATCTCACTCAAGTCCAGGAACTCAGAACGTCTGCAGC 1510

Qy 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAACATTTGTGAACCAATGACAG 752

Db 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAACATTTGTGAACCAATGACAG 1570

Qy 753 AAGCCTGCCTTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGGACTTTGATCATGAAAGAGG 812

Db 1571 AAGCCTGCCTTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGGACTTTGATCATGAAAGAGG 1630

Qy 813 ACTATGAACCTGTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAATTAAGTACAGACA 872

Db 1631 ACTATGAACCTGTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAATTAAGTACAGACA 1690

Qy 873 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932

Db 1691 CTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750

Qy 933 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 992

Db 1751 AACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1810

Qy 993 ATTACTTCAAAATAAAGCATGTAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAA 1052

Db 1811 ATTACTTCAAAATAAAGCATGTAGTGAAGTCTTTTCAAGAGAAATGTGTTTCATAA 1870

Qy 1053 AAGGATATTTATA 1065



Db 1871 AAGGATATTATA 1883

RESULT 14

ADB81363

ID ADB81363 standard; cDNA; 1931 BP.

AC ADB81363;

XX

XX

DT 04-DEC-2003 (first entry)

XX

DE Human caspase recruitment domain 3 (CARD-3) cDNA.

XX

XX human; ss; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;

KW p75; tumour necrosis factor; TNF; neutrophin receptor; cancer;

KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;

KW viral infection; neurological; retinitis pigmentosa; haematologic;

KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 214..1836

FT /\*tag= a

FT /product= "CARD-3 protein"

XX

PN US2002061833-A1.

XX

XX 23-MAY-2002.

XX

PF 26-DEC-2000; 2000US-00748537.

XX

XX 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

XX

XX (BERT/) BERTIN J.

PA (CHAO/) CHAO M V.

XX

PI Bertin J, Chao MV;

XX

XX WPI: 2003-657125/62.

DR P-PSDB; ADB81362.

DR

XX

XX

PT Detecting compounds which alter binding of the caspase recruitment domain

PT (CARD) of CARD-3 polypeptide to the neutrophin receptor p75 is useful

PT to provide compounds for treating CARD-3 mediated disorders.

XX

PS Disclosure; Fig 2; 40pp; English.

XX

XX This invention relates to two novel genes CARD-3 and CARD-4 (caspase

CC recruitment domains), which are mediators of apoptosis and are useful in

CC the identification of compounds that modulate apoptosis. Specifically,

CC CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator

CC of p75 (a member of the tumour necrosis factor (TNF) family), and is

CC believed to provide the switch for cell survival and cell death decisions

CC mediated by this p75 neutrophin receptor. Accordingly these genes, and

CC the proteins encoded thereof, are linked to certain disorders associated

CC with an increased number of cells surviving and proliferating when

CC apoptosis is inhibited. These include cancer, autoimmune disorders e.g.

CC systemic lupus and immune mediated glomerulonephritis, viral infections

CC such as those caused by the herpesvirus, neurological disorders such as

CC retinitis pigmentosa, haematologic diseases including chronic

CC neutropenia, as well as myocardial infarction and strokes. The present

CC invention further describes a novel method for determining whether a test

CC compound alters the binding of CARD-3 to p75, which comprises measuring

CC the binding of a polypeptide containing the CARD domain of CARD-3 to a

CC polypeptide comprising the death domain of p75 in the presence and

CC absence of the test compound, and determining if binding is altered. This

CC polynucleotide is the human CARD-3 cDNA sequence of the invention.

XX

SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Query Match 40.9%; Score 682; DB 9; Length 1931;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 732; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 333 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAAAGAAATGAAATATATCTC 392

DB 1151 AGTTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAAAGAAATGAAATATATCTC 1210

QY 393 TGAACATACCTGTAAATCATGGTCCACAAAGAGGAATCATGTGGATCTCTCAGCTCCATG 452

DB 1211 TGAACATACCTGTAAATCATGGTCCACAAAGAGGAATCATGTGGATCTCTCAGCTCCATG 1270

QY 453 AATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCTTCAAGACAAATGATTTT 512

DB 1271 AATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCTTCAAGACAAATGATTTT 1330

QY 513 TATCTAGAAAAAGCTCAAGACTGTTTATTTTATGAAGCTGCATCAGTCTCTGGAATACACA 572

DB 1331 TATCTAGAAAAAGCTCAAGACTGTTTATTTTATGAAGCTGCATCAGTCTCTGGAATACACA 1390

QY 573 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATCTC 632

DB 1391 GTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATCTC 1450

QY 633 CATGCTCTTCAGCAATATAATCACTCTCAACTGCGAGGAACCTCAGAACTCTGCAGC 692

DB 1451 CATGCTCTTCAGCAATATAATCACTCTCAACTGCGAGGAACCTCAGAACTCTGCAGC 1510

QY 693 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 752

DB 1511 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAG 1570

QY 753 AAGCTGCTTTAAGCAGTCTGATGCTTCTGTCCAGGACTTTGATCATGAAAGAGG 812

DB 1571 AAGCTGCTTTAAGCAGTCTGATGCTTCTGTCCAGGACTTTGATCATGAAAGAGG 1630

QY 813 ACTATGAATCTTTAGTAGTACCAAGCTTCAAGGACCTCAAGAGCTCAAGCAATTTACTAGACA 872

DB 1631 ACTATGAATCTTTAGTAGTACCAAGCTTCAAGGACCTCAAGAGCTCAAGCAATTTACTAGACA 1690

QY 873 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 932

DB 1691 CTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACA 1750

QY 933 AACAAATGGTCTTCAGCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTTAA 992

DB 1751 AACAAATGGTCTTCAGCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTTAA 1810

QY 993 ATTTACTTCAAAATTAAGCATGTAAAGTCAAGAGCAATTTTCAAGAGAAATGTGTTTCATTA 1052

DB 1811 ATTTACTTCAAAATTAAGCATGTAAAGTCAAGAGCAATTTTCAAGAGAAATGTGTTTCATTA 1870

QY 1053 AAGGATATTATA 1065

DB 1871 AAGGATATTATA 1883

RESULT 15

ABX75870

ID ABX75870 standard; cDNA; 1620 BP.

XX ABX75870;

AC ABX75870;

XX

XX 30-APR-2003 (first entry)

XX

XX Human Caspase recruitment domain protein 3, open reading frame.

DE

XX Human; ss; gene; caspase recruitment domain; CARD; CARD-3; CARD-4;

KW CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS;

KW autoimmune disorder; systemic lupus erythematosus; viral infection;

KW immune related glomerulonephritis; acquired immunodeficiency syndrome;

KW neurological disease; Alzheimer's disease; Parkinson's disease;

KW amyotrophic lateral sclerosis; retinitis pigmentosa;

KW spinal muscular atrophy; cerebellar degeneration; haematological disease;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 04:59:21 ; Search time 6741 Seconds  
(without alignments)  
10731.275 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 1669  
Sequence: 1 acctagttattaccagata.....caacagcctgatgtgtaaaa 1669

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 20

Total number of hits satisfying chosen parameters: 676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_hcg\_hum.\*

31: em\_hcg\_inv.\*

32: em\_hcg\_other.\*

33: em\_hcg\_mus.\*

34: em\_hcg\_pln.\*

35: em\_hcg\_rod.\*

36: em\_hcg\_mam.\*

37: em\_hcg\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1333	79.9	2521	9	AY358814	AY358814 Homo sapi
2	990	59.3	116650	9	AC004003	AC004003 Homo sapi
3	990	59.3	320187	9	AF117829	AF117829 Homo sapi
4	879	52.7	2024	6	BD251808	BD251808 Phosphory
5	878	52.6	1886	9	AY358813	AY358813 Homo sapi
6	827	49.6	2033	6	BD127583	BD127583 Primer fo
7	827	49.6	2033	9	AK075213	AK075213 Homo sapi
8	812	48.7	2501	6	AR221453	AR221453 Sequence
9	812	48.7	2501	6	AX429236	AX429236 Sequence
10	812	48.7	2501	9	AF027706	AF027706 Homo sapi
11	812	48.7	2502	6	AR194318	AR194318 Sequence
12	783	46.9	2098	6	BD106658	BD106658 Modulator
13	783	46.9	2098	9	BC004553	BC004553 Homo sapi
14	733	43.9	1889	9	AC139421	AC139421 Homo sapi
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16	708	42.4	1902	9	AF064824	AY358645 Synthetic
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19	682	40.9	1931	6	AR205634	AR216112 Sequence
20	682	40.9	1931	6	AR216112	AR241236 Sequence
21	682	40.9	1931	6	AR241236	AR256252 Sequence
22	682	40.9	1931	6	AR256252	AR391599 Sequence
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26	635	38.0	1623	9	AF078530	AR183235 Sequence
27	632	37.9	1620	6	AR183235	AR205635 Sequence
28	632	37.9	1620	6	AR205635	AR241237 Sequence
29	632	37.9	1620	6	AR241237	AR391599 Sequence
30	632	37.9	1620	6	AR391599	AX082199 Sequence
31	632	37.9	1620	6	AR391600	AX082201 Sequence
32	632	37.9	1620	6	AX082201	BD123999 Novel mol
33	632	37.9	1620	6	BD123999	AR380139 Sequence
34	586	35.1	1060	6	AR380139	AX381606 Sequence
35	220	13.2	299	6	AX381606	BD126039 Primer fo
36	179	10.7	575	6	BD126039	AF461040 Mus muscu
37	26	1.6	1620	10	AF461040	AF487539 Mus muscu
38	26	1.6	1620	10	AF487539	AL807379 Mouse DNA
39	26	1.6	186519	10	AL807379	AJ341343 Homo sapi
40	24	1.4	741	9	HSR341343	AL109815 Plasmodiu
41	24	1.4	80518	2	PFMAL13PA	AC119395 Mus muscu
42	24	1.4	92300	10	AC119395	Continuation (13 o
43	24	1.4	110000	2	PFMAL13_12	AC102277 Mus muscu
44	24	1.4	148851	2	AC102277	AC132407 Mus muscu
45	24	1.4	211970	2	AC132407	

ALIGNMENTS

RESULT 1	AY358814	Homo sapiens clone DNA3305 RIPK2 (UNQ277) mRNA, complete cds.	2521 bp	linear	PRI 03-OCT-2003
AY358814	LOCUS				
DEFINITION	AY358814				
ACCESSION	AY358814				
VERSION	AY358814.1	GI:37182745			
KEYWORDS	FLI_CDNA				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2521)				
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brueh,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,				

Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagstad, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
12975309  
PUBMED  
REFERENCE  
2 (bases 1 to 2521)  
AUTHORS  
Clark, H.F.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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gene

CDS

333	AGTTACAGAGTGTTC	AAAGTGC	CAATTC	CACTAT	GTGTGA	CAGAGAA	AAATG	GAATAT	ATCTC	392
1189	AGTTACAGAGTGTTC	AAAGTGC	CAATTC	CACTAT	GTGTGA	CAGAGAA	AAATG	GAATAT	ATCTC	1248
393	TGAACATACCTGTAA	ATCGT	CCACAGAGGA	ATCAT	GTGAT	CTCTC	CAGCTCC	ATG		452
1249	TGAACATACCTGTAA	ATCGT	CCACAGAGGA	ATCAT	GTGAT	CTCTC	CAGCTCC	ATG		1308
453	AAAATAGTGGTCTCT	CGAACTT	CAAGGTCC	CTCGCAG	CTCCCT	CAAGACA	AAATG	ATTTT		512
1309	AAAATAGTGGTCTCT	CGAACTT	CAAGGTCC	CTCGCAG	CTCCCT	CAAGACA	AAATG	ATTTT		1368
513	TATCTAGAAAAGCTC	CAAGACT	GTATTT	TATGAA	GTGAT	CACTG	TCCTG	GGAAAT	CACA	572
1369	TATCTAGAAAAGCTC	CAAGACT	GTATTT	TATGAA	GTGAT	CACTG	TCCTG	GGAAAT	CACA	1428
573	GTGGGATAGACCAT	TTCTGG	ATCTCA	AAAGG	GTGAT	CTCTG	GATCA	CAAGAC	CACTC	632
1429	GTGGGATAGACCAT	TTCTGG	ATCTCA	AAAGG	GTGAT	CTCTG	GATCA	CAAGAC	CACTC	1488
633	CATGCTCTTCAGCA	ATAATAAT	CACTCT	CACTG	CAGGAA	AACTC	CAGAA	CGTCTG	CAGC	692
1489	CATGCTCTTCAGCA	ATAATAAT	CACTCT	CACTG	CAGGAA	AACTC	CAGAA	CGTCTG	CAGC	1548
693	CTGTGTATAGCC	CAGCTGG	ATTCAG	AGGAA	GCAT	TTGTGA	ACCA	ATGAC	GAC	752

ORIGIN

Query Match	79.9%;	Score 1333;	DB 9;	Length 2521;			
Best Local Similarity	100.0%;	Pred. No. 0;					
Matches 1333;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
QY	333	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGAC	AAGAGAAATGGAATTA	TCTC	392
DB	1189	AGTTACAGAGTGTTC	CAAGTGC	CAATTCACCTATGTGAC	AAGAGAAATGGAATTA	TCTC	1248
QY	393	TGAACATACCTGTAA	ATCATGTGGTCC	ACAGAGGAATCAT	GTGGATCTCTCAGTCC	CATG	452
DB	1249	TGAACATACCTGTAA	ATCATGTGGTCC	ACAGAGGAATCAT	GTGGATCTCTCAGTCC	CATG	1308
QY	453	AAAATAGTGGTCTCT	CGTAAACTTCA	AGGTCCCTCGCAGCT	CTCTCAAGACAATGAT	TTTT	512
DB	1309	AAAATAGTGGTCTCT	CGTAAACTTCA	AGGTCCCTCGCAGCT	CTCTCAAGACAATGAT	TTTT	1368
QY	513	TATCTAGAAAAGCTC	CAAGACTGTTATTT	TATGAACTGCATCA	CTGCTCGGAAATCACA		572
DB	1369	TATCTAGAAAAGCTC	CAAGACTGTTATTT	TATGAACTGCATCA	CTGCTCGGAAATCACA		1428
QY	573	GTGGGATAGCACCAT	TTCTGGATCTCAA	AGGGCTGCATTTCTG	TGATCAAGACCAC	TCTC	632
DB	1429	GTGGGATAGCACCAT	TTCTGGATCTCAA	AGGGCTGCATTTCTG	TGATCAAGACCAC	TCTC	1488
QY	633	CATGCTCTTCAGCAA	ATAATAAACTCA	CTCACTCAGGAGAACT	CAGAACTCGTCGAGC		692
DB	1489	CATGCTCTTCAGCAA	ATAATAAACTCA	CTCACTCAGGAGAACT	CAGAACTCGTCGAGC		1548
QY	693	CTGGTATAGCC	CAGCAGTGGAT	TCAGAGCAAAAGGG	GAAGCATTTGTGAA	CCAAATGACAG	752

RESULT 2  
AC004003  
LOCUS  
DEFINITION Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.  
AC004003  
AC004003  
VERSION 1 GI:2772557

102a

Db	1549	CTGGTATAGCC	CAGCAGT	GGATCC	CAGAGCA	AAAGG	GAAGAC	ATTG	TGAACCA	ATGACAG	1608
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QY	1113	CTTTAT	TGAGG	TTCTT	GGGTA	AAAT	TATAG	CTCC	CTC	CATG	1172
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QY	1413	ACAGA	ATCC	CTGCC	CTTAA	ATCC	CAGC	TTA	TG	CCCT	1472
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QY	1473	ACTCC	ATTAT	TAG	GAT	TAC	ATT	TAA	AGT	TTT	1532
Db	2329	ACTCC	ATTAT	TAG	GAT	TAC	ATT	TAA	AGT	TTT	2388
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QY	1593	TCGCC	ATTTT	TA	ACCT	CAGC	CTTCC	CT	ACTG	TACCA	1652
Db	2449	TCGCC	ATTTT	TA	ACCT	CAGC	CTTCC	CT	ACTG	TACCA	2508
QY	1653	CAGC	CTGAT	GTGT	1665						
Db	2509	CAGC	CTGAT	GTGT	2521						

HTG. Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 116650)  
 Ozersky, P., Holmes, A. and Broy, M.  
 TITLE  
 JOURNAL The sequence of Homo sapiens BAC clone CTA-437L15  
 REFERENCE  
 2 (bases 1 to 116650)  
 Unpublished  
 AUTHORS  
 Waterston, R.  
 TITLE  
 JOURNAL Direct Submission  
 Submitted (15-JAN-1998) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 3 (bases 1 to 116650)  
 Waterston, R.  
 TITLE  
 JOURNAL Direct Submission  
 Submitted (27-JUN-1998) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 4 (bases 1 to 116650)  
 Waterston, R.  
 TITLE  
 JOURNAL Direct Submission  
 Submitted (21-DEC-1999) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
 ----- Summary Statistics  
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 Center project name: H\_RG437L15

NOTICE: This sequence may not represent the entire insert of this  
 clone. It may be shorter because we only sequence overlapping  
 clone sections once, or longer because we provide a small overlap  
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded or sequenced with an alternate  
 chemistry; an attempt was made to resolve all sequencing problems,  
 such as compressions and repeats; all regions were covered by  
 sequence from more than one subclone; and the assembly was  
 confirmed by restriction digest.

MAPPING INFORMATION:  
 This chromosome 8 clone was provided by Dr. Patrick Concannon  
 ([patcon@vmc.org](mailto:patcon@vmc.org)) at the Virginia Mason Research Institute.

SOURCE INFORMATION:  
 Clone CTA-437L15 is from a release of the human BAC library  
 CITB-HS-A. The library contains cloned DNA from human sperm. See:  
 Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.  
 Kim et al., Genomics 34:213-8 (1996). The clone is available from  
 Research Genetics, Inc. (<http://www.resgen.com>).  
 VECTOR: pBelOBAC11  
 Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is CTA-237G1. The actual start of  
 this clone is at base position 1 of CTA-437L15; actual end is at  
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This clone contains STS HS275YF1 (NID:g1051703).

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Matches 990; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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LOCUS	AF117829				
DEFINITION	Homo sapiens chromosome 8 multiple clones map g2i.3, complete sequence.				
ACCESSION	AF117829				
VERSION	AF117829.2				
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 320187)				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Platzer, M., Varon, R., Sperling, K., Reis, A. and Rosenthal, A.				
JOURNAL	Chromosome 8 genomic sequence				
REFERENCE	2 (bases 1 to 320187)				
AUTHORS	Platzer, M. and Varon, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-DEC-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany				
REFERENCE	3 (bases 1 to 320187)				

**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

Platzner,M.  
 Direct Submission  
 Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular  
 Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany  
 On Nov 4, 2003 this sequence version replaced gi:4151947.

----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: http://genome.imb-jena.de/

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: NBSlocusa

Center clone name: RGP-64M4 to SCB-316M22

----- Summary Statistics

Sequencing vector: M13mp18; 100% of reads

Chemistry: Dye-primer ET, Dye-terminator Big Dye;

Consensus quality: 319496 bases at least Q40

Consensus quality: 320184 bases at least Q30

Consensus quality: 320187 bases at least Q20

Quality coverage: 7.63

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 This sequence was finished as follows unless otherwise noted: all  
 regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest.

-----

Neighboring sequence information:

This entry is part of a larger genomic contig. The start of this  
 sequence is directed towards the centromere. The end  
 (318188..320187) of this sequence overlaps with the start of  
 Acc number AF049895. It covers RGP-64M4, SCB-282k6, SCB-273G1  
 entirely and is overlapped by SCB-296N11, SCB-316M22.

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Sequence Quality Assessment:

This entry has been annotated with sequence quality  
 estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the  
 GenBank flat file format but are available as part  
 of this entry's ASN.1 file.

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**FEATURES**

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 VERSION BD251808.1 GI:33061578  
 KEYWORDS JP 2002526035-A/6.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2024)  
 AUTHORS Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J., Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A., Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L.  
 TITLE Phosphorylation effectors  
 JOURNAL Patent: JP 2002526035-A 6 20-AUG-2002;  
 COMMENT INCYTE PHARMACEUTICALS INC  
 OS Homo sapiens (human)  
 FN JP 2002526035-A/6  
 PD 20-AUG-2002  
 PF 28-JUL-1999 JP 2000562510  
 PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR  
 14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR  
 19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR  
 12-JAN-1999 US 60/155233  
 PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J GUEGLER,  
 PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU YOUNG,  
 PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA M LU,  
 PI LEO L SHIH  
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VERSION AY358813.1 GI:37182743  
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REFERENCE 1 (bases 1 to 1886)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiedel,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL 12975309  
PUBMED 2 (bases 1 to 1886)  
AUTHORS Clark,H.F.  
DIRECT SUBMISSION  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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RESULT 6  
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 ACCESSION BD127583  
 VERSION BD127583.1 GI:23222528  
 KEYWORDS JP 2002017375-A/3014.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2033)  
 Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
 Koga,H.  
 TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002017375-A 3014 22-JAN-2002;  
 HELIX RESEARCH INSTITUTE  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002017375-A/3014  
 PD 22-JAN-2002 JP 2000253172  
 PF 07-JUL-2000 JP 2000253172  
 PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO  
 PI ISHII,  
 PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI  
 SHINICHI KOJIMA,  
 PI TETSUO OTSUKI, HISASHI KOGA  
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LOCUS Homo sapiens cDNA FLJ90732 fis, clone PLACE1010081, highly similar
DEFINITION to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
ACCESSION AK075213
VERSION AK075213.1 GI:22761157
KEYWORDS oligo capping, fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kojima-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2033)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
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QY 333 AGTTACAGAGTGTTCAGATGCCATTCACCTATGTGACAGAGAAATGGAATTATCTC 392
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ACCESSION AR221453
VERSION AR221453.1 GI:23328503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2501)
AUTHORS Ward,D.T. and Cowser,L.M.
TITLE Antisense modulation of R1P2 expression
JOURNAL Patent: US 6426221-A 3 30-JUL-2002;
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DEFINITION Sequence 13 from Patent BP1201765.  
ACCESSION AX429236  
VERSION AX429236.1 GI:21540548  
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ORGANISM	synthetic construct									
REFERENCE	artificial sequences.									
AUTHORS	Schubart, D., Habenberger, P., Stein-Gerlach, M. and Bevec, D.									
TITLE	Cellular kinases involved in cytomagalovirus infection and their inhibition									
JOURNAL	Patent: EP 1201765-A 13 02-MAY-2002;									
FEATURES	Axxima Pharmaceuticals Aktiengesellschaft (DE)									
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LOCUS Homo sapiens threonine/threonine kinase RICK (RICK) mRNA, complete cds.  
DEFINITION

ACCESSION AF027706  
VERSION AF027706.1 GI:3123886  
KEYWORDS Homo sapiens  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2501)  
AUTHORS Inohara, N., del Peso, L., Koseki, T., Chen, S. and Nunez, G.  
TITLE RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis  
J. Biol. Chem. 273 (20), 12296-12300 (1998)  
JOURNAL 98241596  
MEDLINE 9575181  
REFERENCE 2 (bases 1 to 2501)  
AUTHORS Inohara, N., Koseki, T., Chen, S., del Peso, L. and Nunez, G.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CGCG 1500 E. Medical Center Dr, Ann Arbor, MI 48109, USA

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DEFINITION Sequence 2 from patent US 6348573.  
ACCESSION AR194318  
VERSION AR194318.1 GI:20240910  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 2502)  
AUTHORS Nunez, G., Inohara, N. and Koseki, T.  
TITLE Compositions and methods for identifying apoptosis signaling pathway inhibitors and activators  
JOURNAL Patent: US 6348573-A 2 19-FEB-2002;  
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QY 333 AGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAGAGAAATGGAATATATCTC 392  
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VERSION A82777.1 GI:6732464  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 2098)  
AUTHORS Boldin, M. and Wallach, D.  
TITLE MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS  
JOURNAL Patent: WO 9855507-A 2 10-DEC-1998;  
BOLDIN MARK (IL); WALLACH DAVID (IL)  
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ACCESSION BD106658
VERSION BD106658.1 GI:23201476
KEYWORDS JP 2002502258-A/1.
SOURCE synthetic construct
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REFERENCE 1 (bases 1 to 2098)
AUTHORS Wallach,D., Boldin,M. and Malinin,N.
TITLE Modulators of intracellular inflammation, cell death and cell
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JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;
YEDA RESEARCH AND DEVELOPMENT CO LTD
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PD 22-JAN-2002
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PR 05-JUN-1997 IL 121011,30-JUN-1997 IL 121199 PR
11-SEP-1997 IL 121746
PI DAVID WALLACH,MARK BOLDIN,NIKOLAI MALININ
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 333 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 392
Db 1197 AGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTC 1256
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1889)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalley,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE
PUBMED 12477932

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JOURNAL  
REFERENCE  
AUTHORS

Unpublished  
2 (bases 1 to 61099)  
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,  
Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T.,  
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Direct Submission  
Submitted (03-FEB-2003) Whitehead Institute/MIT Center for Genome  
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All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
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JOURNAL  
COMMENT

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Project Information  
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\* However, it should not be assumed that this clone  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Perfect score: 531

Sequence: 1 acctagttatccagata.....caacagcctgatgtgtaaaa 1669

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 141681 seqs, 52070155 residues

Word size: 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09771161/runat\_29032004\_124856\_14314/app\_query.fasta\_1.1863  
-DB=SwissProt\_42 -OPMT=fastan -SUFFIX=oli20n2p.rsp -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1 1 19 @runat\_29032004\_124856\_14314 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	42.7	540	1 RIK2_HUMAN	O43353 h receptor-
2	27	5.1	539	1 RIK2_MOUSE	P58801 mus musculus

#### ALIGNMENTS

RESULT 1  
RIK2\_HUMAN  
ID RIK2\_HUMAN STANDARD; PRT; 540 AA.  
AC O43353;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)  
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme  
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).  
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.



DR EMBL; AF461040; AAL96436.1; -.  
 DR MGD; MGI:1891456; RipK2.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR000719; Prot Kinase.  
 DR InterPro; IPR008271; Ser Thr pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR0109; TYRKINASE.  
 DR ProDom; PD000001; Prot Kinase; 1.  
 DR SMART; SM00114; CARD; 1.  
 DR PROSITE; PSS0209; CARD; 1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Apoptosis.  
 FT DOMAIN 18 294 PROTEIN KINASE.  
 FT DOMAIN 431 523 CARD.  
 FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
 FT BINDING 47 47 ATP (BY SIMILARITY).  
 FT ACT\_SITE 146 146 BY SIMILARITY.  
 SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Alignment Scores:  
 Pred. No.: 4.28e-20 Length: 539  
 Score: 27.00 Matches: 27  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 5.08% Indels: 0  
 DB: 1 Gaps: 0

US-09-771-161A-2 (1-1669) x RIK2\_MOUSE (1-539)

Qy 743 CAAATGACAGAGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATC 802  
 Db 449 GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeu 468  
 Qy 803 ATGAAAGAGGACTATGAACCTT 823  
 Db 469 MetLysGluAspTyrGluLeu 475

Search completed: March 29, 2004, 14:32:12  
 Job time : 22.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:24:58 ; Search time 87.5 Seconds  
(without alignments)  
12036.569 Million cell updates/sec

Title: US-09-771-161A-2  
Perfect score: 531  
Sequence: 1 acctagttataccagata.....caacagcctgatgtgtaaaa 1669

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Word size: 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -MODEL=frame+n2p.model -DEV=xlp  
-O=/cn2\_1/USPTO\_spool\_p/US09771161/runat\_29032004\_124857\_14326/app.query.fasta\_1.1863  
-DB=SPTREMBL\_25 -QWAT=fastan -SUFFIX=oli20n2p.rspt -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CN 1 1.95 @runat\_29032004\_124857\_14326 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

- Database : SPTREMBL 25:\*
- 1: sp archaea:\*
  - 2: sp bacteria:\*
  - 3: sp fungi:\*
  - 4: sp human:\*
  - 5: sp invertebrate:\*
  - 6: sp mammal:\*
  - 7: sp mhc:\*
  - 8: sp organelle:\*
  - 9: sp phage:\*
  - 10: sp plant:\*
  - 11: sp rodent:\*
  - 12: sp virus:\*
  - 13: sp vertebrate:\*
  - 14: sp unclassified:\*
  - 15: sp virus:\*
  - 16: sp bacteriap:\*
  - 17: sp archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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No matches found

Search completed: March 29, 2004, 14:35:18  
Job time : 87.5 secs

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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:08:46 ; Search time 59 Seconds  
(without alignments)  
1111.034 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLOQSVSAIHLCDKKK.....PEILVSRSPSLNLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 20

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseq1980s: \*  
2: Geneseq1990s: \*  
3: Geneseq2000s: \*  
4: Geneseq2001s: \*  
5: Geneseq2002s: \*  
6: Geneseq2003as: \*  
7: Geneseq2003bs: \*  
8: Geneseq2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	284	3	AAY59406 Human RIC
2	227	97.8	478	3	AAY59405 Human RIC
3	227	97.8	531	3	AAY59404 Human RIC
4	227	97.8	540	2	AAY92795 Human B1
5	227	97.8	540	3	AAY68774 Amino aci
6	227	97.8	540	4	AAY93621 Human pol
7	227	97.8	540	5	AAY80369 Human cel
8	227	97.8	540	5	AAY27882 Human rec
9	227	97.8	544	3	AAB43570 Human can
10	197	84.9	510	7	ADC99079 Human KPP
11	167	72.0	167	3	AAY59407 Human RIC
12	128	55.2	540	2	AAY31140 Human CAR
13	128	55.2	540	4	AAB20079 Human CAR
14	128	55.2	540	5	ABG31075 Human cas
15	128	55.2	540	5	AAC22107 Protein o
16	128	55.2	540	6	ABU56269 Human Cas
17	128	55.2	540	7	ADB81362 Human cas
18	110	47.4	110	6	ABU56272 Human CAR
19	109	47.0	109	5	AAC22110 Protein o
20	98	42.2	131	5	AAC22109 Protein o
21	98	42.2	131	6	ABU56271 Human Cas
22	92	39.7	92	5	ABJ04754 RICK prot

ALIGNMENTS

RESULT 1  
AAY59406  
ID AAY59406 standard; protein; 284 AA.  
XX  
AC AAY59406;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK protein sequence residues 248-531.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9955134-A2.  
XX  
PD 04-NOV-1999. (b)  
XX  
PF 27-APR-1999; 99WO-US0009183.  
XX  
PR 27-APR-1998; 98US-00069023.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
DR WPI; 2000-072163/06.  
XX  
PT Compositions for identifying apoptosis signaling pathway inhibitors  
XX useful for treating diseases.  
PS Claim 6; Page; 93pp; English.  
XX  
CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
CC kinase) protein of the invention. RICK acts as a positive regulator of  
CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
CC during CD95 signalling. The invention provides methods for identifying  
CC apoptosis signalling pathway inhibitors and activators, and methods and  
CC compositions for screening compounds which will modulate the interactions  
CC of the various compositions identified: ARC, RICK, and the CIDE family of  
CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
CC assays for agents, useful in the diagnosis, prognosis or treatment of  
CC disease associated with excess cell growth and dysregulation of  
CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
CC screening assays to identify inhibitor molecules blocking CD95-mediated  
CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
CC to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene  
CC therapy treatment of disease with increased cell death in muscle tissue  
CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
CC can be used as reagents for the preparation or affinity chromatography  
CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
CC of an essential step in the biochemistry of apoptosis is needed. RICK  
CC interaction with intracellular factors such as CLARP and FADD appears to  
CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates. Note: This sequence was  
CC created using information given in the specification  
XX  
SQ Sequence 284 AA;  
Query Match 97.8%; Score 227; DB 3; Length 284;  
Best Local Similarity 100.0%; Pred. No. 5.5e-22; Indels 0; Gaps 0;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LQSVSSAIHLCDKKKMWLSLNIPIVNHGPQESGSQLHNSGSPETSRSLPAPQDNDFL 65

CC	media, and for diagnostically measuring RICK levels. A specific inhibitor																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates. Note: This sequence was created using information given in the specification																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking C95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8. Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies can be used as reagents for the preparation of affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates

XX Sequence 531 AA;

Query Match 97.8%; Score 227; DB 3; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-222;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGQEESSGSQLHNSGSPETSRSLPAPQNDPL 65  
 DB 305 LQSVSSAIHLCDKKKMWLSLNPVNHGQEESSGSQLHNSGSPETSRSLPAPQNDPL 364

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125  
 DB 365 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 424

QY 126 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 185  
 DB 425 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 484

QY 186 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 232  
 DB 485 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 531

RESULT 4  
 AAW92795  
 ID AAW92795 standard; protein; 540 AA.

AC AAW92795;  
 DT 07-MAY-1999 (first entry)  
 DE Human B1 protein.  
 KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
 KW cell survival pathway; intracellular signalling; AIDS; cancer; human.

OS Homo sapiens.

PN WO9855507-A2.

PD 10-DEC-1998.

PF 01-JUN-1998; 98WO-IL000255.

PR 05-JUN-1997; 97IL-00121011.

PR 30-JUN-1997; 97IL-00121199.

PR 11-SEP-1997; 97IL-00121746.

PA (YEDA ) YEDA RES & DEV CO LTD.

XX Wallach D, Boldin M, Malinin N;

PI

XX

DR WPI; 1999-070258/06.  
 DR N-PSDB; AAX02558.

XX New B1 protein regulates cell death and cell survival pathways -  
 PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
 PT ; for treating AIDS, cancer.  
 XX Claim 4; Fig 3A; 90pp; English.

XX This invention describes the isolation of a novel human B1 protein which  
 CC can interact with, intracellular mediators or modulators of inflammation,  
 CC cell death and/or cell survival pathways, directly or indirectly. Cells  
 CC can be modulated or mediated in inflammation, cell death or cell survival  
 CC pathways or another intracellular signalling activity using B1.  
 CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
 CC oligonucleotides and ribozymes can also be used to regulate the above  
 CC pathways

XX Sequence 540 AA;

Query Match 97.8%; Score 227; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNPVNHGQEESSGSQLHNSGSPETSRSLPAPQNDPL 65

DB 314 LQSVSSAIHLCDKKKMWLSLNPVNHGQEESSGSQLHNSGSPETSRSLPAPQNDPL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125

DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433

QY 126 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 185

DB 434 GIAQWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLD 493

QY 186 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 232

DB 494 TDIQEEPAKVIQKLNKQKQGLQPYPEILVVSRSPLNLLQNKSM 540

RESULT 5  
 AAY68774

ID AAY68774 standard; protein; 540 AA.

AC AAY68774;

DT 16-MAY-2000 (first entry)

DE Amino acid sequence of a human phosphorylation effector PHSP-6.

KW Human; phosphorylation effector; PHSP; proliferative disorder;  
 KW immune disorder; neuronal disorder.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 18..287 /note= "protein kinase family signature sequence"

FT Modified-site 23 /note= "potential phosphorylation site"

FT Modified-site 34 /note= "potential phosphorylation site"

FT Modified-site 58 /note= "potential phosphorylation site"

FT Modified-site 100 /note= "potential glycosylation site"

FT Modified-site 102 /note= "potential phosphorylation site"

FT Modified-site 180 /note= "potential phosphorylation site"

FT Modified-site 183 /note= "potential phosphorylation site"

FT Modified-site /note= "potential phosphorylation site"

FT Modified-site 207 /note= "potential phosphorylation site"  
 FT Modified-site 224 /note= "potential phosphorylation site"  
 FT Modified-site 267 /note= "potential phosphorylation site"  
 FT Modified-site 296 /note= "potential phosphorylation site"  
 FT Modified-site 301 /note= "potential phosphorylation site"  
 FT Modified-site 360 /note= "potential phosphorylation site"  
 FT Modified-site 374 /note= "potential phosphorylation site"  
 FT Modified-site 391 /note= "potential phosphorylation site"  
 FT Modified-site 401 /note= "potential glycosylation site"  
 FT Modified-site 428 /note= "potential phosphorylation site"  
 FT Modified-site 442 /note= "potential phosphorylation site"  
 FT Modified-site 457 /note= "potential phosphorylation site"  
 FT Modified-site 478 /note= "potential glycosylation site"  
 FT Modified-site 478 /note= "potential phosphorylation site"  
 FT Modified-site 478 /note= "potential phosphorylation site"  
 FT Modified-site 484 /note= "potential phosphorylation site"  
 FT Modified-site 537 /note= "potential phosphorylation site"  
 FT Modified-site /note= "potential glycosylation site"  
 PN WO200006728-A2.  
 XX 10-FEB-2000.  
 XX 28-JUL-1999; 99WO-US017132.  
 XX 28-JUL-1998; 98US-0155213P.  
 PR 14-SEP-1998; 98US-0155196P.  
 PR 14-OCT-1998; 98US-0155239P.  
 PR 03-NOV-1998; 98US-0106889P.  
 PR 19-NOV-1998; 98US-0109093P.  
 PR 23-DEC-1998; 98US-0113796P.  
 PR 12-JAN-1999; 99US-0155233P.  
 XX (INCYTE) INCYTE PHARM INC.  
 PA Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI; 2000-183125/16.  
 DR N-PSDB; AAZ46143.  
 XX New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders.  
 XX Claim 1; Page 84-85; 142pp; English.  
 XX AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
 CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
 CC given in the specification). The sequences were isolated from cDNA  
 CC libraries prepared from various human tissues. The PHSP proteins are  
 CC useful for the diagnosis, treatment and prevention of proliferative  
 CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
 CC form pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity  
 XX Sequence 540 AA;

Query Match 97.8%; Score 227; DB 3; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 LQSVSAIHLCDKXKMWLSLNIPVNHGPOEESGSQLHSGSPETSRLPAPQNDL 65  
 DB 314 LQSVSAIHLCDKXKMWLSLNIPVNHGPOEESGSQLHSGSPETSRLPAPQNDL 373  
 QY 66 SRKAQDCYFMKLHHCPCGNSHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 125  
 DB 374 SRKAQDCYFMKLHHCPCGNSHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSRLQ 433  
 QY 126 GIAQWIOQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLLDT 185  
 DB 434 GIAQWIOQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLLDT 493  
 QY 186 TDIQGEFAKIVQKLKDNKQMGLOPYPEILVVSRSPLNLLQNKSM 232  
 DB 494 TDIQGEFAKIVQKLKDNKQMGLOPYPEILVVSRSPLNLLQNKSM 540  
 RESULT 6  
 AAM93621  
 ID AAM93621 standard; protein; 540 AA.  
 XX  
 AC AAM93621;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX Human polypeptide, SEQ ID NO: 3454.  
 DE Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX Homo sapiens.  
 OS  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR N-PSDB; AAK94554.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX  
 PS Claim 8; SEQ ID NO 3454; 1380pp + Sequence Listing; English.  
 XX  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX Sequence 540 AA;

Query Match 97.8%; Score 227; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 65  
 DB 314 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 125  
 DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 433

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
 DB 434 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493

QY 186 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 232  
 DB 494 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 7  
 AAU80369  
 ID AAU80369 standard; protein; 540 AA.  
 AC AAU80369;  
 DT 30-JUL-2002 (first entry)  
 XX Human cellular kinase RICK protein.  
 DE Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 KW RIP; Nck-interacting kinase; MKK3; SRPK-2.  
 XX Homo sapiens.  
 OS  
 PN EP1201765-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 15-OCT-2001; 2001EP-00124604.  
 XX  
 PR 16-OCT-2000; 2000US-0240750P.  
 XX  
 PA (AXXI-) AXXIMA PHARM AG.  
 XX  
 PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
 XX  
 DR WPI; 2002-373930/41.  
 DR N-PSDB; ABK51169.  
 XX  
 PT Identifying agents for treatment or prevention of cytomegalovirus  
 PT infection, comprises contacting test compound with cellular kinase and  
 PT detecting change in cellular kinase activity.  
 XX  
 PS Disclosure; Page 23-24; 49pp; English.  
 XX  
 CC The present invention relates to a new method for identifying compounds  
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
 CC related diseases. The method of the invention comprises contacting a test  
 CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
 CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
 CC activity. The method of the invention can be used to treat and/or prevent  
 CC CMV infections and related diseases. Oligonucleotides that can detect the  
 CC specified kinases can also be used for diagnosis of infection. The  
 CC present amino acid sequence represents the human cellular kinase RICK  
 CC protein of the invention, as described above  
 XX  
 SQ Sequence 540 AA;

Query Match 97.8%; Score 227; DB 5; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 65  
 DB 314 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 125  
 DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 433

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
 DB 434 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493

QY 186 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 232  
 DB 494 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 540

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 65  
 DB 314 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 125  
 DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 433

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
 DB 434 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493

QY 186 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 232  
 DB 494 TDIQGEFAKVIQVKLNDKQMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
 AAU27882  
 ID AAU27882 standard; protein; 540 AA.  
 XX AAU27882;  
 AC AAU27882;  
 DT 27-DEC-2002 (first entry)  
 XX Human receptor interacting protein (RIP)2.  
 DE Human; receptor interacting protein; RIP2; antisense; gene therapy.  
 KW Homo sapiens.  
 OS  
 PN US6426221-B1.  
 XX  
 PD 30-JUL-2002.  
 XX  
 PF 01-AUG-2001; 2001US-00920663.  
 XX  
 PR 01-AUG-2001; 2001US-00920663.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ward DT, Cowser LM;  
 XX  
 DR WPI; 2002-673017/72.  
 DR N-PSDB; AAD45172.  
 XX  
 PT New antisense oligonucleotide that targets regions of a nucleic acid  
 PT encoding human receptor interacting protein (RIP)2, for treating diseases  
 PT associated with RIP2 expression.  
 XX  
 PS Example 15; Col 49-54; 35pp; English.  
 XX  
 CC The invention relates to antisense compounds targeted to a nucleic acid  
 CC encoding human receptor interacting protein (RIP)2 to inhibit its  
 CC expression. Antisense compounds are used for treating diseases associated  
 CC with RIP2 expression. They are also useful in antisense gene therapy. The  
 CC present sequence is human RIP2 protein  
 XX  
 SQ Sequence 540 AA;

Query Match 97.8%; Score 227; DB 5; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1e-221;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 65  
 DB 314 LQSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDFL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 125  
 DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSERLQP 433

QY 126 GIAQWISQKREDIVNQMTAECLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 185  
ID AAB43570 standard; protein; 544 AA.  
XX AC AAB43570;  
XX 08-FEB-2001 (first entry)  
XX Human cancer associated protein sequence SEQ ID NO:1015.  
XX Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;  
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX  
OS Homo sapiens.  
XX WO200055350-A1.  
XX 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US005882.  
XX 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
PI WPI: 2000-587533/55.  
DR N-PSDB; AAC7779.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer.  
XX  
PS Claim 11; Page 1595-1597; 2352pp; English.  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
CC AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnery; immunomodulator;  
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of

CC the present invention  
XX Sequence 544 AA;  
SQ  
Query Match 97.8%; Score 227; DB 3; Length 544;  
Best Local Similarity 100.0%; Pred. No. 1e-221;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 LOSVSAIHLCDKKWELSLNIPVNHGPOBESGSSQLHENGSPETSRSLPAPQNDL 65  
Db 318 LOSVSAIHLCDKKWELSLNIPVNHGPOBESGSSQLHENGSPETSRSLPAPQNDL 377  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSRLQP 125  
Db 378 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSRLQP 437  
QY 126 GIAQWISQKREDIVNQMTAECLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 185  
Db 438 GIAQWISQKREDIVNQMTAECLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDIT 497  
QY 186 TDIQGEFAKVIQKLDKDKQKMGLOPYPEILVVSRSPLNLLQKSM 232  
Db 498 TDIQGEFAKVIQKLDKDKQKMGLOPYPEILVVSRSPLNLLQKSM 544  
RESULT 10  
ADC99079  
ID ADC99079 standard; protein; 510 AA.  
XX AC ADC99079;  
XX 01-JAN-2004 (first entry)  
XX Human KPP protein - SEQ ID 32.  
XX  
KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;  
KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;  
KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
KW cancer; developmental; mental retardation; neurological;  
KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
KW helminthic infection; transgenic; gene therapy; human; enzyme.  
XX  
OS Homo sapiens.  
XX WO2003033680-A2.  
XX 24-APR-2003.  
XX 17-OCT-2002; 2002WO-US033723.  
XX 19-OCT-2001; 2001US-0345474P.  
PR 02-NOV-2001; 2001US-0343910P.  
PR 13-NOV-2001; 2001US-033098P.  
PR 16-NOV-2001; 2001US-033424P.  
PR 30-NOV-2001; 2001US-0334288P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
PI Emerling BM, Forsythe JD, Gandhi AR, Gorvad AE, Griffin JA;  
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
PI Zebbarjadian Y;  
XX WPI: 2003-403214/38.



DR N-PSDB; ADC99131.  
 XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX Claim 1; SEQ ID NO 32; 424pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.  
 XX Sequence 510 AA;  
 XX  
 Query Match 84.9%; Score 197; DB 7; Length 510;  
 Best Local Similarity 100.0%; Pred. No. 3e-191;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 36 ECGSSQLHSGSPETSLPAPQNDFLSRKAQDCYFMKLHCPGNHSDSTSGSOR 95  
 DB 314 ECGSSQLHSGSPETSLPAPQNDFLSRKAQDCYFMKLHCPGNHSDSTSGSOR 373  
 QY 96 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMTACINQSLDAL 155  
 DB 374 AAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQMTACINQSLDAL 433  
 QY 156 LSRDLIMKEDYELVSTKPTRTSKVRLDITDIQGEFAKVIQKLKDKNQGLQPYPEI 215  
 DB 434 LSRDLIMKEDYELVSTKPTRTSKVRLDITDIQGEFAKVIQKLKDKNQGLQPYPEI 493  
 QY 216 LVVSRSPSLNLLQNSM 232  
 DB 494 LVVSRSPSLNLLQNSM 510  
 RESULT 11  
 AAY59407  
 XX ID AAY59407 standard; protein; 167 AA.  
 XX AC AAY59407;  
 XX 21-MAR-2000 (first entry)  
 XX  
 DE Human RICK protein sequence residues 365-531.  
 XX  
 KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
 KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
 KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
 KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
 KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9955134-A2.  
 XX  
 PD 04-NOV-1999.  
 XX  
 XX 27-APR-1999; 99WO-US0009183.  
 PF  
 PR 27-APR-1998; 98US-00069023.  
 XX  
 PA (UNMI ) UNIV MICHIGAN.

XX Nunez G, Inohara N, Koseki T;  
 XX WPI; 2000-072163/06.  
 DR Compositions for identifying apoptosis signaling pathway inhibitors  
 PT useful for treating diseases.  
 PT  
 XX Claim 6; Page; 93pp; English.  
 PS  
 XX This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
 CC kinase) protein of the invention. RICK acts as a positive regulator of  
 CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
 CC during CD95 signalling. The invention provides methods for identifying  
 CC apoptosis signalling pathway inhibitors and activators, and methods and  
 CC compositions for screening compounds which will modulate the interactions  
 CC of the various compositions identified: ARC, RICK, and the CIDE family of  
 CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
 CC assays for agents, useful in the diagnosis, prognosis or treatment of  
 CC disease associated with excess cell growth and dysregulation of  
 CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
 CC screening assays to identify inhibitor and molecules blocking CD95-mediated  
 CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
 CC to identify inhibitors of the enzymatic activity of caspase-8.  
 CC Identification of ARC-like inhibitory compounds may be useful for gene  
 CC therapy treatment of disease with increased cell death in muscle tissue  
 CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
 CC treat e.g. cancer, AIDS, neurodegenerative diseases, aplastic anaemia,  
 CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
 CC can be used as reagents for the preparation or affinity chromatography  
 CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
 CC of an essential step in the biochemistry of apoptosis is needed. RICK  
 CC interaction with intracellular factors such as CLARP and FADD appears to  
 CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
 CC apoptosis factors are potential drug candidates. Note: This sequence was  
 CC created using information given in the specification  
 XX  
 SQ Sequence 167 AA;  
 XX  
 Query Match 72.0%; Score 167; DB 3; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-161;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 66 SRKAQDCYFMKLHCPGNHSDSTSGSORAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
 DB 1 SRKAQDCYFMKLHCPGNHSDSTSGSORAFCDHKTTPCSSAIINPLSTAGNSERLQ 60  
 QY 126 GIAQQWIOSKREDIVNQMTACINQSLDALSRDLIMKEDYELVSTKPTRTSKVRLDIT 185  
 DB 61 GIAQQWIOSKREDIVNQMTACINQSLDALSRDLIMKEDYELVSTKPTRTSKVRLDIT 120  
 QY 186 TDIQGEFAKVIQKLKDKNQGLQPYPEILVVSRSPSLNLLQNSM 232  
 DB 121 TDIQGEFAKVIQKLKDKNQGLQPYPEILVVSRSPSLNLLQNSM 167  
 RESULT 12  
 AAY31140  
 ID AAY31140 standard; protein; 540 AA.  
 XX  
 AC AAY31140;  
 XX  
 XX 25-OCT-1999 (first entry)  
 DT  
 XX Human CARD-3 protein.  
 DE  
 XX  
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;

QY	Db	Accession	Location/Qualifiers	Key	Domain	Location/Qualifiers
QY	165	DYELVSTKPTRTSKVRQLDDTTDIQGEFQKVIQKLNKQMGLOPYPEILVVSRSFSL 224	Location/Qualifiers i. .300 /note= "predicted kinase domain"	Key Domain	1. .400 /note= "kinase domain"	PCSSAIINPLSTAGNSERLOPGIAQOWTQSKREDIVNQWTEACLNQSLDALLSRDLINKE 477
QY	165	DYELVSTKPTRTSKVRQLDDTTDIQGEFQKVIQKLNKQMGLOPYPEILVVSRSFSL 224	Location/Qualifiers 301. .431 /note= "predicted linker domain"	Key Domain	401. .431 /note= "linker domain"	DYELVSTKPTRTSKVRQLDDTTDIQGEFQKVIQKLNKQMGLOPYPEILVVSRSFSL 224
QY	165	DYELVSTKPTRTSKVRQLDDTTDIQGEFQKVIQKLNKQMGLOPYPEILVVSRSFSL 224	Location/Qualifiers 432. .540 /note= "predicted CARD domain"	Key Domain	432. .540 /note= "CARD"	DYELVSTKPTRTSKVRQLDDTTDIQGEFQKVIQKLNKQMGLOPYPEILVVSRSFSL 224
QY	225	NLLQKSM 232		Key Domain		NLLQKSM 232
QY	533	NLLQKSM 540		Key Domain		NLLQKSM 540
QY	23-APR-2001	(first entry)		Key Domain		23-APR-2001 (first entry)
QY	Human	CARD-3 protein.		Key Domain		Human CARD-3 protein.
QY	CARD-3	cardiomyocyte domain; human; cancer; infection;		Key Domain		CARD-3; cardiomyocyte domain; human; cancer; infection;
QY	autoimmune	disease; neurological disease; haematological disease;		Key Domain		autoimmune disease; neurological disease; haematological disease;
QY	immune	disease; inflammation; antitumour; antiseptic; immunomodulator;		Key Domain		immune disease; inflammation; antitumour; antiseptic; immunomodulator;
QY	antiinflammatory;	apoptosis; diagnosis; gene therapy.		Key Domain		antiinflammatory; apoptosis; diagnosis; gene therapy.
QY	Homo sapiens.			Key Domain		Homo sapiens.
QY	Bertin J;			Key Domain		Bertin J;
QY	WPI; 1999-494269/41.			Key Domain		WPI; 1999-494269/41.
QY	N-PSDB; AA209246.			Key Domain		N-PSDB; AA209246.
QY	Novel CARD-3 and CARD-4 genes and polypeptides used or treating			Key Domain		Novel CARD-3 and CARD-4 genes and polypeptides used or treating
QY	regulation of cellular proliferation and differentiation and cell			Key Domain		regulation of cellular proliferation and differentiation and cell
QY	survival.			Key Domain		survival.
QY	Example 2; Fig 2; 181pp; English.			Key Domain		Example 2; Fig 2; 181pp; English.
QY	This invention describes the isolation of novel human caspase recruitment			Key Domain		This invention describes the isolation of novel human caspase recruitment
QY	domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial			Key Domain		domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial
QY	murine CARD-4L protein and genes. The genes and proteins of the invention			Key Domain		murine CARD-4L protein and genes. The genes and proteins of the invention
QY	are involved in the regulation of caspase activation. The caspase			Key Domain		are involved in the regulation of caspase activation. The caspase
QY	recruitment domain (CARD) polynucleotides, polypeptides, homologues and			Key Domain		recruitment domain (CARD) polynucleotides, polypeptides, homologues and
QY	antibodies can be used in screening assays, detection assays, predictive			Key Domain		antibodies can be used in screening assays, detection assays, predictive
QY	medicine and therapeutic and prophylactic methods of treatment. The			Key Domain		medicine and therapeutic and prophylactic methods of treatment. The
QY	methods may be used to diagnose and treat patients which are suffering			Key Domain		methods may be used to diagnose and treat patients which are suffering
QY	from a disorder associated with abnormal level or rate of apoptotic cell			Key Domain		from a disorder associated with abnormal level or rate of apoptotic cell
QY	death, abnormal activity of the Fas/APO-1 receptor complex, abnormal			Key Domain		death, abnormal activity of the Fas/APO-1 receptor complex, abnormal
QY	activity of the TNF receptor complex, or abnormal activity of a caspase.			Key Domain		activity of the TNF receptor complex, or abnormal activity of a caspase.
QY	Diseases that may be treated include cancer (particularly follicular			Key Domain		Diseases that may be treated include cancer (particularly follicular
QY	lymphoma, carcinomas associated with mutations in p53 and hormone-			Key Domain		lymphoma, carcinomas associated with mutations in p53 and hormone-
QY	dependent tumours), autoimmune disorders (e.g. systemic lupus			Key Domain		dependent tumours), autoimmune disorders (e.g. systemic lupus
QY	erythematosus, immune-mediated glomerulonephritis), viral infections,			Key Domain		erythematosus, immune-mediated glomerulonephritis), viral infections,
QY	Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,			Key Domain		Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
QY	retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,			Key Domain		retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,
QY	anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.			Key Domain		anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.
QY	CARD-3 protein interacts with other cellular proteins, and so can be used			Key Domain		CARD-3 protein interacts with other cellular proteins, and so can be used
QY	for regulation of cellular proliferation and differentiation and cell			Key Domain		for regulation of cellular proliferation and differentiation and cell
QY	survival. The CARD proteins may also be used to for screen drugs or			Key Domain		survival. The CARD proteins may also be used to for screen drugs or
QY	compounds which modulate their activity. The CARD-4 gene can express a			Key Domain		compounds which modulate their activity. The CARD-4 gene can express a
QY	long transcript that encodes CARD-4L, a short transcript that encodes			Key Domain		long transcript that encodes CARD-4L, a short transcript that encodes
QY	CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence			Key Domain		CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence
QY	represents the human CARD-3 protein described in the method of the			Key Domain		represents the human CARD-3 protein described in the method of the
QY	invention			Key Domain		invention
QY	Sequence 540 AA;			Key Domain		Sequence 540 AA;
QY	Query Match	55.2%; Score 128; DB 2; Length 540;		Key Domain		Query Match
QY	Best Local Similarity	100.0%; Pred. No. 4.4e-121;		Key Domain		Best Local Similarity</

CC with insufficient or excessive production of CARD-3, -4, -5 or -6  
CC protein, or production of an aberrant protein  
XX  
SQ Sequence 540 AA;

Query Match 55.2%; Score 128; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4.4e-121; Indels 0; Gaps 0;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAECLNQSLDALLSRDLINKE 164  
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAECLNQSLDALLSRDLINKE 472

QY 165 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 224  
DB 473 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 532

QY 225 NLLQNKSM 232  
DB 533 NLLQNKSM 540

RESULT 14  
ABG31075  
ID ABG31075 standard; protein; 540 AA.  
XX  
AC ABG31075;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human caspase recruitment domain protein CARD-3.  
XX  
KW Human; caspase recruitment domain; CARD-3; CARD-4; LRR;  
KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
KW gastrointestinal allergy; insulin-dependent diabetes;  
KW bacterial infection; tuberculosis; lepromatous leprosy;  
KW cell signalling disorder; tissue disorder.  
XX  
OS Homo sapiens.  
XX  
FN WO200253765-A1.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-US049798.  
XX  
PR 29-DEC-2000; 2000US-0258724P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Bertin J, Philpott D, Sansonetti P, Girardin S;  
XX  
DR WPI; 2002-583627/62.  
DR N-PSDB; ABK89280.  
XX  
PT Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.  
XX  
PS Example 2; Fig 2; 139pp; English.  
XX  
CC The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of

CC identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4 are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein  
XX  
SQ Sequence 540 AA;

Query Match 55.2%; Score 128; DB 5; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4.4e-121; Indels 0; Gaps 0;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAECLNQSLDALLSRDLINKE 164  
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAECLNQSLDALLSRDLINKE 472

QY 165 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 224  
DB 473 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKQMGLOPYPEILVWSRPSL 532

QY 225 NLLQNKSM 232  
DB 533 NLLQNKSM 540

RESULT 15  
AAO22107  
ID AAO22107 standard; protein; 540 AA.  
XX  
AC AAO22107;  
XX  
DT 27-SEP-2002 (first entry)  
XX  
DE Protein of human CARD-3 SEQ ID No 2.  
XX  
KW Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's; cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; nootropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.  
XX  
OS Homo sapiens.  
XX  
FN US6369196-B1.  
XX  
PD 09-APR-2002.  
XX  
PF 05-FEB-1999; 99US-00245281.  
XX  
PR 06-FEB-1998; 98US-00019942.  
PR 17-JUN-1998; 98US-00039041.  
PR 08-DEC-1998; 98US-00207359.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Bertin J;  
XX



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:11:47 ; Search time 22 Seconds  
(without alignments)  
544.419 Million cell updates/sec

Title: US-09-771-161a-93

Perfect score: 232

Sequence: 1 MSLQLQSVSSAIHLCDKKK.....PEILVVSRSLSNLLQNKSM 232

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 20

Total number of hits satisfying chosen parameters: 25

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	284	4	US-09-069-023-5
2	227	97.8	478	4	US-09-069-023-4
3	227	97.8	530	4	US-09-069-023-3
4	227	97.8	531	4	US-09-069-023-1
5	227	97.8	540	4	US-09-069-023-27
6	227	97.8	540	4	US-09-345-473E-28
7	167	72.0	167	4	US-09-069-023-6
8	128	55.2	540	3	US-09-019-942-1
9	128	55.2	540	4	US-09-099-041A-2
10	128	55.2	540	4	US-09-245-281-2
11	128	55.2	540	4	US-09-470-271-1
12	128	55.2	540	4	US-09-207-359B-2
13	128	55.2	540	4	US-09-340-620A-2
14	128	55.2	540	4	US-09-865-364-2
15	128	55.2	540	4	US-09-748-537-1
16	110	47.4	110	4	US-09-207-359B-6
17	110	47.4	110	4	US-09-865-364-6
18	109	47.0	109	4	US-09-099-041A-6
19	109	47.0	109	4	US-09-245-281-6
20	109	47.0	109	4	US-09-340-620A-6
21	98	42.2	131	4	US-09-099-041A-5
22	98	42.2	131	4	US-09-245-281-5
23	98	42.2	131	4	US-09-207-359B-5
24	98	42.2	131	4	US-09-340-620A-5
25	98	42.2	131	4	US-09-865-364-5

ALIGNMENTS

```
RESULT 1
US-09-069-023-5
; Sequence 5, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-5

Query Match          97.8%; Score 227; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 3.9e-220;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENS GSPETSRSLPAPQNDFL 65
DB 58 LQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENS GSPETSRSLPAPQNDFL 117
QY 66 SRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 125
DB 118 SRKAQDCYFMKLHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQP 177
QY 126 GIAQWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLDPT 185
DB 178 GIAQWIOSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLDPT 237
QY 186 TDIQGEFAKIVOKLKDKNQKGLQPYPEILVVSRSLSNLLQNKSM 232
DB 238 TDIQGEFAKIVOKLKDKNQKGLQPYPEILVVSRSLSNLLQNKSM 284

RESULT 2
US-09-069-023-4
; Sequence 4, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-4

Query Match          97.8%; Score 227; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 6.2e-220;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENS GSPETSRSLPAPQNDFL 65
DB 252 LQSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENS GSPETSRSLPAPQNDFL 311
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; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-473E-28

Query Match 97.8%; Score 227; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 7e-220;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 LOSVSAIHLCKKMWELSLNIPVNHGPOEESCGSQLHENGSPETSRSLPAPQNDPL 65  
DB 314 LOSVSAIHLCKKMWELSLNIPVNHGPOEESCGSQLHENGSPETSRSLPAPQNDPL 373  
  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCASSAIINPLSTAGNSERLQP 125  
DB 374 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCASSAIINPLSTAGNSERLQP 433  
  
QY 126 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 434 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 493  
  
QY 186 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSLNLLQKSM 232  
DB 494 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSLNLLQKSM 540

RESULT 7  
US-09-069-023-6  
; Sequence 6, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-6

Query Match 72.0%; Score 167; DB 4; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.8e-160;  
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCASSAIINPLSTAGNSERLQP 125  
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QY 126 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185  
DB 61 GIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 120  
  
QY 186 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSLNLLQKSM 232  
DB 121 TDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSLNLLQKSM 167

RESULT 8  
US-09-019-942-1

; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-019-942-1

Query Match 55.2%; Score 128; DB 3; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472  
  
QY 165 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSL 224  
DB 473 DYELVSTKPTRTSKVRQLLDTTDIOGEFAKVIQKLDKDKNQKMGLOPYPEILVVSRSFSL 532  
  
QY 225 NLLQKSM 232  
DB 533 NLLQKSM 540  
  
RESULT 9  
US-09-099-041A-2  
; Sequence 2, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-2

Query Match      55.2%; Score 128; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 10
US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES-OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-2

Query Match      55.2%; Score 128; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 11
US-09-470-271-1
; Sequence 1, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
```

```
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-470-271-1

Query Match      55.2%; Score 128; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.2e-120;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLKDNKQMGLOQYPPEILVVSRSPSL 532

Qy 225 NLLQNKSM 232
Db 533 NLLQNKSM 540

RESULT 12
US-09-207-359B-2
; Sequence 2, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-207-359B-2

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472

QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 224  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

RESULT 13  
 US-09-340-620A-2  
 ; Sequence 2, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US/09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US/09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US/09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-340-620A-2

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 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
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 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472

QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 224  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

RESULT 14  
 US-09-865-364-2  
 ; Sequence 2, Application US/09865364  
 ; Patent No. 6613521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/865,364  
 ; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-865-364-2

Query Match 55.2%; Score 128; DB 4; Length 540;  
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 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472

QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 224  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

RESULT 15  
 US-09-748-537-1  
 ; Sequence 1, Application US/09748537  
 ; Patent No. 6680167  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-748-537-1

Query Match 55.2%; Score 128; DB 4; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-120;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 164  
 DB 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKE 472

QY 165 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 224  
 DB 473 DYELVSTKPTRTSKVRQLDITDIQGEFPAKIVIVQKLDKDKQKGLQPYPEILLVWSRPSL 532

QY 225 NLLQNKSM 232  
 DB 533 NLLQNKSM 540

Search completed: March 29, 2004, 14:15:28  
 Job time : 23 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:12:57 ; Search time 43 Seconds  
(without alignments)  
1411.757 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1065169 seqs, 261661801 residues

Word size : 20  
Total number of hits satisfying chosen parameters: 24

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	232	100.0	232	9	US-09-771-161A-93
2	227	97.8	540	9	US-09-771-161A-184
3	227	97.8	540	9	US-09-862-027-28
4	227	97.8	540	10	US-09-981-397A-14
5	227	97.8	544	9	US-09-925-301-1015
6	128	55.2	540	9	US-09-748-537-1
7	128	55.2	540	9	US-09-728-721-2
8	128	55.2	540	13	US-10-133-780-1
9	128	55.2	540	13	US-10-105-931-2
10	128	55.2	540	13	US-10-118-984-2
11	128	55.2	540	14	US-10-295-981-2
12	109	47.0	109	9	US-09-728-721-6
13	109	47.0	109	13	US-10-105-931-6
14	109	47.0	109	13	US-10-118-984-6
15	109	47.0	109	14	US-10-295-981-6

Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 21, Appli  
Sequence 21, Appli  
Sequence 21, Appli  
Sequence 10, Appli  
Sequence 11, Appli

16 98 42.2 131 9 US-09-728-721-5  
17 98 42.2 131 13 US-10-105-931-5  
18 98 42.2 131 13 US-10-118-984-5  
19 98 42.2 131 14 US-10-295-981-5  
20 92 39.7 92 13 US-10-014-269-21  
21 92 39.7 92 13 US-10-002-974-21  
22 92 39.7 92 14 US-10-314-506-21  
23 90 38.8 90 9 US-09-841-879B-10  
24 89 38.4 89 9 US-09-931-071-11

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

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Matches 232; Conservative 0; Mismatches 0;  
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DB 1 MYSLOQSVSSAIHLCDKKKMELSINIPVNHGQPESCGSSQLHNSGSPETSRSLPAQ 60  
QY 61 DNDFLSRKAQDCYFMKLHPCGNHSDSTISGSQRAAFCDHKHTTCCSSAIINPLSTAGNS 120  
DB 61 DNDFLSRKAQDCYFMKLHPCGNHSDSTISGSQRAAFCDHKHTTCCSSAIINPLSTAGNS 120  
QY 121 ERLQFGIAQOWTQSKREDIVNQTEACLNQSLDALLSRDLINKEDYELVSTKPTRTSKVR 180  
DB 121 ERLQFGIAQOWTQSKREDIVNQTEACLNQSLDALLSRDLINKEDYELVSTKPTRTSKVR 180  
QY 181 QLLDITTDIQGEFAKVIQKLNKQMGLOQPYPEILVVSRSPLNLLQNKSM 232  
DB 181 QLLDITTDIQGEFAKVIQKLNKQMGLOQPYPEILVVSRSPLNLLQNKSM 232

RESULT 2  
US-09-771-161A-184  
; Sequence 184, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 273  
 ; SOFTWARE: Patent version 3.0  
 ; SEQ ID NO 184  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-771-161A-184

Query Match 97.8%; Score 227; DB 9; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESGSSQLHNSGSPETSRSLPAPQNDL 65  
 DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESGSSQLHNSGSPETSRSLPAPQNDL 373  
 QY 66 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
 DB 374 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433  
 QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
 DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493  
 QY 186 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 232  
 DB 494 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 540

RESULT 3

US-09-862-027-28  
 ; Sequence 28, Application US/09862027  
 ; Patent No. US20020142428A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hodge, Martin R.  
 ; TITLE OF INVENTION: No. US20020142428A1 Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/234862  
 ; CURRENT APPLICATION NUMBER: US/09/862,027  
 ; CURRENT FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: US 09/345,473  
 ; PRIOR FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 82  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-862-027-28

Query Match 97.8%; Score 227; DB 9; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESGSSQLHNSGSPETSRSLPAPQNDL 373  
 QY 66 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
 DB 374 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433  
 QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
 DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493  
 QY 186 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 232  
 DB 494 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 540

RESULT 4

US-09-981-397A-14  
 ; Sequence 14, Application US/09981397A  
 ; Publication No. US20030082519A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axixima Pharmaceuticals AG  
 ; APPLICANT: Schubart, Daniel  
 ; APPLICANT: Habenberger, Peter  
 ; APPLICANT: Stein-Gerlach, Matthias  
 ; APPLICANT: Bevec, Dorian  
 ; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
 ; TITLE OF INVENTION: Inhibition  
 ; FILE REFERENCE: AXM-004.1 US  
 ; CURRENT APPLICATION NUMBER: US/09/981,397A  
 ; CURRENT FILING DATE: 2002-06-28  
 ; PRIOR APPLICATION NUMBER: 60/240,750  
 ; PRIOR FILING DATE: 2000-10-16  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-981-397A-14

Query Match 97.8%; Score 227; DB 10; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 LQSVSSAIHLCDKKMELSLNIPVNHGPOESGSSQLHNSGSPETSRSLPAPQNDL 65  
 DB 314 LQSVSSAIHLCDKKMELSLNIPVNHGPOESGSSQLHNSGSPETSRSLPAPQNDL 373  
 QY 66 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 125  
 DB 374 SRKAQDCYFMKLHCHPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 433  
 QY 126 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 185  
 DB 434 GIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRLD 493  
 QY 186 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 232  
 DB 494 TDIOGEFAKVIQKLDKQMGLOPYPEILVVSRSPLNLLQKSM 540

RESULT 5

US-09-925-301-1015  
 ; Sequence 1015, Application US/09925301  
 ; Patent No. US20020052308A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA106  
 ; CURRENT APPLICATION NUMBER: US/09/925,301  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1694  
 ; SOFTWARE: Patent version 2.0  
 ; SEQ ID NO 1015  
 ; LENGTH: 544  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-925-301-1015

Query Match 97.8%; Score 227; DB 9; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 318 LOSVSAIHLCDKKMELSLNIPVNHGPOBSCSSQLHENSQSPETSRSLPAPQDNDFL 377

Qy 66 SRKAQDCYFMKLHCPGNHWDSTTSGSQAFAFCDHKTTPCSSAIINPLSTAGNSERLOP 125

Db 378 SRKAQDCYFMKLHCPGNHWDSTTSGSQAFAFCDHKTTPCSSAIINPLSTAGNSERLOP 437

Qy 126 GIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 185

Db 438 GIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT 497

Qy 186 TDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 498 TDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPLNLLQNKSM 544

RESULT 6

US-09-748-537-1

Sequence 1, Application US/09748537

Patent No. US20020061833A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

APPLICANT: Chao, Moses V.

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-316001

CURRENT APPLICATION NUMBER: US/09/748,537

CURRENT FILING DATE: 2000-12-26

PRIOR APPLICATION NUMBER: US/09/999,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-748-537-1

Query Match 55.2%; Score 128; DB 9; Length 540;

Best Local Similarity 100.0%; Pred. No. 4e-116;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 413 PCSSAIINPLSTAGNSERLOPQIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 224

Db 473 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 532

Qy 225 NLLQNKSM 232

Db 533 NLLQNKSM 540

RESULT 7

US-09-728-721-2

Sequence 2, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/340,620

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US/09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US/09/999,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US/09/019,942

PRIOR FILING DATE: 1998-02-06

US-09-728-721-2

Query Match 55.2%; Score 128; DB 9; Length 540;

Best Local Similarity 100.0%; Pred. No. 4e-116;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLOPQIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKE 164

Db 413 PCSSAIINPLSTAGNSERLOPQIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 224

Db 473 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 532

Qy 225 NLLQNKSM 232

Db 533 NLLQNKSM 540

RESULT 8

US-10-133-780-1

Sequence 1, Application US/10133780

Publication No. US20020123115A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-133-780-1

Query Match 55.2%; Score 128; DB 13; Length 540;

Best Local Similarity 100.0%; Pred. No. 4e-116;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-728-721-2

Query Match 55.2%; Score 128; DB 9; Length 540;

Best Local Similarity 100.0%; Pred. No. 4e-116;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLOPQIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKE 164

Db 413 PCSSAIINPLSTAGNSERLOPQIAQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKE 472

Qy 165 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 224

Db 473 DYELVSTKPTRTSKVRQLLDTTDIQGEERFAKVIQKLNKQKMGLOPYPEILVVSRSPL 532

Qy 225 NLLQNKSM 232

Db 533 NLLQNKSM 540

RESULT 8

US-10-133-780-1

Sequence 1, Application US/10133780

Publication No. US20020123115A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-133-780-1

Query Match 55.2%; Score 128; DB 13; Length 540;

Best Local Similarity 100.0%; Pred. No. 4e-116;

Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 532
Qy 225 NLLQKSM 232
Db 533 NLLQKSM 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-2

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Query Match 55.2%; Score 128; DB 13; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 532
Qy 225 NLLQKSM 232
Db 533 NLLQKSM 540

```

```

RESULT 10
US-10-118-984-2
; Sequence 2, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-2

Query Match 55.2%; Score 128; DB 13; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 532
Qy 225 NLLQKSM 232
Db 533 NLLQKSM 540

RESULT 11
US-10-295-981-2
; Sequence 2, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-2

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Query Match 55.2%; Score 128; DB 14; Length 540;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 164
Db 413 PCSSAIINPLSTAGNSERLQPGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKE 472
Qy 165 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 224
Db 473 DYELVSTKPTRTSKVRQLDITDIQGEFAKVIIVQKLNKQKMGLOPYPEILVVSRSPL 532
Qy 225 NLLQKSM 232
Db 533 NLLQKSM 540

RESULT 12
US-09-728-721-6
; Sequence 6, Application US/09728721
; Patent No. US20020061845A1

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; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-6

Query Match          47.0%; Score 109; DB 9; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 183
DB 1 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 13
US-10-105-931-6
; Sequence 6, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-6

Query Match          47.0%; Score 109; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 183
DB 1 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 14
US-10-118-984-6
; Sequence 6, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-6

Query Match          47.0%; Score 109; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 183
DB 1 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 60

QY 184 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 232
DB 61 DTTDIQGEFAKVIQVKLNQKMGLOPYPEILVVSRSFSLNLLQKSM 109

RESULT 15
US-10-295-981-6
; Sequence 6, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-6

Query Match          47.0%; Score 109; DB 14; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.4e-98;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 183
DB 1 QPGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLL 60

```





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:10:51 ; Search time 20 Seconds  
(without alignments)  
1115.822 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQLQSVSSAIHLCDKKK.....PEILVVSRSPSLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:\*  
1: Piri:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						

No matches found

Search completed: March 29, 2004, 14:14:52  
Job time : 20 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:09:41 ; Search time 17 Seconds  
(without alignments)  
710.604 Million cell updates/sec

Title: US-09-771-161a-93

Perfect score: 232

Sequence: 1 MYSLQLQSVSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 20

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	540	1 RIK2 HUMAN	O43353 h receptor-
2	27	11.6	539	1 RIK2_MOUSE	P58801 mus musculus

#### ALIGNMENTS

#### RESULT 1

RIK2 HUMAN  
ID RIK2 HUMAN STANDARD; PRT; 540 AA.  
AC O43353;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)  
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme  
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).  
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RX MEDLINE=98241596; PubMed=9575181;  
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;  
RT "RICK, a novel protein kinase containing a caspase recruitment domain,  
interacts with CLARP and regulates CD95-mediated apoptosis.";  
RL J. Biol. Chem. 273:12296-12300(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RC TISSUE=Endothelial cells;

RX MEDLINE=98307936; PubMed=9642260;  
RA McCarthy J.V., Ni J., Dixit V.M.;  
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing  
kinase.";  
RL J. Biol. Chem. 273:16968-16975(1998).  
RN [3]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.  
RX MEDLINE=98381580; PubMed=9705938;  
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,  
RA Mattmann C., Tschopp J.;  
RT "Identification of CARDIAK, a RIP-like kinase that associates with  
caspase-1.";  
RL Curr. Biol. 8:885-888(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Ozersky P., Holmes A., Broy M.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Platzer M., Varon R.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting R.W., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
receptor complex.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,  
peripheral blood leukocytes, spleen, kidney, testis, prostate,  
pancreas and lymph node.  
CC -!- PTM: Autophosphorylated.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; AF027706; AAC34970.1; -  
DR EMBL; AF078530; AAC27722.1; -  
DR EMBL; AF064824; AAC25668.1; -  
DR EMBL; AC004003; AAC24561.1; -  
DR EMBL; AF117829; AAD04634.1; -

```
DR EMBL; BC004553; AAH04553.1; --
DR Genew; HGNC:10020; RPK2.
DR MIM; 603455; --
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; PROTEIN KINASE ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT NP_BIND 24 32 CARD.
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146 K-A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 47 47 K-S: REDUCES FAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D-S: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;

Query Match 97.8%; Score 227; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.4e-233;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQSVSSAIHLCDKKKELSLNIPVNHGQPEESGSSQHSOLHENSQSPETSRSLPAPQNDL 65
DB 314 LQSVSSAIHLCDKKKELSLNIPVNHGQPEESGSSQHSOLHENSQSPETSRSLPAPQNDL 373

QY 66 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAINPLSTAGNSERLQ 125
DB 374 SRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAINPLSTAGNSERLQ 433

QY 126 GIAQOMIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRLD 185
DB 434 GIAQOMIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTTSKVRLD 493

QY 186 TDIQGEFEFAKVIQKLDKNDKQMGLOPYPEILVVSRSFSLNLLQNSM 232
DB 494 TDIQGEFEFAKVIQKLDKNDKQMGLOPYPEILVVSRSFSLNLLQNSM 540

RESULT 2
RIK2 MOUSE
ID_RIK2_MOUSE STANDARD; PRT; 539 AA.
AC P58801;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).
GN RPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097;
RA Chin A.I.; Dempsey P.W.; Bruhn K.; Miller J.F.; Xu Y.; Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
```

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RT immune responses.";
RL Nature 416:190-194(2002).
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/C-IAP1 and BIRC2/C-IAP2, TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
EMBL; AF461040; AAL96436.1; --
MGD; MGI:1891456; RPK2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
FT DOMAIN 18 294 PROTEIN KINASE.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Query Match 11.6%; Score 27; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 QMTEACLNQSLDALLSRDLIMKEDYEL 168
DB 449 QMTEACLNQSLDALLSRDLIMKEDYEL 475

Search completed: March 29, 2004, 14:13:21
Job time : 17 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:10:16 ; Search time 45 Seconds  
(without alignments)  
1626.672 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQLOSVSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 20

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
-----					

No matches found

Search completed: March 29, 2004, 14:14:19  
Job time : 45 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 11:22:08 ; Search time 4002 Seconds  
(without alignments)  
2512.640 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table:  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 20

Total number of hits satisfying chosen parameters: 39

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlh  
-O=/cn2 1/USPTO spool/US09771161/runat\_29032004.124851.19858/app.query.fasta\_1.391  
-DB=GenEmbl -QFMT=fastap -SUFFIX=oli20p2n.rge -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=20 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1 1 2496 @runat\_29032004.124851.19858 -NCPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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ALIGNMENTS

RESULT 1  
AF078530  
LOCUS  
DEFINITION Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete  
ACCESSION AF078530  
VERSION AF078530.1 GI:3342909

1623 bp mRNA linear PRI 28-JUL-1998

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db	1180	TGGGACAGCACCATTCTTGGATCTCAAGGGCTGCAATTCGTGATCACAAGACCACTCCA	123
Qy	106	CysSerSerAlaIleAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro	125
Db	1240	TGCTCTTCTCAGCAATAATAATCCACTCTCACTCAGGAACTCAGAACTGTCAGCCT	1299
Qy	126	GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu	145
Db	1300	GGTATAGCCAGCAGTGGATCCAGACCAAGGAGAACATTTGTGAACCAATGACAGAA	1359
Qy	146	AlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAsp	165
Db	1360	GCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGAC	1419
Qy	166	TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr	185
Db	1420	TATGAACCTTGTGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGCAATTTACTAGACACT	1479
Qy	186	ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys	205
Db	1480	ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAACAAA	1539
Qy	206	GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn	225
Db	1540	CAATGGGTCTTTCAGCCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAAT	1599
Qy	226	LeuLeuGlnAsnLysSerMet	232
Db	1600	TTACTTCAAAATAAAGCATG	1620
RESULT 2			
AY335645			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
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QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
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DEFINITION Homo sapiens clone DNA43306 RIPK2 (UNQ277) mRNA, complete cds.
ACCESSION AY358813
VERSION AY358813.1 GI:3718743
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1886)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1886)
AUTHORS Clark,H.F.
Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
JOURNAL Location/Qualifiers
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ACCESSION	BC004553		
VERSION	BC004553.2	GI:33871163	
KEYWORDS	MGC.		
SOURCE	Homo sapiens	(human)	
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1889)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Brownstein, R.A., S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,		

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerich, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
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2 (bases 1 to 1889)	
Strausberg, R.	
Direct Submission	
Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
On Aug 19, 2003 this sequence version replaced gi:13528713.	
Contact: MGC help desk	
Email: <a href="mailto:cgabbs@mail.nih.gov">cgabbs@mail.nih.gov</a>	
Tissue Procurement: ATCC/DCID/DTP	
CDNA Library Preparation: Rubin Laboratory	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;	
Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>	
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Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.I., Masciello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsougeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	
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FEATURES  
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CDS

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Query Match: 97.84% Indels: 0
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VERSION AF064824.1 GI:3290171
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REFERENCE 1 (bases 1 to 1902)
AUTHORS Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C. and Tschopp J.
TITLE Identification of CARDIAK, a RIP-like kinase that associates with
caspase-1
JOURNAL Curr. Biol. 8 (1998) In press
REFERENCE 2 (bases 1 to 1902)
AUTHORS Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C. and Tschopp J.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-1998) Institute of Biochemistry, University of
Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066,
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ACCESSION BD251808
VERSION BD251808.1 GI:33061578
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2024)
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A.,
Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.I.
Phosphorylation effectors
Patent: JP 2002526035-A 6 20-AUG-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002526035-A/6
PD 20-AUG-2002
PF 28-JUL-1999 JP 2000362510
PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR
14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR
19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR
12-JAN-1999 US 60/155233
PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J
GUEGLER,
PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU
YOUNG,
PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA
PI M LU,
PI LEO L SHIH
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PC C12N15/09,A61K38/00,A61K45/00,A61P1/04,A61P1/16,A61P3/10 PC
,A61P5/14,A61P5/38,
PC A61P7/00,A61P9/10,A61P11/00,A61P17/00,A61P19/02,A61P19/06, PC
A61P21/04
PC A61P25/00,A61P25/08,A61P25/14,A61P25/16,A61P25/18,A61P25/28,
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PC A61P31/10,A61P31/12,A61P31/18,A61P33/00,A61P35/00,A61P35/02,
PC A61P37/00,
PC A61P37/08,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
12,C12N9/16,
PC C12Q1/68,G01N33/50,G01N33/566,C12N15/00,C12N5/00,A61K37/02 CC
PC C12Q1/68,G01N33/50,G01N33/566,C12N15/00,C12N5/00,A61K37/02 CC
Incyte Clone Number: 156108
FH Key Location/Qualifiers
FT source 1..2024
FT /organism='Homo sapiens (human)'.
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1..2024
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/db_xref='taxon:9606'
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Alignment Scores: 6.73e-218 Length: 2024
Pred. No.: 227.00 Matches: 227
Score: 227.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-771-161A-93 (1-232) x BD251808 (1-2024)
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Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
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Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1322 TCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCAGTCTCTGGAAATCAGAGT 1381
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105
Db 1382 TGGATAGCACCACCTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAAGACCACTCCA 1441
Qy 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
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Qy 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
Db 1502 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGCACAGAA 1561
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Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
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Db 1802 TTACTTCAAAATAAAGCATG 1822

RESULT 7
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LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION
ACCESSION BD127583.1 GI:23222528
VERSION JP 2002017375-A/3014
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2033)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 3014 22-JAN-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3014
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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Pred. No.: 6,75e-218 Length: 2033
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x BD127583 (1-2033)

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QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1218 ACATACCTGTAAATCATGGTCACAGAGGAATCATGTGGATCCCTCAGCTCCATGAA 1277
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1278 AATAGTGGTTCCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTTAA 1337
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db 1338 TCTAGAAAAGCTCAGACTGTTATTTATGAAGCTCATCACTGTCTCTGGAATCACAGT 1397
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QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
Db 1518 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTACCAATGACAGAA 1577
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Db 1638 TATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1697
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QY 226 LeuLeuGlnAsnLysSerMet 232
Db 1818 TTACTTCAAAATAAAGCATG 1838

RESULT 8
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LOCUS Homo sapiens cDNA FLJ90732 fis, clone PLACE1010081, highly similar
DEFINITION to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
ACCESSION AK075213
VERSION AK075213.1 GI:22761157
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2033)
AUTHORS Isogai,T. and Otsuki,T.
JOURNAL Direct Submission
TITLE Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5' & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
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US-09-771-161A-93 (1-232) x AK075213 (1-2033)

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QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1218 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1277
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPheLeu 65
DB 1278 AATAGTGGTTCCTCGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1337
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB 1338 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGGAATATCAGT 1397
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105
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QY 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
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QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
DB 1518 GGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTGTGAACCAAAATGACAGAA 1577
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DB 1578 GCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1637
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DB 1638 TATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAGACCTCAAAGACCAATTTACTAGACACT 1697
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
DB 1698 ACTGACATCCAGAGAGAAATTTGCTAAAGTTATAGTACAAAATTTGAAAGATACAAA 1757
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
DB 1758 CAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTCTTAGATCACCATCTTTAAAT 1817
QY 226 LeuLeuGlnAsnLysSerMet 232
DB 1818 TTACTTTCAAAATAAAGCATG 1838

RESULT 9
LOCUS A82777 2098 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9855507.
ACCESSION A82777
VERSION A82777.1 GI:6732464
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2098)
AUTHORS Boldin,M. and Wallach,D.
TITLE MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL
SURVIVAL PATHWAYS
JOURNAL Patent: WO 9855507-A 2 10-DEC-1998;
BOLDIN MARK (IL); WALLACH DAVID (IL)
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ORIGIN

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Score: 227.00 Matches: 227
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DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x A82777 (1-2098)

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QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB 1379 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGGAATATCAGT 1438
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QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
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RESULT 10
BD106658
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LOCUS BD106658 2098 bp DNA linear PAT 18-SEP-2002  
DEFINITION Modulators of intracellular inflammation, cell death and cell survival pathways.  
ACCESSION BD106658  
VERSION BD106658.1 GI:23201476  
KEYWORDS JP 2002502258-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 2098)  
AUTHORS Wallach,D., Boldin,M. and Malinin,N.  
TITLE Modulators of intracellular inflammation, cell death and cell survival pathways  
JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;  
YEDA RESEARCH AND DEVELOPMENT CO LTD  
COMMENT PN JP 2002502258-A/1  
PD 22-JAN-2002  
PF 01-JUN-1998 JP 1999501993 121011,30-JUN-1997 IL 121199 PR  
PR 05-JUN-1997 IL 121746  
11-SEP-1997 IL 121746  
PI DAVID WALLACH, MARK BOLDIN, NIKOLAI MALININ  
PC C12N15/12, C07K14/47, C07K16/18, C12Q1/68, A61K38/17, G01N33/68 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
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Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
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QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
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DB 1319 AATAGTGGTTCCTCGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1378  
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DB 1859 TTACTTCAAAATAAAAGCATG 1879  
RESULT 11  
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LOCUS AR221453 2501 bp DNA linear PAT 26-SEP-2002  
DEFINITION Sequence 3 from patent US 6426221.  
ACCESSION AR221453  
VERSION AR221453.1 GI:23328503  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2501)  
AUTHORS Ward,D.T. and Cowsett,L.M.  
TITLE Antisense modulation of RIP2 expression  
JOURNAL Patent: US 6426221-A 3 30-JUL-2002;  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
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QY      186   ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnLys 205
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QY      206   GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
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QY      226   LeuLeuGlnAsnLysSerMet 232
Db      1824  TTACTTCAAAATAAAGCATG 1844

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LOCUS   AX429236
DEFINITION AX429236 Sequence 13 from Patent EP1201765.
ACCESSION AX429236
VERSION   AX429236.1 GI:21540548
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.

REFERENCE 1
AUTHORS  Schubart,D., Habenberger,P., Stein-Gerlach,M. and Bevec,D.
TITLE     Cellular kinases involved in cytomagalovirus infection and their
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JOURNAL   Patent: EP 1201765-A 13 02-MAY-2002;
          Axxima Pharmaceuticals Aktiengesellschaft (DE)
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    97.84%      Indels:    0
DB:             6          Gaps:      0

US-09-771-161A-93 (1-232) x AX429236 (1-2501)

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QY      26   AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
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QY      46   AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      1284 AATAGTGGTCTCTCGAATCTTCAAGGTCCCTCGACCTCCTCAAGACAATGATTTTAA 1343
QY      66   SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db      1344 TCTAGAAAGACTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCGAAATCAGT 1403
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QY      166   TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
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QY      186   ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnLys 205
Db      1704 ACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1763
QY      206   GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
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QY      226   LeuLeuGlnAsnLysSerMet 232
Db      1824 TTACTTCAAAATAAAGCATG 1844

RESULT 13
LOCUS   AF027706
DEFINITION Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
ACCESSION AF027706
VERSION   AF027706.1 GI:3123886
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE 1 (bases 1 to 2501)
AUTHORS  Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
TITLE     RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis
JOURNAL   J. Biol. Chem. 273 (20), 12296-12300 (1998)
MEDLINE   98241596
PUBMED    9575181
REFERENCE 2 (bases 1 to 2501)
AUTHORS  Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
TITLE     Direct Submission
JOURNAL   Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor, MI 48109, USA

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polyA_signal
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Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     97.84%      Indels:       0
DB:              9          Gaps:          0

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QY      26 AnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB      1224 AACATACCTGTAAATCATGGTCCACAAAGGGAATCATGTGGATCTCTCAGCTCCATGAA 1283
QY      46 AnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB      1284 AATAGTGGTTCCTCGAAACTTCAGAGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1343
QY      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB      1344 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCTGGAATCACAGT 1403
QY      86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105
DB      1404 TGGGATAGCACCATTCTCGTGTCTCAAGGGCTGCATCTGTGATCACAAAGACCCTCCA 1463
QY      106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
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DB      1524 GGTATAGCCAGCAGTGGATCCAGACAAAAGGAAGACATTGTGAACAAATGACAGAA 1583
QY      146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
DB      1584 GCCTGCTCTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGGAACCTTGATGATGAAGAGGAC 1643
QY      166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
DB      1644 TATGAACTTGTAGTACCAGGCTCAAGACCTCAANAAGTCAAGAAATTAATGACACT 1703
QY      186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
DB      1704 ACTGACATCCAGGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAAA 1763
QY      206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225
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DEFINITION      Sequence 2 from patent US 6348573.
ACCESSION      AR194318
VERSION        AR194318.1      GI:20240910
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 2502)
AUTHORS      Nunez,G., Inohara,N. and Koseki,T.
TITLE        Compositions and methods for identifying apoptosis signaling
              pathway inhibitors and activators
JOURNAL       Patent: US 6348573-A 2 19-FEB-2002;
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QY      26 AnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB      1225 AACATACCTGTAAATCATGGTCCACAAAGGGAATCATGTGGATCTCTCAGCTCCATGAA 1284
QY      46 AnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB      1285 AATAGTGGTTCCTCGAAACTTCAGAGTCCCTGCCAGCTCCTCAAGACAAATGATTTTAA 1344
QY      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB      1345 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCTGGAATCACAGT 1404
QY      86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105
DB      1405 TGGGATAGCACCATTCTCGTGTCTCAAGGGCTGCATCTGTGATCACAAAGACCCTCCA 1464
QY      106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
DB      1465 TGCCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGACGCTCGAGCCCT 1524
QY      126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
DB      1525 GGTATAGCCAGCAGTGGATCCAGACAAAAGGAAGACATTGTGAACAAATGACAGAA 1584
QY      146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
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VERSION AY358814.1 GI:37182745  
KEYWORDS FLI CDNA.  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2521)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
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Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wleand,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
12975309  
REFERENCE 2 (bases 1 to 2521)  
AUTHORS Clark,H.F.  
TITLE Direct Submission  
SUBMITTED (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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ORIGIN

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Query Match: 97.84% Indels: 0  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 13:59:15 ; Search time 61 Seconds  
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1074.607 Million-cell updates/sec

Title: US-09-771-161A-93

Perfect score: 1206

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

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5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

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8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	1182	98.0	540	5	AAE27882	Human rec	AAE27882 Human rec
9	1182	98.0	544	3	AAW43570	Human can	AAW43570 Human can
10	1176	97.5	540	2	AAV31140	Human CAR	AAV31140 Human CAR
11	1176	97.5	540	4	AAW20079	Human CAR	AAW20079 Human CAR
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42	122.5	10.2	953	7	ABJ72227	Human nuc
43	121.5	10.1	953	5	ABG31076	Human cas
44	119	9.9	100	5	AAO22112	Human CAR
45	119	9.9	100	6	ABU56274	Human CAR

#### ALIGNMENTS

##### RESULT 1

AA59406

ID AA59406 standard; protein; 284 AA.

XX AA59406;

AC AA59406;

XX DT 21-MAR-2000 (first entry)

XX DE Human RICK protein sequence residues 248-531.

XX KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;

XX KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;

XX KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;

XX KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;

XX KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.

XX OS Homo sapiens.

XX PN WO9955134-A2.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US009183.

XX PR 27-APR-1998; 98US-00069023.

XX PA (UNMI ) UNIV MICHIGAN.

XX PI Nunez G, Inohara N, Koseki T;

XX DR WPI; 2000-072163/06.

XX PT Compositions for identifying apoptosis signaling pathway inhibitors

XX PT useful for treating diseases.

XX PS Claim 6; Page; 93pp; English.

XX CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP

XX CC kinase) protein of the invention. RICK acts as a positive regulator of

XX CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

XX CC during CD95 signalling. The invention provides methods for identifying

XX CC apoptosis signalling pathway inhibitors and activators, and methods and

XX CC compositions for screening compounds which will modulate the interactions

XX CC of the various compositions identified: ARC, RICK, and the CIDE family of

XX CC activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

XX CC assays for agents, useful in the diagnosis, prognosis or treatment of

XX CC disease associated with excess cell growth and dysregulation of

XX CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC screening assays to identify inhibitor molecules blocking CD95-mediated  
CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
CC to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene  
CC therapy treatment of disease with increased cell death in muscle tissue  
CC and cardiac disorders. Therapeutic compositions of CIDBs can be used to  
CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
CC can be used as reagents for the preparation or affinity chromatography  
CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
CC of an essential step in the biochemistry of apoptosis is needed. RICK  
CC interaction with intracellular factors such as CLARP and FADD appears to  
CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates. Note: This sequence was  
CC created using information given in the specification  
XX  
SQ

Query Match 98.0%; Score 1182; DB 3; Length 284;  
Best Local Similarity 99.6%; Pred. No. 2.1e-115;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLOSVSAIHLCDKKKWLNLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 57 KLOSVSAIHLCDKKKWLNLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 116  
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISSGQRAAFCDHKTTPCSSAIINPLSTAGNERLQ 124  
DB 117 LSRKAQDCYFMKLHHCPCGNHSDSTISSGQRAAFCDHKTTPCSSAIINPLSTAGNERLQ 176  
QY 125 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 177 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 236  
QY 185 TTDIOGEEFAKVIQKLKONKQGLQPYPEILVVSRSPLNLLQKSM 232  
DB 237 TTDIOGEEFAKVIQKLKONKQGLQPYPEILVVSRSPLNLLQKSM 284

RESULT 2  
AA59405  
ID AAY59405 standard; protein; 478 AA.  
XX AC AAY59405;  
XX 21-MAR-2000 (first entry)  
XX Human RICK protein sequence residues 54-531.  
XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX

OS Homo sapiens.  
XX  
XX WO9955134-A2.  
XX 04-NOV-1999.  
XX 27-APR-1999; 99WO-US009183.  
XX 27-APR-1998; 98US-00069023.  
XX (UNMI ) UNIV MICHIGAN.  
XX Nunez G, Inohara N, Koseki T;  
XX WPI; 2000-072163/06.  
XX  
XX Compositions for identifying apoptosis signalling pathway inhibitors  
XX useful for treating diseases.  
PT

XX Claim 6; Page; 93pp; English.  
PS  
XX  
CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP  
CC kinase) protein of the invention. RICK acts as a positive regulator of  
CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
CC during CD95 signalling. The invention provides methods for identifying  
CC apoptosis signalling pathway inhibitors and activators, and methods and  
CC compositions for screening compounds which will modulate the interactions  
CC of the various compositions identified: ARC, RICK, and the CIDE family of  
CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening of  
CC assays for agents, useful in the diagnosis, prognosis or treatment of  
CC disease associated with excess cell growth and dysregulation of  
CC apoptosis. Complexes containing RICK and CLARP can be used in drug  
CC screening assays to identify inhibitor molecules blocking CD95-mediated  
CC apoptosis. Overexpression of ARC in an in vitro cell system can be used  
CC to identify inhibitors of the enzymatic activity of caspase-8.  
CC Identification of ARC-like inhibitory compounds may be useful for gene  
CC therapy treatment of disease with increased cell death in muscle tissue  
CC and cardiac disorders. Therapeutic compositions of CIDBs can be used to  
CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
CC can be used as reagents for the preparation or affinity chromatography  
CC media, and for diagnostically measuring RICK levels. A specific inhibitor  
CC of an essential step in the biochemistry of apoptosis is needed. RICK  
CC interaction with intracellular factors such as CLARP and FADD appears to  
CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates. Note: This sequence was  
CC created using information given in the specification  
XX

SQ Sequence 478 AA;  
Query Match 98.0%; Score 1182; DB 3; Length 478;  
Best Local Similarity 99.6%; Pred. No. 4.6e-115;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLOSVSAIHLCDKKKWLNLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 251 KLOSVSAIHLCDKKKWLNLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 310  
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISSGQRAAFCDHKTTPCSSAIINPLSTAGNERLQ 124  
DB 311 LSRKAQDCYFMKLHHCPCGNHSDSTISSGQRAAFCDHKTTPCSSAIINPLSTAGNERLQ 370  
QY 125 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 371 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 430  
QY 185 TTDIOGEEFAKVIQKLKONKQGLQPYPEILVVSRSPLNLLQKSM 232  
DB 431 TTDIOGEEFAKVIQKLKONKQGLQPYPEILVVSRSPLNLLQKSM 478

RESULT 3  
AA59404  
ID AAY59404 standard; protein; 531 AA.  
XX AC AAY59404;  
XX 21-MAR-2000 (first entry)  
XX Human RICK protein sequence.  
XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.  
XX  
XX Homo sapiens.  
XX WO9955134-A2.  
XX



XX Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 18. .287  
FT /note= "protein kinase family signature sequence"  
FT 23  
FT /note= "potential phosphorylation site"  
FT 34  
FT /note= "potential phosphorylation site"  
FT 58  
FT /note= "potential phosphorylation site"  
FT 100  
FT /note= "potential glycosylation site"  
FT 102  
FT /note= "potential phosphorylation site"  
FT 180  
FT /note= "potential phosphorylation site"  
FT 183  
FT /note= "potential phosphorylation site"  
FT 207  
FT /note= "potential phosphorylation site"  
FT 224  
FT /note= "potential phosphorylation site"  
FT 267  
FT /note= "potential phosphorylation site"  
FT 296  
FT /note= "potential phosphorylation site"  
FT 301  
FT /note= "potential phosphorylation site"  
FT 360  
FT /note= "potential phosphorylation site"  
FT 374  
FT /note= "potential phosphorylation site"  
FT 391  
FT /note= "potential glycosylation site"  
FT 401  
FT /note= "potential phosphorylation site"  
FT 428  
FT /note= "potential phosphorylation site"  
FT 442  
FT /note= "potential phosphorylation site"  
FT 457  
FT /note= "potential glycosylation site"  
FT 478  
FT /note= "potential phosphorylation site"  
FT 478  
FT /note= "potential phosphorylation site"  
FT 484  
FT /note= "potential phosphorylation site"  
FT 537  
FT /note= "potential glycosylation site"  
XX WO200006728-A2.  
XX 10-FEB-2000.  
XX 28-JUL-1999; 99WO-US017132.  
XX 28-JUL-1998; 98US-0155213P.  
XX 14-SEP-1998; 98US-0155196P.  
XX 14-OCT-1998; 98US-0155239P.  
XX 03-NOV-1998; 98US-0106889P.  
XX 19-NOV-1998; 98US-0109093P.  
XX 22-DEC-1998; 98US-0113796P.  
XX 12-JAN-1999; 99US-0155233P.  
XX (INCY-) INCYTE PHARM INC.  
XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI

PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX WPI; 2000-183125/16.  
DR N-PSDB; AAZ46143.  
XX  
FT New human phosphorylation effectors useful for the diagnosis, treatment  
FT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 1; Page 84-85; 142pp; English.  
XX  
CC AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
CC given in the specification). The sequences were isolated from CDNA  
CC libraries prepared from various human tissues. The PHSP proteins are  
CC useful for the diagnosis, treatment and prevention of proliferative  
CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
CC form pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity  
XX  
SQ Sequence 540 AA;  
Query Match 98.0%; Score 1182; DB 3; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.6e-115;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLOSVSATHLCKKMKWELSLNIPVNHGPOEESGSSQLHENSGETSRLPAPQDNDF 64  
DB :|||||  
313 KQSVSSATHLCKKMKWELSLNIPVNHGPOEESGSSQLHENSGETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISSGQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 124  
DB :|||||  
373 LSRKAQDCYFMKLHCPGNHSDSTISSGQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIQSKREDIVNQMTAEACINQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLLD 184  
DB :|||||  
433 PGIAQOWIQSKREDIVNQMTAEACINQSLDALLSRDLIMKEDYELVSTKPTTSKVRQLLD 492  
QY 185 TTDTIQEEFAKIVQKLKONKONGLOPYPEILVVRSPSLNLLQNKSM 232  
DB :|||||  
493 TTDTIQEEFAKIVQKLKONKONGLOPYPEILVVRSPSLNLLQNKSM 540  
RESULT 6  
AAM93621  
ID AAM93621 standard; protein; 540 AA.  
XX  
AC AAM93621;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide, SEQ ID NO: 3454.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping.  
XX Homo sapiens.  
XX  
FN EF1130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;









CC	identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, such as immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein	CC
XX	Sequence 540 AA;	XX
SQ		SQ
Query Match	97.5%; Score 1176; DB 5; Length 540;	
Best Local Similarity	99.1%; Pred. No. 2.4e-114;	
Matches 226; Conservative	1; Mismatches 1; Indels 0; Gaps 0;	
QY	5 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGETSRSLPAPQDNDF 64	QY
Db	313 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGETSRSLPAPQDNDF 372	Db
QY	65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 124	QY
Db	373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 432	Db
QY	125 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184	QY
Db	433 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492	Db
QY	185 TTDIOGEEFAKVIQVKLKNQKQGLQPYPEILVVSRSPLNLLQNKSM 232	QY
Db	493 TTDIOGEEFAKVIQVKLKNQKQGLQPYPEILVVSRSPLNLLQNKSM 540	Db
RESULT 13		
AAO22107		
ID	AAO22107 standard; protein; 540 AA.	ID
XX		XX
AC	AAO22107;	AC
XX		XX
DT	27-SEP-2002 (first entry)	DT
XX		XX
DE	Protein of human CARD-3 SEQ ID No 2.	DE
XX		XX
KW	Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;	KW
KW	cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;	KW
KW	nootropic; antiataemic; caspase Recruitment Domain; CARD; CARD-4L; p53;	KW
KW	cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;	KW
KW	hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;	KW
KW	systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;	KW
KW	anaemia; neutropenia; myelodysplastic syndrome; human.	KW
XX		XX
OS	Homo sapiens.	OS
XX		XX
PN	US6369196-B1.	PN
XX		XX
PD	09-APR-2002.	PD
XX		XX
PF	05-FEB-1999; 99US-00245281.	PF
XX		XX
PR	06-FEB-1998; 98US-00019942.	PR
PR	17-JUN-1998; 98US-0009041.	PR
PR	08-DEC-1998; 98US-00207359.	PR
XX		XX

CC	identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, such as immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence represents human CARD-3 protein	CC
XX	Sequence 540 AA;	XX
SQ		SQ
Query Match	97.5%; Score 1176; DB 4; Length 540;	
Best Local Similarity	99.1%; Pred. No. 2.4e-114;	
Matches 226; Conservative	1; Mismatches 1; Indels 0; Gaps 0;	
QY	5 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGETSRSLPAPQDNDF 64	QY
Db	313 QLOSVSSAIHLCDKKKMWLSLNIPVNHGPOESCGSSQLHENSGETSRSLPAPQDNDF 372	Db
QY	65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 124	QY
Db	373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 432	Db
QY	125 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184	QY
Db	433 PGTAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492	Db
QY	185 TTDIOGEEFAKVIQVKLKNQKQGLQPYPEILVVSRSPLNLLQNKSM 232	QY
Db	493 TTDIOGEEFAKVIQVKLKNQKQGLQPYPEILVVSRSPLNLLQNKSM 540	Db
RESULT 12		
ABG31075		
ID	ABG31075 standard; protein; 540 AA.	ID
XX		XX
AC	ABG31075;	AC
XX		XX
DT	21-OCT-2002 (first entry)	DT
XX		XX
DE	Human caspase recruitment domain protein CARD-3.	DE
XX		XX
KW	Human; caspase recruitment domain; CARD-3; CARD-4; LRR;	KW
KW	leucine rich repeat; LPS; lipopolysaccharide; NF-kB;	KW
KW	nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;	KW
KW	systemic lupus erythematosus; immune-mediated glomerulonephritis;	KW
KW	arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;	KW
KW	atopic condition; asthma; allergy; psoriasis; contact dermatitis;	KW
KW	gastrointestinal allergy; insulin-dependent diabetes;	KW
KW	bacterial infection; tuberculosis; lepromatous leprosy;	KW
KW	cell signalling disorder; tissue disorder.	KW
XX		XX
OS	Homo sapiens.	OS
XX		XX
PN	WO200253765-A1.	PN
XX		XX
PD	11-JUL-2002.	PD
XX		XX
PF	20-DEC-2001; 2001WO-US049798.	PF
XX		XX
PR	29-DEC-2000; 2000US-0258724P.	PR
XX		XX
PA	(MILL-) MILLENNIUM PHARM INC.	PA
XX		XX
PI	Bertin J, Philpott D, Sansonetti P, Girardin S;	PI
XX		XX
DR	WPI; 2002-583627/62.	DR
DR	N-PSDB; ABK89280.	DR
XX		XX
PT	Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.	PT
XX		XX
PS	Example 2; Fig 2; 139pp; English.	PS
XX		XX
CC	The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of	CC

PA (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 PI  
 XX WPI; 2002-391988/42.  
 DR N-PSDB; AAL40752, AAL40753.  
 XX  
 PT Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD  
 PT -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's  
 PT disease, cancers and viral infections.  
 XX  
 XX Example 2; Fig 2; 116pp; English.  
 PS  
 XX The invention relates to novel isolated Caspase Recruitment Domain (CARD)  
 CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may  
 CC be used to treat disorders associated with decreased CARD expression by  
 CC supplementing the patient's own production of CARD. Disorders associated  
 CC with the expression and activity of CARD include cancers (particularly  
 CC follicular lymphomas, carcinomas associated with mutations in p53, and  
 CC hormone-dependent tumours such as breast cancer, prostate cancer, and  
 CC ovarian cancer), autoimmune disorders (such as systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections  
 CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),  
 CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,  
 CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal  
 CC muscular atrophy, and various forms of cerebellar degeneration), anaemia  
 CC associated with chronic disease, aplastic anaemia, chronic neutropenia,  
 CC and the myelodysplastic syndromes. This sequence represents a human CARD  
 CC protein relating to the invention  
 XX  
 XX Sequence 540 AA;  
 SQ

Query Match 97.5%; Score 1176; DB 5; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
 DB 313 KLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
 DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
 QY 125 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 433 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 QY 185 TTDIQGEPAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232  
 DB 493 TTDIQGEPAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 14  
 ABUS6269 standard; protein; 540 AA.  
 XX  
 AC ABUS6269;  
 XX  
 DT 30-APR-2003 (first entry)  
 XX  
 DE Human Caspase recruitment domain protein, CARD-3.  
 XX  
 KW Human; caspase recruitment domain; CARD; CARD-3; CARD-4; CARD-4L;  
 KW CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS; autoimmune disorder;  
 KW systemic lupus erythematosus; viral infection;  
 KW immune related glomerulonephritis; acquired immunodeficiency syndrome;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular atrophy; cerebellar degeneration; haematological disease;  
 KW anaemia; neutropaenia; myelodysplastic syndrome; myocardial infarction;  
 KW stroke; chromosome 7.  
 XX

OS Homo sapiens.  
 XX  
 PN US6469140-B1.  
 PD 22-OCT-2002.  
 XX  
 PF 08-DEC-1998; 98US-00207359.  
 XX  
 PR 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Bertin J;  
 XX  
 XX WPI; 2003-147109/14.  
 DR N-PSDB; ABX75869, ABX74870.  
 XX  
 PT Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
 PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
 PT detection assays, predictive medicine, and in therapeutic applications.  
 XX  
 PS Example 2; Fig 2; 99pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide, comprising at least 25  
 CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
 CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
 CC polypeptide. Also included is an isolated fusion protein, comprising the  
 CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
 CC polypeptide. The CARD polypeptide is useful in screening assays,  
 CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
 CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
 CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
 CC prophylactic treatments (in diseases associated with apoptotic cell death  
 CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
 CC immune related glomerulonephritis), viral infections, AIDS (acquired  
 CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
 CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
 CC haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic  
 CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
 CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
 CC identify other proteins, which bind to or interact with other CARD  
 CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
 CC human CARD-4 is located on chromosome 7. The present sequence is a human  
 CC CARD protein  
 XX  
 SQ Sequence 540 AA;  
 Query Match 97.5%; Score 1176; DB 6; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-114;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
 DB 313 KLOSVSSAIHLCDKKKMKELSLNIPVNHGQPEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
 QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
 DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
 QY 125 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
 DB 433 PGIAQOWIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
 QY 185 TTDIQGEPAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232  
 DB 493 TTDIQGEPAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 15  
 ADB81362 standard; protein; 540 AA.  
 ID ADB81362



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:07:10 ; Search time 22 Seconds  
(without alignments)  
544.419 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLOQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNSKM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A-COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/6C-COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/6D-COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	98.0	284	US-09-069-023-5	Sequence 5, Appli
2	1182	98.0	478	US-09-069-023-4	Sequence 4, Appli
3	1182	98.0	530	US-09-069-023-3	Sequence 3, Appli
4	1182	98.0	531	US-09-069-023-1	Sequence 1, Appli
5	1182	98.0	540	US-09-069-023-27	Sequence 27, Appli
6	1182	98.0	540	US-09-345-473B-28	Sequence 28, Appli
7	1176	97.5	540	US-09-019-942-1	Sequence 1, Appli
8	1176	97.5	540	US-09-099-041A-2	Sequence 2, Appli
9	1176	97.5	540	US-09-245-281-2	Sequence 2, Appli
10	1176	97.5	540	US-09-470-271-1	Sequence 1, Appli
11	1176	97.5	540	US-09-207-359B-2	Sequence 2, Appli
12	1176	97.5	540	US-09-340-620A-2	Sequence 2, Appli
13	1176	97.5	540	US-09-865-364-2	Sequence 2, Appli
14	1176	97.5	540	US-09-748-537-1	Sequence 1, Appli
15	867	71.9	167	US-09-069-023-6	Sequence 6, Appli
16	632	52.4	131	US-09-099-041A-5	Sequence 5, Appli
17	632	52.4	131	US-09-245-281-5	Sequence 5, Appli
18	632	52.4	131	US-09-207-359B-5	Sequence 5, Appli
19	632	52.4	131	US-09-340-620A-5	Sequence 5, Appli
20	632	52.4	131	US-09-865-364-5	Sequence 5, Appli
21	548	45.4	110	US-09-207-359B-6	Sequence 6, Appli
22	548	45.4	110	US-09-865-364-6	Sequence 6, Appli
23	544	45.1	109	US-09-099-041A-6	Sequence 6, Appli
24	544	45.1	109	US-09-245-281-6	Sequence 6, Appli
25	544	45.1	109	US-09-340-620A-6	Sequence 6, Appli
26	149.5	12.4	109	US-09-340-620A-71	Sequence 71, Appli
27	122.5	10.2	164	US-09-245-281-41	Sequence 41, Appli

28	122.5	10.2	164	US-09-207-359B-41	Sequence 41, Appli
29	122.5	10.2	164	US-09-340-620A-41	Sequence 41, Appli
30	122.5	10.2	164	US-09-865-364-41	Sequence 41, Appli
31	122.5	10.2	249	US-09-245-281-39	Sequence 39, Appli
32	122.5	10.2	249	US-09-207-359B-39	Sequence 39, Appli
33	122.5	10.2	249	US-09-340-620A-39	Sequence 39, Appli
34	122.5	10.2	249	US-09-865-364-39	Sequence 39, Appli
35	122.5	10.2	409	US-09-207-359B-46	Sequence 46, Appli
36	122.5	10.2	409	US-09-865-364-46	Sequence 46, Appli
37	122.5	10.2	953	US-09-099-041A-8	Sequence 8, Appli
38	122.5	10.2	953	US-09-245-281-8	Sequence 8, Appli
39	122.5	10.2	953	US-09-207-359B-8	Sequence 8, Appli
40	122.5	10.2	953	US-09-340-620A-8	Sequence 8, Appli
41	122.5	10.2	953	US-09-865-364-8	Sequence 8, Appli
42	119	9.9	100	US-09-099-041A-10	Sequence 10, Appli
43	119	9.9	100	US-09-245-281-10	Sequence 10, Appli
44	119	9.9	100	US-09-207-359B-10	Sequence 10, Appli
45	119	9.9	100	US-09-340-620A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Query Match	98.0%	Score 1182;	DB 4;	Length 284;
Best Local Similarity	99.6%	Pred. No. 1.9e-125;		
Matches 227;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	5	QLQSVSSAIHLCDKKKMELSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF	64	
Db	57	QLQSVSSAIHLCDKKKMELSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF	116	
QY	65	LSRKAQDCYFKMLHPCGNHSDWSTISGSORAAFCDHKTTPCCSSALINPLSTAGNSERLQ	124	
Db	117	LSRKAQDCYFKMLHPCGNHSDWSTISGSORAAFCDHKTTPCCSSALINPLSTAGNSERLQ	176	
QY	125	PGIAQWQISQKREEDIVNQWTEACLNQSLDALLSRDLINKEDYELVSTKTRTSKVRQLLD	184	
Db	177	PGIAQWQISQKREEDIVNQWTEACLNQSLDALLSRDLINKEDYELVSTKTRTSKVRQLLD	236	
QY	185	TTDIGEEFAKVIQKLDKDKMGLOPYPEILVVSRSPLNLLQNSKM	232	
Db	237	TTDIGEEFAKVIQKLDKDKMGLOPYPEILVVSRSPLNLLQNSKM	284	

RESULT 2  
US-09-069-023-4  
; Sequence 4, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 478  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-4

Query Match 98.0%; Score 1182; DB 4; Length 478;  
Best Local Similarity 99.6%; Pred. No. 4.2e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 251 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 310  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
Db 311 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 370  
Qy 125 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 371 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 430  
Qy 185 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db 431 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 478

RESULT 3  
US-09-069-023-3  
; Sequence 3, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-3

Query Match 98.0%; Score 1182; DB 4; Length 530;  
Best Local Similarity 99.6%; Pred. No. 5e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 303 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 362  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
Db 363 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 422  
Qy 125 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 423 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 482  
Qy 185 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 232

Db 483 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 530

RESULT 4  
US-09-069-023-1  
; Sequence 1, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-1

Query Match 98.0%; Score 1182; DB 4; Length 531;  
Best Local Similarity 99.6%; Pred. No. 5e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 304 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 363  
Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
Db 364 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 423  
Qy 125 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
Db 424 PGIAQOWIQSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 483  
Qy 185 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 232  
Db 484 TTDIQGEFAKVIQKLDKKNKMGLOPYPEILVVSRSPLNLLQNKSM 531

RESULT 5  
US-09-069-023-27  
; Sequence 27, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-27

Query Match 98.0%; Score 1182; DB 4; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.1e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
Db 313 KLOSVSAAIHLCDKKKMWLSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 232  
DB 493 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 540

RESULT 6

US-09-345-473E-28  
; Sequence 28, Application US/09345473E  
; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin  
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-345-473E-28

Query Match 98.0%; Score 1182; DB 4; Length 540;  
Best Local Similarity 99.6%; Pred. No. 5.1e-125;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 232  
DB 493 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 540

RESULT 7

US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95

3/7/00

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-019-942-1

Query Match 97.5%; Score 1176; DB 3; Length 540;

Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 232  
DB 493 TTDIQGEFAKVIQKLDKDKMGLQPYPEILVVSRSPLNLLQNSM 540

RESULT 8

US-09-099-041A-2

; Sequence 2, Application US/09099041A

; Patent No. 6340576

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-076001

; CURRENT APPLICATION NUMBER: US/09/099,041A

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 09/019,942

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-099-041A-2

Query Match 97.5%; Score 1176; DB 4; Length 540;

Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 QLOSVSSAIHLCDKKMELSLNIPVNHGPOEESGSSQLHNSGSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 124  
Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 432  
QY 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
QY 185 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 232  
Db 493 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 540

## RESULT 9

US-09-245-281-2  
; Sequence 2, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-245-281-2

Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 OLOSVSSAIHLCDKKKWEISLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 64  
Db 313 KLOSVSSAIHLCDKKKWEISLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 124  
Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 432  
QY 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
QY 185 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 232  
Db 493 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 540

## RESULT 10

US-09-470-271-1  
; Sequence 1, Application US/09470271  
; Patent No. 6410689  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA

; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/470,271  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/019,942  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-470-271-1

Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 OLOSVSSAIHLCDKKKWEISLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 64  
Db 313 KLOSVSSAIHLCDKKKWEISLNIPVNHGPOEESCGSSQLHENSGETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 124  
Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDDHKTTPCSSLAIINPLSTAGNSERLQ 432  
QY 125 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 184  
Db 433 PGIAQWIOSKREDIVNQMTACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLDD 492  
QY 185 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 232  
Db 493 TTDIQGEFAKVIIVOKLKDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 540

## RESULT 11

US-09-207-359B-2  
; Sequence 2, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; CURRENT FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-207-359B-2



Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
  
QY 185 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 232  
DB 493 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 540

RESULT 12  
US-09-340-620A-2  
; Sequence 2, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US/09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-620A-2

Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
  
QY 185 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 232  
DB 493 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 540

RESULT 13  
US-09-865-364-2  
; Sequence 2, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:

APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-112001  
CURRENT APPLICATION NUMBER: US/09/865,364  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US/09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US/09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US/09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-865-364-2

Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432  
  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
  
QY 185 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 232  
DB 493 TTDIQEEFAKIVQKLKDKNQKMGLOPYPEILLVWSRSPSLNLLQKSM 540

RESULT 14  
US-09-748-537-1  
; Sequence 1, Application US/09748537  
; Patent No. 6680167  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Chao, Moses V.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-316001  
; CURRENT APPLICATION NUMBER: US/09/748,537  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US/09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-748-537-1

Query Match 97.5%; Score 1176; DB 4; Length 540;  
Best Local Similarity 99.1%; Pred. No. 2.5e-124;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 KLOSVSSAIHLCDKKKMWLSLNPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124

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Db 373 LSRKAQDCYFMKHLHPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEFAKVIQVKLKDKNQKMGLOPYPEILVVSRSPSLNLQNKSM 232
Db 493 TTDIQGEFAKVIQVKLKDKNQKMGLOPYPEILVVSRSPSLNLQNKSM 540

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RESULT 15
US-09-069-023-6
; Sequence 6, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-6

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Query Match 71.9%; Score 867; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 SRKAQDCYFMKHLHPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 125
Db 1 SRKAQDCYFMKHLHPCGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQ 60

QY 126 GIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 185
Db 61 GIAQOWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 120

QY 186 TTDIQGEFAKVIQVKLKDKNQKMGLOPYPEILVVSRSPSLNLQNKSM 232
Db 121 TTDIQGEFAKVIQVKLKDKNQKMGLOPYPEILVVSRSPSLNLQNKSM 167

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Search completed: March 29, 2004, 14:10:44  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:08:11 ; Search time 43 Seconds  
(without alignments)  
1411.757 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLQNKSM 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/ECTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1206	100.0	232	9	US-09-771-161A-93
2	1182	98.0	540	9	US-09-771-161A-184
3	1182	98.0	540	9	US-09-862-027-28
4	1182	98.0	540	10	US-09-981-397A-14
5	1182	98.0	540	9	US-09-925-301-1015
6	1176	97.5	540	9	US-09-748-537-1
7	1176	97.5	540	9	US-09-728-721-2
8	1176	97.5	540	13	US-10-133-780-1
9	1176	97.5	540	13	US-10-105-931-2
10	1176	97.5	540	13	US-10-118-984-2
11	1176	97.5	540	14	US-10-295-981-2
12	632	52.4	131	9	US-09-728-721-5
13	632	52.4	131	13	US-10-105-931-5
14	632	52.4	131	13	US-10-118-984-5
15	632	52.4	131	14	US-10-295-981-5

16	544	45.1	109	9	US-09-728-721-6	Sequence 6, Appli
17	544	45.1	109	13	US-10-105-931-6	Sequence 6, Appli
18	544	45.1	109	13	US-10-118-984-6	Sequence 6, Appli
19	544	45.1	109	14	US-10-295-981-6	Sequence 6, Appli
20	461	38.2	92	13	US-10-014-269-21	Sequence 21, Appl
21	461	38.2	92	13	US-10-002-974-21	Sequence 21, Appl
22	461	38.2	92	14	US-10-314-506-21	Sequence 21, Appl
23	451	37.4	90	9	US-09-841-879B-10	Sequence 10, Appl
24	447	37.1	89	9	US-09-931-071-11	Sequence 11, Appl
25	149.5	12.4	109	9	US-09-728-721-71	Sequence 71, Appl
26	149.5	12.4	109	14	US-10-295-981-71	Sequence 71, Appl
27	143.5	11.9	95	9	US-09-841-879B-12	Sequence 12, Appl
28	122.5	10.2	164	9	US-09-728-721-41	Sequence 41, Appl
29	122.5	10.2	164	13	US-10-118-984-41	Sequence 41, Appl
30	122.5	10.2	164	14	US-10-295-981-41	Sequence 41, Appl
31	122.5	10.2	249	9	US-09-728-721-39	Sequence 39, Appl
32	122.5	10.2	249	13	US-10-118-984-39	Sequence 39, Appl
33	122.5	10.2	249	14	US-10-295-981-39	Sequence 39, Appl
34	122.5	10.2	507	15	US-10-401-194-3	Sequence 3, Appli
35	122.5	10.2	953	9	US-09-728-721-8	Sequence 8, Appli
36	122.5	10.2	953	13	US-10-105-931-8	Sequence 8, Appli
37	122.5	10.2	953	13	US-10-118-984-8	Sequence 8, Appli
38	122.5	10.2	953	14	US-10-013-477-12	Sequence 12, Appl
39	122.5	10.2	953	14	US-10-295-981-8	Sequence 8, Appli
40	122.5	10.2	953	14	US-10-028-374-4	Sequence 4, Appli
41	122.5	10.2	953	14	US-10-183-770-4	Sequence 4, Appli
42	119	9.9	100	9	US-09-728-721-10	Sequence 10, Appl
43	119	9.9	100	13	US-10-105-931-10	Sequence 10, Appl
44	119	9.9	100	13	US-10-118-984-10	Sequence 10, Appl
45	119	9.9	100	14	US-10-295-981-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 93  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

Query Match	100.0%;	Score 1206;	DB 9;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 3.4e-111;		
Matches 232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MYSLQLOQSVSSAIHLCDKKKMSLNI	PVNHGCPQESCGSSQLHNSGSPETSRSLPAQ	60
Db	1	MYSLQLOQSVSSAIHLCDKKKMSLNI	PVNHGCPQESCGSSQLHNSGSPETSRSLPAQ	60
QY	61	DNDFLSRQAQDCYFMKLHHCPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNS	120	
Db	61	DNDFLSRQAQDCYFMKLHHCPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNS	120	
QY	121	ERLQFGIAQOWTQSKREDIVNOMTACLNQSLDALLSRDLINKEDYELVSTKPTRTSKVR	180	

Db 121 ERLQPGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180

Qy 181 OLDDTTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 232

Db 181 OLDDTTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 232

RESULT 2

US-09-771-161A-184

; Sequence 184, Application US/09771161A

; Patent No. US2002011081A1

; GENERAL INFORMATION:

; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES

; FILE REFERENCE: 802620-2005.1

; CURRENT APPLICATION NUMBER: US/09/771,161A

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 09/724,676

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 135619

; PRIOR FILING DATE: 2000-04-12

; NUMBER OF SEQ ID NOS: 273

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 184

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-771-161A-184

Query Match 98.0%; Score 1182; DB 9; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSIAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 64

Db 313 KLOSVSSAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 540

RESULT 3

US-09-862-027-28

; Sequence 28, Application US/09862027

; Patent No. US20020142428A1

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof

; FILE REFERENCE: 35800/234862

; CURRENT APPLICATION NUMBER: US/09/862,027

; CURRENT FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: US 09/345,473

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-862-027-28

Query Match 98.0%; Score 1182; DB 9; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSIAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 64

Db 313 KLOSVSSAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 540

RESULT 4

US-09-981-397A-14

; Sequence 14, Application US/09981397A

; Publication No. US20030082519A1

; GENERAL INFORMATION:

; APPLICANT: Axxima Pharmaceuticals AG

; APPLICANT: Schubart, Daniel

; APPLICANT: Habenberger, Peter

; APPLICANT: Stein-Gerlach, Matthias

; APPLICANT: Bevec, Dorian

; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their

; FILE REFERENCE: AXM-004.1 US

; CURRENT APPLICATION NUMBER: US/09/981,397A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: 60/240,750

; PRIOR FILING DATE: 2000-10-16

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-397A-14

Query Match 98.0%; Score 1182; DB 10; Length 540;

Best Local Similarity 99.6%; Pred. No. 2.7e-108;

Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QLOSVSIAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 64

Db 313 KLOSVSSAHLCDKXKXWELSLNIPVNHGPOEESCGSSQLHENSQSPETSRLPAPQDNDF 372

Qy 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124

Db 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

Qy 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184

Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

Qy 185 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 232

Db 493 TTDIOGEEFAKVIQKLNKQKMGLOPYPEILVVSRSPSLNLLQKSM 540

RESULT 5

US-09-925-301-1015

; Sequence 1015, Application US/09925301

; Patent No. US20020052308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106  
CURRENT APPLICATION NUMBER: US/09/925,301  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05882  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1694  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 1015  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-301-1015

Query Match  
Best Local Similarity 98.0%; Score 1182; DB 9; Length 544;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 64  
DB 317 KLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 376  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 377 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 436  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 437 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 496  
QY 185 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 232  
DB 497 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 544

RESULT 6  
US-09-748-537-1  
Sequence 1, Application US/09748537  
Patent No. US20020061833A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
APPLICANT: Chao, Moses V.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
CURRENT APPLICATION NUMBER: US/09/748,537  
CURRENT FILING DATE: 2000-12-26  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-748-537-1

Query Match  
Best Local Similarity 97.5%; Score 1176; DB 9; Length 540;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 232  
DB 493 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
US-10-133-780-1  
Sequence 1, Application US/10133780  
Publication No. US20020123115A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 232  
Db 493 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 7  
US-09-728-721-2  
Sequence 2, Application US/09728721  
Patent No. US20020061845A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/728,721  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/340,620  
PRIOR FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-728-721-2

Query Match  
Best Local Similarity 97.5%; Score 1176; DB 9; Length 540;  
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMLSLNIPVNHGPQEESSQLHNSGSPETSRLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCHPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432  
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184  
DB 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492  
QY 185 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 232  
DB 493 TTDIOGEFAKVIQKLDKDKMGLOPYPEILVWSRSPSLNLLQKSM 540

RESULT 8  
US-10-133-780-1  
Sequence 1, Application US/10133780  
Publication No. US20020123115A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/133,780  
 FILING DATE: 26-Apr-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/019,942  
 FILING DATE: 06-FEB-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meiklejohn, Ph.D., Anita L.  
 REGISTRATION NUMBER: 35,283  
 REFERENCE/DOCKET NUMBER: 07334/068001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 540 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-133-780-1

Query Match 97.5%; Score 1176; DB 13; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSIAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
 :|||||  
 Db 313 KLQSVSSAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
 :|||||  
 Db 373 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
 :|||||

QY 125 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184  
 :|||||  
 Db 433 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492  
 :|||||

QY 185 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 540  
 :|||||

RESULT 9

US-10-105-931-2  
 ; Sequence 2, Application US/10105931  
 ; Publication No. US20020150987A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/10/105,931  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-105-931-2

Query Match 97.5%; Score 1176; DB 13; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSIAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
 :|||||  
 Db 313 KLQSVSSAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
 :|||||  
 Db 373 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
 :|||||

QY 125 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184  
 :|||||  
 Db 433 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492  
 :|||||

QY 185 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 540  
 :|||||

RESULT 10

US-10-118-984-2  
 ; Sequence 2, Application US/10118984  
 ; Publication No. US20020197693A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/10/118,984  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-118-984-2

Query Match 97.5%; Score 1176; DB 13; Length 540;  
 Best Local Similarity 99.1%; Pred. No. 1.1e-107;  
 Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSIAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64  
 :|||||  
 Db 313 KLQSVSSAHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372  
 :|||||

QY 65 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 124  
 :|||||  
 Db 373 LSRKAQDCYFMKLHCPGNHSDSTTSGSORAAFCDHKTTPCSAIINPLSTAGNSERLQ 432  
 :|||||

QY 125 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 184  
 :|||||  
 Db 433 PGIAQQWIOSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVROLLD 492  
 :|||||

QY 185 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 232  
 :|||||  
 Db 493 TTDIQGEFAKVIQKLNKQKMGLOPYPEILVVSRLNLLQNKSM 540  
 :|||||

RESULT 11

US-10-295-981-2  
 ; Sequence 2, Application US/10295981  
 ; Publication No. US20030120055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001

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; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-2

Query Match      97.5%; Score 1176; DB 14; Length 540;
Best Local Similarity 99.1%; Pred. No. 1.1e-107;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
DB 313 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
DB 373 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQWQISQKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
DB 433 PGIAQWQISQKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEFPAKIVQKLDKQKMGLOPYPEILVWSRSPSLNLQKSM 232
DB 493 TTDIQGEFPAKIVQKLDKQKMGLOPYPEILVWSRSPSLNLQKSM 540

RESULT 12
US-09-728-721-5
; Sequence 5, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-5

Query Match      52.4%; Score 632; DB 9; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
; :|||||
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DB 13 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 123
DB 73 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 131

RESULT 13
US-10-105-931-5
; Sequence 5, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5

Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
DB 13 QLOSVSAAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
QY 65 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 123
DB 73 LSRKAQDCYFMKLHCHPCGNHNSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 131

RESULT 14
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5

Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.3e-54;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

Qy 5 QLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 64  
Db 13 KLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 72  
Qy 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 123  
Db 73 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 131

RESULT 15  
US-10-295-981-5  
; Sequence 5, Application US/10295981  
; Publication No. US20030120055A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/10/295,981  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-981-5

Query Match 52.4%; Score 632; DB 14; Length 131;  
Best Local Similarity 98.3%; Pred. No. 1.3e-54;  
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 64  
Db 13 KLOSVSSAIHLCDKKKMWLSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQDNDF 72  
Qy 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 123  
Db 73 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERL 131

Search completed: March 29, 2004, 14:11:39  
Job time : 43 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:06:05 ; Search time 20 Seconds  
(without alignments)  
1115.822 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVSRSPSLNLLQNSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	8.3	943	2 S44636	f22b7.5 protein -
2	98	8.1	830	2 T00029	Miranda protein -
3	93	7.7	692	2 T32980	hypothetical prote
4	92.5	7.7	618	2 S68450	apoptosis inhibito
5	90	7.5	2288	2 T29999	hypothetical prote
6	89	7.4	242	2 S71757	MADS box protein D
7	89	7.4	1360	2 T33922	hypothetical prote
8	89	7.4	1944	2 A55117	tsq24 protein - mo
9	88	7.3	283	2 B81996	RNA polymerase sig
10	88	7.3	524	2 S35551	transcription fact
11	88	7.3	1135	2 T30561	Scythe protein - A
12	88	7.3	2368	2 S46005	ESR1 protein - yea
13	87.5	7.3	340	2 T27389	hypothetical prote
14	87	7.2	147	2 F84869	hypothetical prote
15	87	7.2	1205	2 T41987	hypothetical prote
16	86.5	7.2	407	2 T52092	transforming prote
17	86.5	7.2	528	2 T17415	DNA-binding protei
18	86.5	7.2	1203	2 T17415	mycellial surface a
19	85.5	7.1	212	2 G75458	conserved hypothet
20	85.5	7.1	455	1 JC4338	tryptophan dimethy
21	85.5	7.1	1758	2 T30560	resistance protein
22	85	7.0	690	2 A24545	triacylglycerol li
23	85	7.0	3898	1 GNMVHC	genome polyprotein
24	84.5	7.0	224	2 S23728	MADS box protein T
25	84.5	7.0	810	2 S69652	hypothetical prote
26	84	7.0	691	2 B89797	glycerol ester hyd
27	83.5	6.9	201	2 S65712	hypothetical prote
28	83.5	6.9	486	2 I55449	gene P22A protein
29	83.5	6.9	956	2 T40953	hypothetical prote

30	83	6.9	576	2 S59829	hypothetical prote
31	83	6.9	853	2 S58375	aryl hydrocarbon r
32	83	6.9	1544	2 T29482	hypothetical prote
33	82.5	6.8	591	2 T25636	hypothetical prote
34	82.5	6.8	1129	2 T25635	hypothetical prote
35	82.5	6.8	1175	2 T25634	hypothetical prote
36	82	6.8	383	2 A56084	interleukin-lbeta
37	82	6.8	427	2 S53021	G-box-binding prot
38	82	6.8	622	2 S45129	VPS27 protein - ye
39	82	6.8	721	2 S31824	gene Mx protein -
40	82	6.8	884	2 T40690	hypothetical prote
41	81.5	6.8	243	2 S71756	MADS box protein D
42	81.5	6.8	489	2 S50548	hypothetical prote
43	81.5	6.8	651	2 D72042	conserved hypothet
44	81.5	6.8	651	2 E86581	CHLPN 76 kDa homol
45	81.5	6.8	715	2 I40729	hypothetical 76k p

ALIGNMENTS

RESULT 1  
S44636  
f22b7.5 protein - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Dec-1997  
C:Accession: S44636  
R:Anderson, K.  
submitted to the EMBL Data Library, March 1993  
A:Description: Sequence of the C. elegans cosmid F22B7.  
A:Reference number: S44628  
A:Accession: S44636  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-943 <AND>  
A:Cross-references: EMBL:112018; NID:g156298; PID:g156307  
C:Genetics:  
A:Introns: 83/2; 250/2; 453/1; 484/2; 519/1; 553/3; 580/3; 632/3; 729/3; 830/2; 905/1  
C:Superfamily: dnaJ amino-terminal homology  
F:531-595/Domain: dnaJ amino-terminal homology <DNJ>

Query Match	8.3%	Score 100.5;	DB 2;	Length 943;
Best Local Similarity	19.4%	Pred. No. 2;		
Matches	45;	Conservative 44;	Mismatches 84;	Indels 59; Gaps 10;
QY	25	LNIPVNHGQESCGSSQLHENSQSPETSRSLPAPQDNDFLSRKAQDCYFMKLHCPGNH	84	
DB	349	IDVANNQERSEIATDQDVCLAIIDSSPDPTSS-----NDMINK-----FVVELEHATNVE	397	
QY	85	SWDSTISG-----SQRAAFCDHKTPCSSLII--NPLS	115	
DB	398	TWEMIVNGIIDDQKKPVAIEKKENEPEVDMMDLIFSMSSRMDQRTFLPAARFIPRPVS	457	
QY	116	TAG-----NSERLQPGIAQMIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVST	171	
DB	458	SASKTKTSHRILPGLRANWTQVMKVLGMFV---LNRS-SGLIHRSPVLLAQ---VST	510	
QY	172	KPTRTSKVRQLDITDIOGEEPAKVI-VOKLKDNK-----QMGLOPYEPI	215	
DB	511	PTTSTTKLAQLHTHALSKEDYKTLGVDDKSDAKAKAYQLAKKYPHDV	562	

RESULT 2  
T00029  
Miranda protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 17-Nov-2000  
C:Accession: T00029  
R:Ikeshima-Kataoka, H.; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F.  
Nature 390, 625-629, 1997  
A:Title: Miranda directs Prospero to a daughter cell during Drosophila asymmetric division  
A:Reference number: Z14067; MUID:98065952; PMID:9403694  
A:Accession: T00029

A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A;Residues: 1-830 <IKE>  
A;Cross-references: EMBL:AB005661; NID:g2749776; PIDN:BAA24111.1; PID:g2749777  
A;Experimental source: strain Canton-S  
C;Genetics:  
A;Cross-references: FlyBase:FBgn0021776  
A;Map position: 92B-C

Query Match 8.1%; Score 98; DB 2; Length 830;  
Best Local Similarity 21.3%; Pred. No. 2.7;  
Matches 44; Conservative 39; Mismatches 78; Indels 46; Gaps 8;

Qy 12 AIHLCDKKKMSLNIPVNHGPOEESGSSQLHENSPTSRLPAPQDNDFLSRKAQD 71  
Db 64 AVRFASSSKEAKFAIP-----KDDKSKGLRFTPLSPQLRFRPTPSHTDTATSG-- 117  
Qy 72 CYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQFGIAQOW 131  
Db 118 -----SGASTAA-----STPLHSAATTPVKEAKSRLKGEALQY 153  
Qy 132 -IQSKREDIVNQWTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQ 189  
Db 154 EIRKHNELIESQLSDVLRHVLDQKEAKLREHELATSK---TDLRLIEALTSENLS 210  
Qy 190 GEEPAKVIQKLNKDKMKGLOPYEIL 216  
Db 211 HKAL-----NEQMG-QEHADLL 226

RESULT 3  
T32980  
hypoetical protein T21D12.7 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
A;Accession: T32980  
R;Du, Z.; Maggi, L.  
A;Description: The sequence of C. elegans cosmid K02D7.  
A;Reference number: 221259  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-692 <DUZ>  
A;Cross-references: EMBL:AF045645; PIDN:AAC02606.1; GSPDB:GN00022; CESP:T21D12.7  
A;Experimental source: strain Bristol N2; clone K02D7  
C;Genetics:  
A;Gene: CESP:T21D12.7  
A;Map position: 4  
A;Introns: 29/1; 89/1; 127/1; 186/1; 233/1; 291/1; 379/3; 586/3; 611/3; 643/3

Query Match 7.7%; Score 93; DB 2; Length 692;  
Best Local Similarity 18.6%; Pred. No. 5.8;  
Matches 48; Conservative 35; Mismatches 67; Indels 108; Gaps 11;

Qy 8 SVSSAHLHC-----DKKMSLSLNIPVNHGPOEESGSSQLHENSPTS 53  
Db 427 SFGARHLCCPKKCKVIVYDPDKR-----PIRCFPGDQSC-----PIST 468  
Qy 54 RSLPAPQDNFLSR--KAQDCYFMKLH-----HC 80  
Db 469 DCLPALENSESFLNTAIDVFFCCHTVTSIFSCPDGASPLDPNSGQPATCLASNPFS 528  
Qy 81 PGNHSDSTISGSORAAFCDHKTTPCSSAI-----NPLSTAGNSERLQPG 126  
Db 529 PAEHSCTALMDGS--TACCPITQPLCVLEALVSDGSPKTCGLWDNNTCPQCKQKAMDG 586  
Qy 127 IAQWIOSKREDIVNQWTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTT 186  
Db 587 ILQK-----MHHSISVILA--LVISISHALLTSDPSNFA-IRQFPRPM 626  
Qy 187 DIQGE-----EFAKVI 197

Db 627 SMSSECNTPDEAHFCKTI 644

RESULT 4  
S68450  
apoptosis inhibitor hiap-2 - human  
C;Species: Homo sapiens (man)  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jul-2000  
A;Accession: S68450  
R;Lisbon, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996  
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of TAP A;Reference number: A58182; MUID:96149249; PMID:8552191  
A;Accession: S68450  
A;Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A;Residues: 1-618 <LS>  
A;Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAC50372.1; PID:g1184318  
C;Function:  
A;Description: apoptotic suppressor  
C;Superfamily: RING finger homology  
C;Keywords: apoptosis; zinc finger  
F;567-611/Domain: RING finger homology <RNG>

Query Match 7.7%; Score 92.5; DB 2; Length 618;  
Best Local Similarity 24.5%; Pred. No. 5.5;  
Matches 27; Conservative 24; Mismatches 46; Indels 13; Gaps 2;

Qy 132 IQSKREDIVNQWTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIOGE 191  
Db 461 IRKNRMALFQQLT--CVLPILDNLLKANVINQEHDIIRKQTKIPLQARELIDTIWVKN 518  
Qy 192 EFAKVIQKLNKDKMKGLOPYEILVSVSRPSLNLLQNK 230  
Db 519 AAANIFKCNLCKEIDSTLYKNLFDVKMKNVPTEDVSGLSLEQLRRLQEE 568

RESULT 5  
T29999  
hypoetical protein ZC8.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
A;Accession: T29999  
R;Latreille, P.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A;Description: The sequence of C. elegans cosmid ZC8.  
A;Reference number: Z20719  
A;Accession: T29999  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A;Residues: 1-2288 <LAT>  
A;Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4  
A;Experimental source: strain Bristol N2; clone ZC8  
C;Genetics:  
A;Gene: CESP:ZC8.4  
A;Map position: X  
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/1

Query Match 7.5%; Score 90; DB 2; Length 2288;  
Best Local Similarity 20.8%; Pred. No. 53;  
Matches 47; Conservative 40; Mismatches 85; Indels 54; Gaps 10;

Qy 5 QLOSVSVAIHLCDKKKMSLSLN-----IPVNHGPOEESGSSQLHENSPTS 49  
Db 712 ELEHAQKAAHLAEQQLKEIKIQRDDYQKQDEHARHLFDIRHKLKLEIKRQDLKNGA- 770  
Qy 50 PETSRLPAPQDNDFLSRKAQ-----DCVFVKMLHHCPCGNHSDSTISGSORAAFCDHK 102  
Db 771 -----RNDELKRLQTTSDYESQINLRRH-----NDELDTTIKGHQ-----GK 810  
Qy 103 TTPCSSAIINPLSTAGNSERLQFGIAQOWIOSKREDIVNQWTEA-CLNOSLDALLSRDLIM 162  
Db 811 ITHLENEL---HSRSGBEIKLND--LNQRLQKQKQDILNQKLNK--LDGDVQAL--KETIR 861

QY 163 KEDYELVSTKPTSTSKVRLQLDTRTDIQGEFF--AKVIVOKLKDKNQ 206  
DB 862 KLENELEKLRNENKELVGEARDAANOQLSRANLLNKELEDTKQ 907

RESULT 6  
S71757  
MADS box protein DEPH200 - garden snapdragon  
C;Species: Antirrhinum majus (garden snapdragon)  
C;Date: 11-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 20-Jun-2000  
C;Accession: S71757  
R;Davies, B.; Egge-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer, H.  
EMBO J. 15, 4330-4343, 1996  
A;Title: Multiple interactions amongst floral homeotic MADS box proteins.  
A;Reference number: S71756; MUID:97015133; PMID:8861961  
A;Accession: S71757  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-242 <DAV>  
A;Cross-references: EMBL:X95459; NID:g1239958; PIDN:CAA64743.1; PID:g1239959  
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog  
C;Keywords: DNA binding; transcription regulation  
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
F;94-159/Domain: domain K <KDO>

Query Match 7.4%; Score 89; DB 2; Length 242;  
Best Local Similarity 21.1%; Pred. No. 3.1;  
Matches 48; Conservative 30; Mismatches 65; Indels 84; Gaps 7;

QY 15 LCDKKKWEKLSLNPVNHGPOEESCGSQLHE-----NSGSPETSRSLPAPQDNDFLS 66  
DB 38 LCD---AEVALIIIFSNGKLYEFCSTSMLETLERQKCNYPETNVS-----83

QY 67 RKAQDCYFMKLRHCPGNHSDSTISGSQRAAFCDHKHTPCSSAIINPLSTAGNSERLQPG 126  
DB 84 -----TREALELS 91

QY 127 IAQOQTSQK-REDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTSTSKVRLQLD 185  
DB 92 SQOEYIKLKARYEALQSRNLLGDLGLNLSKELESLESLERQKDMSLKQINRSTQAMLD 151

QY 186 -TDIQGEFFA-----KVIVOKLKDKNQMLQPYP---EILVWSRSPS 223  
DB 152 LTLDLQKHEALNEANSLKRLMDGSGQISLQWNPNAEDHVGYGRQPS 198

RESULT 7  
T33922  
hypothetical protein Y8A9A.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T33922  
R;Courtney, L.; Langston, Y.; Drone, K.; Mead, K.  
submitted to the EMBL Data Library, February 1999  
A;Description: The sequence of C. elegans cosmid Y8A9A.  
A;Reference number: Z21439  
A;Accession: T33922  
A;Status: preliminary; translated from GB/EMBL/DBDB  
A;Molecule type: DNA  
A;Residues: 1-1360 <COU>  
A;Cross-references: EMBL:AF1254461; PIDN:AAD12852.1; GSPDB:GN00020; CESP:Y8A9A.2  
A;Experimental source: strain Bristol N2; clone Y8A9A  
C;Genetics:  
A;Gene: CESP:Y8A9A.2  
A;Map position: 2  
A;Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1

Query Match 7.4%; Score 89; DB 2; Length 1360;  
Best Local Similarity 20.5%; Pred. No. 32;  
Matches 39; Conservative 25; Mismatches 68; Indels 58; Gaps 7;

QY 8 SVSSAIHLCDKKWEKLSLNPVNHGPOEESCGSQLHEN-----SGSPETSRSLPAPQD 61

A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA0049

```

Query Match      7.3%; Score 88; DB 2; Length 283;
Best Local Similarity 23.2%; Pred. No. 4.6;
Matches 52; Conservative 27; Mismatches 85; Indels 60; Gaps 9;

Qy 61 DNDPLSRKAQD-----CYFMKLHHCPGNHSD--STISGSO-----RAAFCDRHKT 104
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 DNPLLERKDTDFSDAEFSHYTAPARQIGDGEDMLSNAGEQDFKQYLHAQVCEHPLS 101
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 105 PCSAAINPLSTAGNSERLOPGIAQOIQSKREIVN-----QMTBACLNQSLDAL--- 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 DOESACVCHILIDFLDE-----QGYLTDSIEDILDTHTPLEWMLDEAMLKQALTALKKF 153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 156 -----LSRDLIMK-EDVELYSTPTRTSKVRQLLDTTIDIQGEFAKVIIVOKLQDNK 205
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 154 DPAGVAADNLNESLILQIERSGECAPKPSALHIVRNALDSIDGNRSQTLARIKKRLPQTD 213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 206 Q-----MGLOPYPEILVVRSPS-----LNLQNKSM 232
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 214 SGTLEAALDLIASLNPPFVAGFASSTPTPYSDAANLAFRGM 257
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 10  
S3551  
transcription factor IIF chain RAP74 - African clawed frog  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 09-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jul-2000  
C/Accession: S35551  
R/Gong, D.W.; Hasegawa, S.; Wada, K.; Roeder, R.G.; Nakatani, Y.; Horikoshi, M.  
Nucleic Acids Res. 20, 6736, 1992  
A/Title: Elucidation of three putative structural subdomains by comparison of primary st  
A/Reference number: S35551; MUID:33126122; PMID:1480494  
A/Accession: S35551  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-524 <GON>  
A/Cross-references: EMBL:Z17426; NID:g65029; PIDN:CAA78999.1; PID:g65030  
C/Genetics:  
A/Gene: RAP74  
C/Keywords: DNA binding; transcription regulation

Query Match.	7.3%;	Score 88;	DB 2;	Length 524;
Best Local Similarity	23.9%;	Pred. No. 11;		
Matches 54;	Conservative 22;	Mismatches 90;	Indels 60;	Gaps 9;
QY	27	IPVNHGPOEESCGSQLHENSGPSPTS-----RSLPAPQDNDFLSRKAQDCY	73	
DB	290	LPGKIKAKAEEGPKGLDEQSESESESEEEKAEPEEGEEKKATPQDNK---KKKGGD--	345	
QY	74	FMKLHCPGNHSDWTISGSGORAAFCDHKTTP-----CSSAIIN-----PLSTAGN	119	
DB	346	-----SSDESETSESDIDGASSLFFMQKKKTPPKKDKKGGSSNSRSGNSRPGTSPOTGN	401	
QY	120	SERLQPGIAQOWIQSKREDIVNQWTEACLQSLDA-----LLSRDL	160	
DB	402	TSSTLRAAAKLEQSKRGTVSN--TPAAKRLKMEAGQNTSGKSTPOPGSKTSPSSGDI	459	
QY	161	IMKED--YELVSTKPTRTSKVRQLLDT--TDIQEEFAKIVQKLK	202	
DB	460	OLTVEEAVRRYLTTRKPMITKLLKKFOTKKTKGLSSEOTVNWLAOLLK	505	

RESULT 11  
T30561  
Scythe protein - African clawed frog  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 11-May-2000  
C/Accession: T30561  
R/Thress, K.; Henzel, W.; Shillinglaw, W.; Kornbluth, S.  
EMBO J. 17. 6135-6143, 1998

A;Title: Scythe: a novel reaper-binding apoptotic regulator.  
A;Reference number: Z20860; MUID:99016035; PMID:9795223  
A;Accession: T30561  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1135 <THR>  
A;Cross-references: EMBL:AF098511; NID:g3983138; PID:g398313  
C;Function:

Query Match	7.3%;	Score 88;	DB 2;	Length 1135;
Best Local Similarity	23.1%;	Pred. No. 31;		
Matches	30;	Conservative	26;	Mismatches 40; Indels 34; Gaps 5;
Qy	112	NPLSTAGNSERLPGTIAQQWIOSKRRDIVNQ-----MTEACL-----	148	
Db	1002	HPTEQDGGSEQWAASVPPEWPFVIRQDMQNRKIKQPPPLSDAYLSGMPAKRRKTWQGE	1061	
Qy	149	-NOSLDALLSRDLIMKEDVELSVTKPTRTSK-VRQLLDTTIDIQG---EEFAKVIIVOKLKD	203	
Db	1062	PHLSLSEAVSRAM-----KATGAKPESSAEVCVRRELDNLSAQGRYREQLCQDIQKTLQD	1115	
Qy	204	NKOMGLQPYYP	213	
Db	1116	NESYSQAORFP	1125	

RESULT 12

S46005  
ESRI protein - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: MEC1 protein; protein YBR1012; protein YBR136w  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 26-Aug-1994 #sequence revision 09-Sep-1994 #text\_change 29-Oct-1999  
C;Accession: S46005; S46578; S47954; S64650  
R;Becan, A.M.; Herber, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45995  
A;Accession: S46005  
A;Molecule type: DNA  
A;Residues: 1-2368 <BEC>  
A;Cross-references: EMBL:Z36005; NID:G536429; PIDN:CAA85094.1; PID:G536430;  
A;Experimental source: strain S288C  
R;Becan, A.M.; Cullin, C.; Grzybowska, E.; Lacroute, F.; Nasr, F.; Ozier-Ka  
Yeast 10 (Suppl.A), S1-S11, 1994  
A;Title: The sequence of 29.7kb from the right arm of chromosome II reveals  
A;Reference number: S46569; MUID:94337817; PMID:8091856

EMBO J. 17, 6135-6143, 1998

A:Molecule type: DNA  
A:Residues: 1-715, P, 717-1254, Q, 1256-1275, G, 1277-2368 <WEI>  
A:Cross-references: EMBL:U31109; NID:9950172; PIDN:AAA74482.1; PID:G950173  
C:Genetics:  
A:Gene: SGD:BSR1; MEC1  
A:Cross-references: SGD:S0000340; MIPS:YBR136W  
A:Map position: 2R  
C:Function:  
A:Description: required for mitotic cell growth, DNA repair, and meiotic recombination  
A:Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein  
F:74-90/Domain: transmembrane #status predicted <TM1>  
F:218-234/Domain: transmembrane #status predicted <TM2>  
F:771-787/Domain: transmembrane #status predicted <TM3>  
F:722-938/Domain: transmembrane #status predicted <TM4>  
F:1152-1169/Domain: transmembrane #status predicted <TM5>  
F:1315-1331/Domain: transmembrane #status predicted <TM6>  
F:1682-1689/Region: nucleotide-binding motif A (P-loop)  
F:1918-1934/Domain: nucleotide-binding motif A (P-loop)  
F:2126-2142/Domain: transmembrane #status predicted <TM8>  
F:1688/Binding site: ATP/GTP (Lys) #status predicted

Query Match 7.3%; Score 88; DB 2; Length 2368;  
Best Local Similarity 22.3%; Pred. No. 83;  
Matches 56; Conservative 38; Mismatches 105; Indels 52; Gaps 11;

QY 14 HLCDDKKK-----MELSLNIPVNHGPOEESGSSQ-----LHNSGSPETSRSILPAPQDNDF 64  
DB 491 HLCDEIKTGNPFVRINPNRP-----EAGKSEIFRILHSN-----FLSHPNIDEF 535  
QY 65 LSKKAQDCYFMKLHH-----CPGNHSDSTISGQRAAFCDHKTTPCSSALINPL 114  
DB 536 -SESLSGLFSLHRIFFSHFQPKLTGNGQINKSPKLVQKCFMNSRYRLRLSTRILPL 594  
QY 115 ---STAGNERLQPGIAQOWIOSKREDIV-----NOMTEACLNOSLDALLSR--DLI 161  
DB 595 FNISDSHNSDEHTALIFLQSQKLPVVKENLVIAWTQTLTSDNDVFTLLKLIDIF 654  
QY 162 MKEDYELVSTKPTRTSKVRQLDITDIQ-GEFPAKIVIVQKLKDN---KOMGLQPYPEILAV 217  
DB 655 NSDDYSLRIMMTLQIKNMAKILKTPYQLLSPLPVLRLQGLNVERKVGQNLIELAG 714  
QY 218 VSRSPSLNLLQ 228  
DB 715 YSSKTILDIFQ 725

RESULT 13  
T27389  
hypothetical protein Y75B8A.29 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27389  
R.Barlow, K.  
submitted to the EMBL Data Library, November 1998  
A:Reference number: Z20361  
A:Accession: T27389  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-340 <WIL>  
A:Cross-references: EMBL:AL033514; NID:e1343251; PIDN:CAA22089.1; CESP:Y75B8A.29  
A:Experimental source: clone Y75B8A  
C:Genetics:  
A:Gene: CESP:Y75B8A.29  
A:Introns: 116/3; 216/3; 267/3

Query Match 7.3%; Score 87.5; DB 2; Length 340;  
Best Local Similarity 23.3%; Pred. No. 6.6;  
Matches 37; Conservative 34; Mismatches 63; Indels 25; Gaps 6;

QY 75 MKLHCPGNHSDSTISGQRAAFCDHKTTPCSSALINPLSTAGNSERLQPGIAQOWIOS 134  
DB 26 VKLEH---ESSDNNESSGSGNFVF-----NFLMSQLQNMG-----PVEIKQVEEA 67

A:Molecule type: DNA  
A:Residues: 135 KR-EDIVNOMTEACLNQSLDAL-LSRDLIMKEDYELVSTKPTRTSKVRQLDITDIQGBE 192  
DB 68 KMLDDIEYTDNNYNEGYSKMDTDGDLWEDEFKLNKDPKMDKREOERHRQMAKNRE 127  
QY 193 FAKVIVQKLKDNKOMGLQPYPEILVSRSPSLNLLQNK 231  
DB 128 YARKVCVQKKDQK-----HAIIRNQIKKRIQLLNKKT 161

RESULT 14  
F84869  
hypothetical protein At2g43720 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84869  
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: F84869  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-147 <STO>  
A:Cross-references: GB:AE002093; NID:G2281098; PIDN:AAB64034.1; GSPDB:GNO0139  
C:Genetics:  
A:Gene: At2g43720  
A:Map position: 2

Query Match 7.2%; Score 87; DB 2; Length 147;  
Best Local Similarity 24.2%; Pred. No. 2.3;  
Matches 37; Conservative 25; Mismatches 43; Indels 48; Gaps 8;

QY 53 SRSLPAPQDNFSLRKAQDCYFMKLHCPGNHSDSTISGQRAAFCDHKTTPCSSALIN 112  
DB 25 SOSLSLSPV-QDHINFITLOKAYFKAYEC-----FQRTTHAE-----ISRCAESCSV 70  
QY 113 PLSTAGN-----SERLOPG-----IAQWIOSKREDIVNOMTEACLNQSLDA 154  
DB 71 PITNAQNVFDNEMSVFQERLNLVVCQDKFEVAQK--QKTRSEAVNDL-EHCVQTVD- 126  
QY 155 LLSRDLIMKEDYELVSTKPTRTSKVRQLDITTD 187  
DB 127 -----EAVKTLPLNLVSRMKKALSITD 147

RESULT 15  
T41987  
hypothetical protein U86 - human herpesvirus 7 (strain JI)  
C:Species: human herpesvirus 7  
A:Variety: Strain JI  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T41987  
R.Nicholas, J.  
submitted to the EMBL Data Library, December 1995  
A:Description: Determination and analysis of the complete nucleotide sequence of human he  
A:Reference number: Z22022  
A:Accession: T41987  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1205 <NIC>  
A:Cross-references: EMBL:U43400; PIDN:AAC54747.1  
A:Experimental source: strain JI  
C:Genetics:  
A:Note: U86

Query Match 7.2%; Score 87; DB 2; Length 1205;  
Best Local Similarity 22.6%; Pred. No. 41;  
Matches 52; Conservative 34; Mismatches 98; Indels 46; Gaps 10;

QY 8 SVSSAIHLCDKKKMELSLN-----IPVNHGPOEESGSS--QLHNSGSPETSRSILPAP 59

Db	833	SKRTCKVCNNKQDSQSETQCKHLISIRSNSEHSISESTYQSCKNKNS-ETLRSRRS	891
Qy	60	QDNDFLSRKAQDCYFMKLLHPCGNHSDSTISGSORAAFCDDHKTTPCSSAIINPLSTAGN	119
Db	892	SESDCKKRSRSC-----SNHSWS--GSTQSKRVDDIDFTGAKSIPN-----	933
Qy	120	SERLQPGIAQOWIQSKREDIVNQWTE-----ACLNQSLDALLSRDLIMKED	165
Db	934	-EYEQKSTNKPFFKNKRNARKRFSDDSDSSMQLFYKKRISGTQKSDSELSDNDLSYREY	992
Qy	166	YELVSTKPTTSKV-ROLLDTTIOGEEPAKIVQKLKDNKQMGLOPYPE	214
Db	993	VKLQEQKQSAKFKVQGRVPTKDFE-KLFRKTI--RAFYKQIPKPFPE	1039

Search completed: March 29, 2004, 14:10:09  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 14:02:15 ; Search time 18 Seconds  
(without alignments)  
671.126 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQLQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNSM 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1182	98.0	540	1 RIK2 HUMAN	043353 h receptor-
2	839.5	69.6	539	1 RIK2_MOUSE	P58801 mus musculus
3	122.5	10.2	953	1 CAR4_HUMAN	Q9Y239 homo sapien
4	100.5	8.3	943	1 YLM5_CAEEL	P34408 caenorhabdi
5	96.5	8.0	953	1 CAR4_MOUSE	Q8bbh0 mus musculus
6	92.5	7.7	618	1 BIR2_HUMAN	Q13490 homo sapien
7	90	7.5	357	1 REPI_ZYGBA	P13776 zygosacchar
8	89	7.4	1544	1 ANCI_MOUSE	P53995 mus musculus
9	88	7.3	524	1 T2FA_XENLA	Q04870 xenopus lae
10	88	7.3	2368	1 ESRI1_YEAST	P38111 saccharomyc
11	86.5	7.2	365	1 SYAP_MOUSE	Q9d5v6 mus musculus
12	86.5	7.2	407	1 MYC_ASTVU	Q17103 asterias vu
13	86.5	7.2	612	1 BIR2_MOUSE	Q62210 mus musculus
14	86.5	7.2	1088	1 MRTE_HUMAN	Q9uhh7 homo sapien
15	85	7.0	627	1 ABPX_YEAST	Q08641 saccharomyc
16	85	7.0	690	1 LIP_STAAR	P10335 staphylococ
17	85	7.0	3898	1 POLG_HCVA	P19712 hog cholera
18	84.5	7.0	224	1 AGL9_LYCES	Q42464 lycopersico
19	84.5	7.0	733	1 ACE1_TIRE	Q9p8w3 trichoderna
20	84	7.0	690	1 LIP_STAAR	Q8nyc2 staphylococ
21	83.5	6.9	486	1 ZASA_HUMAN	Q15172 h serine/th
22	83.5	6.9	805	1 HIFA_XENLA	Q918a9 xenopus lae
23	83.5	6.9	2567	1 M18B_HUMAN	Q8iug5 homo sapien
24	83	6.9	853	1 AHR_RAT	P41738 rattus norv
25	83	6.9	1499	1 PGFI_HUMAN	Q9Y498 homo sapien
26	81.5	6.8	489	1 YEN5_YEAST	P39970 saccharomyc
27	81	6.7	721	1 MX_ANAPL	P33238 anas platyr
28	81	6.7	1203	1 SMC2_XENLA	P50533 xenopus lae
29	80.5	6.7	1878	1 BR11_CANFA	Q95153 canis fami
30	80	6.6	647	1 LK1_RAT	Q95169 rattus norv
31	80	6.6	918	1 YNEC_CAEEL	P30845 caenorhabdi
32	79.5	6.6	943	1 YMI1_YEAST	P39523 saccharomyc
33	79.5	6.6	1324	1 IRS2_HUMAN	Q9Y4h2 homo sapien

## ALIGNMENTS

## RESULT 1

ID	RIK2_HUMAN	STANDARD;	PRT;	540 AA.
AC	O43353;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)			
DE	(RIP-2) (CARD-containing CLARP kinase) (Receptor-interacting protein 2)			
DE	associated kinase) (CARD-containing IL-1 beta converting enzyme			
GN	RIPK2 OR RICK OR RIP2 OR CARDIAK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RA	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain,			
RT	interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=98307936; PubMed=9642260;			
RA	McCarthy J.V., Ni J., Dixit V.M.;			
RT	"RIP2 is a novel NF-kappaB-activating and cell death-inducing			
RT	kinase.";			
RL	J. Biol. Chem. 273:16968-16975(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.			
RX	MEDLINE=98381580; PubMed=9705938;			
RA	Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,			
RA	Mattmann C., Tschopp J.;			
RT	"Identification of CARDIAK, a RIP-like kinase that associates with			
RT	caspase-1.";			
RL	Curr. Biol. 8:885-888(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Ozereky P., Holmes A., Brody M.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBDJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Platzter M., Varon R.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBDJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

O62640 sus scrofa  
Q9M367 arabidopsis  
Q03569 caenorhabdi  
P53667 homo sapien  
Q35800 rattus norv  
O61221 mus musculus  
O74522 schizosacch  
P07866 saccharomyc  
Q03489 petunia hyb  
Q91a06 lactococcus  
Q9v1e5 drosophila  
P70478 rattus norv

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,  
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,  
CC pancreas and lymph node.  
CC -1- PM: Autophosphorylated.  
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF027706; AAC34970.1; -  
CC EMBL: AF078530; AAC27722.1; -  
CC EMBL: AF064824; AAC25668.1; -  
CC EMBL: AC004003; AAC24561.1; -  
CC EMBL: AF117829; AAD04634.1; -  
CC EMBL: BC004553; AAH04553.1; -  
CC Genew: HGNC:10020; RIPK2.  
CC MIM: 603455; -  
CC GO: GO:0004674; F:protein serine/threonine kinase activity; TAS.  
CC GO: GO:0004871; F:signal transducer activity; TAS.  
CC GO: GO:0006915; P:apoptosis; TAS.  
CC GO: GO:0006954; P:inflammatory response; TAS.  
CC GO: GO:0007165; P:signal transduction; TAS.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR000719; Prot\_kinase.  
CC InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
CC InterPro: IPR001245; Tyr\_pkinase.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00069; pkinase; 1.  
CC PRINTS: PR00109; TYRKINASE.  
CC ProDom: PD000001; Prot\_kinase; 1.  
CC SMART: SM00114; CARD; 1.  
CC PROSITE: PS02029; CARD; 1.  
CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
CC PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation; Apoptosis.  
FT DOMAIN 18 294 PROTEIN KINASE.  
FT DOMAIN 432 524 CARD.  
FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
FT BINDING 47 47 ATP.  
FT ACT\_SITE 146 146  
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.  
FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.

FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.  
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;  
Query Match 98.0%; Score 1182; DB 1; Length 540;  
Best Local Similarity 99.6%; Pred. No. 1.5e-91;  
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QLQSVSSAIHLCDKKKMKELSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64  
DB 313 KLQSVSSAIHLCDKKKMKELSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 372  
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGQRAAFCDHKHTPCSSALINPLSTAGNSERLQ 124  
DB 373 LSRKAQDCYFMKLHCPGNHSDSTISGQRAAFCDHKHTPCSSALINPLSTAGNSERLQ 432  
QY 125 PGIAQQMIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRSKVQLQLD 184  
DB 433 PGIAQQMIQSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKPTRSKVQLQLD 492  
QY 185 TTDIOGEEFAKIVQKLKDKNQKMGLOPYPEILLVSRSPSLNLQKSM 232  
DB 493 TTDIOGEEFAKIVQKLKDKNQKMGLOPYPEILLVSRSPSLNLQKSM 540  
RESULT 2  
RIK2 MOUSE STANDARD; PRT; 539 AA.  
AC P58801;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).  
GN RIPK2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=21891093; PubMed=11894097;  
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;  
RT "Involvement of receptor-interacting protein 2 in innate and adaptive  
RT immune responses";  
RL Nature 416:190-194(2002).  
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -1- PTM: Autophosphorylated (By similarity).  
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AF461040; AAL96436.1; -  
CC MGD: MGI:1891456; Ripk2.  
CC InterPro: IPR001315; CARD.  
CC InterPro: IPR000719; Prot\_kinase.  
CC InterPro: IPR008271; Ser\_Thr\_pkin\_AS.  
CC InterPro: IPR001245; Tyr\_pkinase.  
CC Pfam: PF00619; CARD; 1.  
CC Pfam: PF00069; pkinase; 1.



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DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN_KINASE.
FT DOMAIN 431 523 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Query Match 69.6%; Score 839.5; DB 1; Length 539;
Best Local Similarity 71.9%; Pred. No. 7.6e-63;
Matches 164; Conservative 20; Mismatches 43; Indels 1; Gaps 1;

QY 5 QIQSVSSAIHLCDKKMELSLNIPVNHGPOEESCGSSQLHNSGPGTSSRLPAPQDNDF 64
DQ :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 313 KIQSSSTIHLCD-KKMDLSLNPANHPPOEESCGSSLLSRNTGPGPSRSLAPQDKGF 371
QY 65 LSRKAQDCYFMKLHCHPCGNHSDSTISGQRAAFCDHKTPCSSLINPLSTAGNSERLQ 124
DQ :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 372 LSGAQDQCSLKAHCHPCGNHSDGIVSPVPGAFCDDRASSCSLAVISPLVKGSRPP 431
QY 125 PGIAQWIOSKREDIVNQMTAEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLLD 184
DQ :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 432 IGIAQWIOSKREAIVSQNTAEACLNQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLLD 491
QY 185 TTDIOGEFAKVIQKLDKNQKGLQPYEPIILVGRSPSLNLLQNSM 232
DQ :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 492 TSDIOGEFAKVIQKLDKNQKGLQPYEPIILVGRSPSLNLLQNSM 539

RESULT 3
CAR4_HUMAN STANDARD; PRT; 953 AA.
ID CAR4_HUMAN
AC Q9Y239; OBTWFS;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4 (Nod1 protein).
GN CAR4 OR NOD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Endothelial cells;
RC SEQUENCE FROM N.A.
RX MEDLINE=99240667; PubMed=10224040;
RA Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R.,
RA Grant J.R., Kelly J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,
RA Glucksmann M.A., DiStefano P.S.;
RT "Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member
RT that activates NF-kappaB."
RL J. Biol. Chem. 274:12955-12958 (1999).
RN [2]
RC SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.
RP TISSUE=Breast;
RX MEDLINE=99262599; PubMed=10329646;
RA Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R.,
RA Merino J., Liu D., Ni J., Nunez G.;
RT "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-
RT kappaB."
RL J. Biol. Chem. 274:14560-14567 (1999).
RN [3]
RC SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Roshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RN FUNCTION.
RX MEDLINE=21264704; PubMed=11058605;
RA Inohara N., Ogura Y., Chen F.P., Muto A., Nunez G.;
RT "Human Nod1 confers responsiveness to bacterial lipopolysaccharides."
RL J. Biol. Chem. 276:2551-2554 (2001).
CC -!- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-
CC B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers
CC responsiveness to intracellular bacterial lipopolysaccharides
CC (LPS).
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD
CC interaction.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal
CC muscle, pancreas, spleen and ovary. Also detected in placenta,
CC lung, liver, kidney, thymus, testis, small intestine and colon.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF126484; AAD29125.1; -;
CC EMBL; AF149774; AAD43922.1; -;
CC EMBL; AF113925; AAD28350.1; -;
CC EMBL; BC040339; AAH40339.1; -;
CC GenSeq; HGNC:16390; CARD4.
CC MIM; 605980;
CC GO; GO:0008656; F: caspase activator activity; TAS.
CC GO; GO:0006915; P: apoptosis; TAS.
CC GO; GO:0007165; P: signal transduction; TAS.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR007091; LRR_RNinh.
CC InterPro; IPR007111; NACHT_NTPase.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF05729; NACHT; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS50837; NACHT; 1.
KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.
FT DOMAIN 15 105 CARD.
FT NP_BIND 196 531 NACHT.
FT NP_BIND 202 209 ATP (POTENTIAL).
FT REPEAT 632 656 LRR 1.
FT REPEAT 702 725 LRR 2.
FT REPEAT 727 750 LRR 3.
FT REPEAT 755 778 LRR 4.
FT REPEAT 783 806 LRR 5.

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FT REPEAT      839   862   LRR 6.
FT REPEAT      867   891   LRR 7.
FT REPEAT      895   918   LRR 8.
FT REPEAT      923   946   LRR 9.
FT MUTAGEN     41    41    V-SQ: ABOLISHES CASPASE-9 ACTIVATION AND
FT MUTAGEN     208   208   INTERACTION WITH RICK.
FT MUTAGEN     447   447   K-R: REDUCES CASPASE-9 ACTIVATION.
FT CONFLICT    447   447   R -> H (IN REF. 3).
SQ SEQUENCE    953 AA; 107690 MW; 0A9DF5FC6487E21A CRC64;

Query Match      10.2%; Score 122.5; DB 1; Length 953;
Best Local Similarity 37.1%; Pred. No. 0.021;
Matches 39; Conservative 19; Mismatches 36; Indels 11; Gaps 6;

QY 130 QWTQSKREDIVNQMTER-CLNQSLDALLSRDLTKMEDYELVSTKPTKSKVQLLDTTDI 188
DB 21 QLLKSNRELIVTHRTQCL---VDNLLKNDYFSAEDAIVCACPQPKDKVKRLDLVQS 77

QY 189 QGE---EFKAVIVQKLDKDKQMGLOPYPELLVVSRSPLNLLQNK 230
DB 78 KGEVSEFFYLILQLQAD-AYVDLRPW--LLEIGFSPSL-LTQSK 118

RESULT 4
YLW5_CABEL STANDARD; PRT; 943 AA.
AC P34408;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein F22B7.5 in chromosome III.
GN F22B7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
RA Lathelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -!- SIMILARITY: Contains 1 GoLoco domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
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CC -----
CC EMBL; L12018; AAA65459.1; -.
CC PIR; S44636; S44636.
CC HSSP; P08622; 1XEL.
CC WormPep; F22B7.5; CE00158.
CC InterPro; IPR002939; DnaJ_C.
CC InterPro; IPR001305; DnaJ_CXXCXGK.
CC InterPro; IPR001623; DnaJ_N.
CC InterPro; IPR003109; GoLoco.

DR InterPro; IPR008971; HSP40_DnaJ_pdp.
DR InterPro; IPR003095; Hsp DnaJ.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGK; 1.
DR Pfam; PF02188; GoLoco; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR SMART; SM00390; GoLoco; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS0076; DnaJ_2; 1.
DR PROSITE; PS0877; GoLoco; 1.
KW Hypothetical protein.
FT DOMAIN     424   445   GOLOCO.
FT DOMAIN     531   595   J-DOMAIN.
SQ SEQUENCE    943 AA; 105926 MW; 9847F95977E0418E CRC64;

Query Match      8.3%; Score 100.5; DB 1; Length 943;
Best Local Similarity 19.4%; Pred. No. 1.4;
Matches 45; Conservative 44; Mismatches 84; Indels 59; Gaps 10;

QY 25 LNIPIVNHGQERSCGSSQLHENSGETSRSLPAPQDNDFLSKQAQDCYFMKLHHCNGH 84
DB 349 IDVAMNQERSETATDQDVCLADSSPDPTSS-----NDMNK-----FVVELEHATNVE 397

QY 85 SWDSTISG-----SRAAFCDHKHTPCSSAI--NPLS 115
DB 398 TWEMIVNGIIDDOKKPAIEKKEKEEPVDMMDLIFSSSRMDDQRTLPAAEPIPRPVS 457

QY 116 TAG---NSERLQPGIAQOWIOSKREDIVNQWTEACINOSLDALLSRDLTKMEDYELVST 171
DB 458 SASKTKTKSHRILPGLRANWTKVQSMKVLGMFV---LNRS-SGLIHSVPLLAQ---VST 510

QY 172 KPRTSKVQLLDTTDIQGEFAKVI-VOKLKNK-----QMGLOPYPEI 215
DB 511 PTTSTTKLAQLHTHALSKEDYIKTLGVDKKSDAKAIKKAYFQIAKKYHPDV 562

RESULT 5
CAR4_MOUSE STANDARD; PRT; 953 AA.
ID CAR4_MOUSE
AC Q8B8B0; Q8BUT6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4.
GN CARD4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=NOD; TISSUE=Cerebellum, and Spleen;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirani L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Ciothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
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FT REPEAT 727 750 LRR 3.
FT REPEAT 755 778 LRR 4.
FT REPEAT 783 806 LRR 5.
FT REPEAT 839 862 LRR 6.
FT REPEAT 867 890 LRR 7.
FT REPEAT 895 918 LRR 8.
FT REPEAT 923 946 LRR 9.
FT VARIANT 884 S -> A (in strain Czech II).
SQ SEQUENCE 953 AA; 107739 MW; 39C639621CEB1A58 CRC64;

Query Match 8.0%; Score 96.5; DB 1; Length 953;
Best Local Similarity 35.5%; Pred No. 3.2;
Matches 27; Conservative 13; Mismatches 29; Indels 7; Gaps 3

QY 132 IQSKREDIV-NQMTAEACINSLDALLSRDLIMKEDYELVSTKPTRTSKVRLQLDITDQ 190
Db 23 LKINRHLVNIIRNTQL---VDNLLNGVFSAEAEIVCACTPKDKVRKILDVLVQSKG 79
QY 191 E---EFAKIVQKLKD 203
Db 80 EEVSEFFLYVLOQLED 95

RESULT 6
BIR2_HUMAN STANDARD; PRT; 618 AA.
ID BIR2_HUMAN Q13450; Q16516;
AC Q13450; Q16516;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
DE protein 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TRAF signaling complex
DE protein 2) (IAP homolog B).
GN BIRC2 OR API1 OR IAP2 OR MIHB.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertont-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:349-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [16]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [17]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [18]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [19]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [20]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [21]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [22]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [23]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [24]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [25]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [26]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors."
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [27]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Farkusch M., Hawkins C.J., Puls K.L.,
```

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP STRUCTURE BY NMR OF 266-363.  
 RX MEDLINE=93332054; PubMed=10404221;  
 RA Hinds M.G., Norton R.S., Vaux D.B., Day C.L.;  
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
 RT repeat.";  
 RL Nat. Struct. Biol. 6:648-651(1999).  
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
 CC LEUKOCYTES.  
 CC -1- SIMILARITY: Belongs to the IAP family.  
 CC -1- SIMILARITY: Contains 3 BIR repeats.  
 CC -1- SIMILARITY: Contains 1 CARD domain.  
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.  
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 CC EMBL; L49431; AAC41942.1; -;  
 DR EMBL; U45879; AAC50372.1; -;  
 DR EMBL; U37547; AAC50508.1; -;  
 DR EMBL; BC016174; AAH16174.1; -;  
 DR EMBL; BC028578; AAH28578.1; -;  
 DR PIR; S68450; S68450.  
 DR PDB; 1QBH; 20-OCT-99.  
 DR Genew; HGNC:590; BIRC2.  
 DR MIM; 601712; -;  
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR InterPro; IPR001370; BIR.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SM00238; BIR; 3.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS0209; CARD; 1.  
 DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS00089; ZF\_RING\_2; 1.  
 KW Apoptosis; zinc-finger; Repeat; 3D-structure.  
 FT REPEAT 46 113 BIR 1.  
 FT REPEAT 184 250 BIR 2.

FT REPEAT 269 336 BIR 3.  
 FT DOMAIN 453 543 CARD.  
 FT ZN\_FING 571 606 RING-TYPE.  
 FT CONFLICT 157 157 S -> P (IN REF. 2).  
 FT CONFLICT 308 308 C -> G (IN REF. 2).  
 FT CONFLICT 414 414 Q -> L (IN REF. 2).  
 FT CONFLICT 514 514 L -> W (IN REF. 2).  
 FT TURN 269 270  
 FT HELIX 271 274  
 FT HELIX 287 293  
 FT TURN 294 294  
 FT TURN 296 297  
 FT TURN 301 304  
 FT STRAND 309 309  
 FT HELIX 322 325  
 FT TURN 326 328  
 FT STRAND 333 333  
 FT TURN 334 343  
 FT HELIX 344 351  
 FT TURN 353 354  
 SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;  
 Query Match 7.7%; Score 92.5; DB 1; Length 618;  
 Best Local Similarity 24.5%; Pred. No. 3.9;  
 Matches 27; Conservative 24; Mismatches 46; Indels 13; Gaps 2;  
 QY 132 IQSKREDIVNQMTAEALNQSLDALLSRDLIMKDEYELVSTKPTRTSKVRLDTDTIQGE 191  
 Db 461 IRKNRVALFQOLT--CVLPILDNLNKKANVINKQEHDIKQKTOIPQARELIDTILVKGN 518  
 QY 192 EFAKVTIVQKLKD-----NKQMGLQVPYPEILVWSRSPSLNLQNK 230  
 Db 519 AAANIFKNCLEKIDSTLYKNLFVDKNNKYIPTEDVSGLSLEQLRRLQEE 568  
 RESULT 7  
 REPI\_ZYGBA STANDARD; PRT; 357 AA.  
 ID REPI\_ZYGBA AC P13776;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-AUG-1990 (Rel. 15, Last annotation update)  
 DE Trans-acting factor B (REPI).  
 GN B.  
 OS Zygosaccharomyces bailii.  
 OG Plasmid pSB2.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.  
 OX NCBI\_TaxID=4954;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IFO 1047;  
 RX MEDLINE=88058763; PubMed=3680169;  
 RA Uchatsu I., Sakamoto S., Imura I., Toh-E A.;  
 RT "yeast plasmids resembling 2 micron DNA: regional similarities and  
 RT diversities at the molecular level.";  
 RL J. Bacteriol. 169:5537-5545(1987).  
 CC -1- FUNCTION: PLASMID PARTITION REQUIRE REPI, REP2, AND A CIS-ACTING  
 CC DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN  
 CC THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA  
 CC REP2.  
 CC -1- SIMILARITY: TO THE P GENE PRODUCT OF PSR1.  
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 CC EMBL; M18274; AAA35283.1; -;  
 DR InterPro; IPR008897; Yeast\_TAF.





Query Match	7.3%; Score 88; DB 1; Length 2368;
Best Local Similarity	22.3%; Pred. No. 54;
Matches	56; Conservative 38; Mismatches 105; Indels 52; Gaps 11;
QY	14 HLCDDKKK-----MELSLNIPVNHGPOEESGSGSQ-----LHNSGSPETSRLPAPQDNDF 64
DB	491 HLCDEIKTGNPVRINP-----EAAGSEIFRILHSN-----FLSHPNIDF 535
QY	65 LSKAQCQCFMKLHH-----CPGNHSDSTIGSQRAAFCDHKTTPCCSAINPL 114
DB	536 -SESLSGLILFSLHRIFSHFQPPKLTGNGQINKSPKLVCKFMNSRYRLRLSTRIEPL 594
QY	115 ---STAGNERLOPAGTAQWIOQSKREDIV-----NMTACLNQSLDALLSR--DLI 161
DB	595 FNISDSHNSDEHTAFILRFLOSKLPVVKENLVIAWTQTLTTSNDVFTLLKLIDIF 654
QY	162 MKEDYELVSTKPTRTSKVQLDITDIO-GEFAKVIIVKLDN---KMGLOPYPEILV 217
DB	655 NDDVSLRIMTLOIKWMAKILKTPYQLLSPILPVLKQNLVERKVGQNLIELLG 714
QY	218 VSRSPSLNLLQ 228
DB	715 YSSKTILDFQ 725
RESULT 11	
SYAP MOUSE	
ID	SYAP MOUSE STANDARD; PRT; 365 AA.
AC	Q9D5V6; Q9D870;
DT	10-OCT-2003 (Rel. 42, Created)
DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Synapse associated protein 1.
GN	SYAP1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J;
RC	TISSUE=Dorsal root ganglion, Small intestine, and Testis;
RX	MEDLINE=22354683; PubMed=12466851;
RA	Okazaki Y., Furuno M., Kasukawa T.,
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA	Blake J.A., Bratt T.A., Brusic V., Clothia C., Corbani L.E., Cousins S.,
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA	Kongaya A., Kurochkin I.V., Lee Y., Lenhard R., Lyons P.A.,
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA	Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA	Wilm L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA	Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA	Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA	Birney E., Hayashizaki Y.;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573 (2002).
RN	[2]
RP	SEQUENCE FROM N.A.
QY	114 LSTAGNSERLOPAGTAQWIOQSKREDIVNQ-----MTEACLNQSLDALLSRDLIMKEDYEL 168
DB	220 ISLIQSAQLTALAAQQASGKEKSSNRDNLPLTEAVRPKTPPVVVKSLKQSDDEE 279
QY	169 VSTKTRTSKVQLDITDIOGEFAKVIIVKLDNKKQ 206
DB	280 ISTSPGVSEFVSADFATCTSLNQEDLRKEMEQLVLDKKQ 317
RESULT 12	
MYC ASTVU	
ID	MYC ASTVU STANDARD; PRT; 407 AA.
AC	Q17103;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Myo protein (c-myc) (fragment).
GN	MYC.
OS	Asterias vulgaris (Northern sea star).
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC	Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Asterias.
OX	NCBI_TaxID=7605;
RN	[1]
RP	SEQUENCE FROM N.A.

```

RX MEDLINE=93026376; PubMed=1408141;
RA Walker C.W., Boom J.D., Marsh A.G.;
RT "First non-vertebrate member of the myc gene family is seasonally
RT expressed in an invertebrate testis.";
RL Oncogene 7:2007-2012(1992).
CC -1- FUNCTION: Participates in the regulation of gene transcription.
CC Binds DNA both in a non-specific manner and also specifically to
CC recognizes the core sequence CAC[GA]TG. Seems to activate the
CC transcription of growth-related genes (By similarity).
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (BHLH) domain.
CC
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CC
DR ENBL; M80364; AAA27788.1; -.
DR PIR; S27774; S27774.
DR HSP; P25912; IHLO.
DR TRANSFAC; T03463; -.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF01056; Myc_N_term; 1.
DR PRINTS; PR00044; LEUZIPPRMYC.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH; 1.
KW Nuclear protein; DNA-binding; Transcription regulation; Activator.
FT NON_TER 1
FT DNA_BIND 321 334 BASIC DOMAIN.
FT DOMAIN 335 374 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 380 401 LEUCINE-ZIPPER (POTENTIAL).
SQ SEQUENCE 407 AA; 45673 MW; F4E52DD01182113A CRC64;

Query Match 7.2%; Score 86.5; DB 1; Length 407;
Best Local Similarity 21.9%; Pred. No. 7.1;
Matches 59; Conservative 40; Mismatches 91; Indels 79; Gaps 14;

QY 19 KQELSLNIPV--NHGPOE--ESCGSSQLHNSGSPETSRLPAPQNDL----- 65
DB 43 KPELYTPTPLSPHNDKESDHPRHQDGDGSPSRSYQHLMDDDLPLVNPQVPLL 102
QY 66 -----SRKAQDCYPMKLHCPGNHSDSTISGSQRAAFCDHK-----TTP 105
DB 103 DLSSAPPIAALIQC-----WSSIIAERRKLFMKSEKKHAEERATKKASTP 150
QY 106 CSSAINPL---STAGNSERLOP-GIAQQWIOSKREDIVNQMTACLNQSLDALLSDLI 161
DB 151 SSGVMLPPLVPASVYSGDCVDSAVCPYPLSLRDLFSSGT-----NTPSDSEEEIDVV 206
QY 162 MKED-----YELSTKP--TRTSKVRQLD-----TTDIOGEPAKVI---VOKLK 202
DB 207 TVEKKHSHVHKINTRYHQSTKVRQHLHRPISVALVGLRGPSTAILSTPIPKLK 266
QY 203 DNKQMGLOPPEILVSRPSLNLLQNK 231
DB 267 --TEGNLEEVKQILQKS-----NLIRSS 288

RESULT 13
BIR2_MOUSE
ID BIR2_MOUSE STANDARD; PRT; 612 AA.
AC Q62210; Q08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis
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DE protein 2) (MIAP2) (MIAP-2).
GN BIRC2 OR BIRC3 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins.";
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.";
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBUNIT: Interacts with SMAC and with PRS25; these interactions
CC inhibit apoptotic suppressor activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung,
CC liver, skeletal muscle, kidney and testis.
CC -1- SIMILARITY: Belongs to the IAP family.
CC -1- SIMILARITY: Contains 3 BIR repeats.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
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DR ENBL; L49433; AAC42078.1; -.
DR HSP; U88909; AAC3532.1; -.
DR HSP; Q13490; 1QBH.
DR MGD; MGI:1197009; Birc3.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 46 113 BIR 1.
FT REPEAT 177 243 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 447 537 CARD.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C10D CRC64;

Query Match 7.2%; Score 86.5; DB 1; Length 612;
Best Local Similarity 23.6%; Pred. No. 12;
Matches 26; Conservative 21; Mismatches 50; Indels 13; Gaps 2;
```



QY 132 IQSKREDIVNMTAEACNLSLDALLSRDLIMKEDYELVSTKPTRSKVQLDITDDIQE 191  
 DB 455 IKRKNALFQQLTHVL--PILNLLASVITKQEHDIIRKQTQIPQLQARELIDTVLKG 512  
 QY 192 EFAKVIQKLDK-----NKGMLQPYEILVWSRSPSLNLQNK 230  
 DB 513 AAANIFKSLKEIDSTLYENLFVEKNKXIPTDVSGLSLEQLRLQEE 562

## RESULT 14

MRTEB HUMAN  
 ID MRTEB HUMAN STANDARD; PRT; 1088 AA.  
 AC Q9ULH7; Q86W2; Q8N226;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Myocardin-related transcription factor B (MRTF-B).  
 GN MRTF B OR KIAA1243.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Thymus;  
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,  
 RA Arita M., Matsushino K., Yuuki H., Hara H., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,  
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;  
 RT "NEO human cDNA sequencing project";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Medulla oblongata;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Scherch A.J., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE OF 261-1088 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirotsawa M., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro";  
 RL DNA Res. 6:337-345(1999).  
 CC -!- FUNCTION: Poor transcriptional factor which uses the canonical  
 CC single or multiple CArG boxes DNA sequence. Acts as a cofactor of  
 CC serum response factor (SRF) with the potential to modulate SRF  
 CC target genes (By similarity).

CC -!- SUBUNIT: Interacts with SRF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Comment=Full isoforms so far detected are isoform 2 and isoform  
 CC 3;  
 CC Name=1;  
 CC IsoId=Q9ULH7-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9ULH7-2; Sequence=VSP\_007653, VSP\_007654, VSP\_007655;  
 CC Note=No experimental confirmation available;  
 CC Name=3;  
 CC IsoId=Q9ULH7-3; Sequence=VSP\_007656, VSP\_007657;  
 CC Note=No experimental confirmation available;  
 CC -!- DOMAIN: The N-terminal region is required for nuclear localization  
 CC and the C-terminal region mediates transcriptional activity (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 3 RPEL repeats.  
 CC -!- SIMILARITY: Contains 1 SAP domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC -----  
 CC EMBL; AK093577; BAC04200.1; -;  
 CC EMBL; BC047761; AAH47761.1; -;  
 CC EMBL; AB033069; BAA86557.2; -;  
 CC InterPro: IPR004018; RPEL\_repeat.  
 CC InterPro: IPR003034; SAP.  
 CC Pfam: PF02755; RPEL; 3.  
 CC Pfam: PF02037; SAP; 1.  
 CC SMART; SM00707; RPEL; 3.  
 CC SMART; SM00513; SAP; 1.  
 CC PROSITE; PS50800; SAP; 1.  
 CC Transcription regulation; Nuclear protein; Coiled coil; Repeat;  
 CC Alternative splicing.  
 CC REPEAT 1. 65  
 CC REPEAT 2. 84 109  
 CC REPEAT 3. 128 153  
 CC DOMAIN 389 423  
 CC DOMAIN 545 601  
 CC DOMAIN 671 787  
 CC VARSPLIC 1 41  
 CC -----  
 CC MIDSSKQOQGPPEILTAGDFEPLKEKECLEGSNQSLKEV  
 CC -> M (in isoform 2).  
 CC /FTID=VSP\_007653.  
 CC PLNDKNSGNSALNNATPNTPRNTSTPVRKPGPLPSSLD  
 CC DLKVELTELKRLGVPVSGTKPDILIER -> AYHTVSEVH  
 CC MVRVACIPFQSLSSIGSEFLQVRNAPSOLFQICLLLBHQ  
 CC NSTRCEKSVSIIIPGINS (in isoform 2).  
 CC /FTID=VSP\_007654.  
 CC Missing (in isoform 2).  
 CC /FTID=VSP\_007655.  
 CC PLNDKNSGNSALNNATPNTPRNTSTPVRKPGPLPSSLD  
 CC DLKVELTELKRLGVPVSGTKPDILIERLKPYQEVNNSGLA  
 CC AGGIVAVSSAIVTSNPVTVALPVTTLHN -> YGGAHAI  
 CC LNAGFSVFMNRYKLKPKVCECHLFLVSLNDFHFFVIRAYHTV  
 CC SEVHMVRVACIPFQSLSSIGSEFLQVRNAPSOLFQICLL  
 CC LEHQNSTRCEKSVSIIIPGINS (in isoform 3).  
 CC /FTID=VSP\_007656.  
 CC Missing (in isoform 3).  
 CC /FTID=VSP\_007657.  
 CC K -> R (in REF. 1).  
 CC QUERY MATCH 7.2%; Score 86.5; DB 1; Length 1088;  
 CC MATCHES 38; Conservative 32; Mismatches 59; Indels 41; Gaps 6;  
 CC -----  
 CC QY 81 PGNHSDSTIGSRAAFCDHKHTTP-CSS-----AIIINPLSTAGNSRERLQPGIAQ 129

Db 610 PGHSVSKDQKHGSLGSIKDEASLPDCSSRQPIPVASHAVGPVSTGG-----QTLVAK 664  
Qy 130 QWI-----OSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180  
Db 665 KAVIKQIEVPVGAQEQSVVVSQFVSVSQGPPPAVNAQ-----PQALLTIQTA 712  
Qy 181 QLLDITDIOGEEFAKVIQV----KLKDNKQMGQVPEILVWRSRSLNL 226  
Db 713 QLLLPVSIQSSVTSVQLPVGSLKQTSPOAGMTQPOIATAAQIPTAAL 762

RESULT 15

ABPX YEAST  
ID ABPX YEAST STANDARD; PRT; 627 AA.  
AC Q08641; Q08644;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Actin-binding protein ABP140.  
GN ABP140 OR YOR233W/YOR240W.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / FY1679;  
RX MEDLINE=97127829; PubMed=8972580;  
RA Boyer J., Michaux G., Fairhead C., Gaillon L., Dujon B.;  
RT "Sequence and analysis of a 26.9 kb fragment from chromosome XV of  
RL the yeast Saccharomyces cerevisiae.";  
RN Yeast 12:1575-1586(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97313270; PubMed=9169874;  
RA Dujon B., Albermann K., Aldea M., Alexandraki D., Ansong W.,  
RA Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,  
RA Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,  
RA Criepluch C., Daigman-Fornier B., Dang D.V., de Haan M., Delius H.,  
RA Durand P., Fairhead C., Feldmann H., Gaillon L., Gallison F.,  
RA Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,  
RA Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,  
RA Hernandez Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,  
RA Hollenberg C.P., Hughes B., Jauniaux J.-C., Kaloogeropoulos A.,  
RA Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,  
RA Maarse C., Madania A., Mannhaupt G., Marck C., Martin R.P.,  
RA Mewes H.-W., Michaux G., Paces V., Farie-McDermott A.G., Pearson B.M.,  
RA Perrin A., Pettersson B., Poch O., Pohl T.M., Poirey R.,  
RA Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,  
RA Schwager C., Schweizer M., Sor F., Sterky F., Tarassov I.A.,  
RA Teodoru C., Tettelin H., Thierry A., Tobiasch E., Tzermia M.,  
RA Uhlen M., Unsel M., Valens M., Vandenbol M., Vetter I., Vleck C.,  
RA Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,  
RA Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";  
RL Nature 387:98-102(1997).  
[3]  
RP PARTIAL SEQUENCE FROM N.A., SEQUENCE OF 1-12; 38-72; 102-115; 244-286;  
RP 560-574 AND 598-608, FUNCTION, AND SUBCELLULAR LOCATION.  
RC STRAIN=BU5457;  
RX MEDLINE=98127445; PubMed=9467951;  
RA Asakura T., Sasaki T., Nagano F., Satoh A., Obaishi H., Nishioka H.,  
RA Inamura H., Hotta K., Tanaka K., Nakanishi H., Takai Y.;  
RT "Isolation and characterization of a novel actin filament-binding  
RL protein from Saccharomyces cerevisiae.";  
RL Oncogene 16:121-130(1998).  
CC -1- FUNCTION: Potential methyltransferase (By similarity). Binds F-  
CC actin and shows weak F-actin crosslinking activity.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and cortical cytoskeleton.  
CC -1- MISCELLANEOUS: A ribosomal frameshift occurs between the codons  
CC for Leu-276 and Gly-277.  
CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. METL

CC family.  
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CC  
CC EMBL; Z75147; CAA99460.1; ALT\_SEQ.  
CC EMBL; Z75147; CAA99461.1; ALT\_SEQ.  
CC GermOnline; I43827; -.  
CC SGD; S0005765; ABP140.  
CC GO; GO:0005884; C:actin filament; IDA.  
CC GO; GO:0003780; F:actin cross-linking activity; IDA.  
CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IDA.  
CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IDA.  
CC InterPro; IPR001601; Methyltransf.  
CC InterPro; IPR000051; SAM\_bind.  
CC Transferase; Methyltransferase; Cytoskeleton; Actin-binding;  
KW Ribosomal frameshift.  
FT INIT MET 0  
SQ SEQUENCE 627 AA; 71354 MW; D4E55F9485412F39 CRC64;  
  
Query Match 7.0%; Score 85; DB 1; Length 627;  
Best Local Similarity 18.8%; Pred. No. 17;  
Matches 41; Conservative 47; Mismatches 92; Indels 38; Gaps 7;  
  
Qy 22 ELSLNPVNHGPOESCGSSQLHNSGSPETSRLPAPQDNDFLSRKAQDCYFMKLHCP 81  
Db 180 EEDADIEQNSGKRETAENASQAQNDGSTTTTSKKNKKKKKKKKKKR----- 229  
Qy 82 GNHSWDSSTISGSORAAFCDDHKTTTSCSAIINPLSTAGNSERLQP---GIAQQ----WIQS 134  
Db 230 GNVTNANVDDSTKTGENDDTTGTTSITTSATQEVNDLEVDVDDSCLDGIDQHNREHLKA 289  
Qy 135 KREDIVNQTEACLNQSL-DALLSRDLIMKEDYELVSTKPTRTSK-----VRLDIT 186  
Db 290 LTQDVKEETLENTAHEGRGDNQDQNAVEKSDFEKSDTEGSRIGRDLPFEGKRNLTES 349  
Qy 187 DI-----QGEEFAKVIQVOKLKNQMGQVPE 214  
Db 350 DVWDHNDVNDVWEEGEEVQQAEEKIQPK---HPVPE 384  
  
Search completed: March 29, 2004, 14:08:38  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 29, 2004, 14:03:30 ; Search time 45 Seconds  
(without alignments)  
1626.672 Million cell updates/sec

Title: US-09-771-161A-93

Perfect score: 1206

Sequence: 1 MISLQSQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	27.8	584	13 Q8JHU4	Q8JHU4 brachydanio
2	99	8.2	461	12 Q8J861	Q8J861 spodoptera
3	98.5	8.2	537	11 Q8R489	Q8R489 cavia porce
4	98	8.1	799	5 Q8IN63	Q8IN63 drosophila
5	98	8.1	829	5 Q9VDR7	Q9VDR7 drosophila
6	98	8.1	830	5 Q45116	Q45116 drosophila
7	98	8.1	830	5 Q44224	Q44224 drosophila
8	97.5	8.1	869	10 Q9FTV4	Q9FTV4 oryza sativ
9	97	8.0	285	13 Q8JFU4	Q8JFU4 brachydanio
10	96	8.0	1169	16 Q7ZAJ1	Q7ZAJ1 scaphylococ
11	95.5	7.9	791	16 Q8A9V6	Q8A9V6 bacteroides
12	95.5	7.9	2063	11 Q8QTB4	Q8QTB4 mus musculus
13	94.5	7.8	589	11 Q9QZC6	Q9QZC6 rattus norv
14	94.5	7.8	589	11 Q8ESE8	Q8ESE8 rattus norv
15	94.5	7.8	896	11 Q91X10	Q91X10 mus musculus
16	93.5	7.8	571	16 Q87L04	Q87L04 vibrio para

17	93.5	7.8	1229	15	Q8D169	Q8D169 yersinia pe
18	93	7.7	692	5	Q965M1	Q965M1 caenorhabdi
19	92.5	7.7	923	13	Q902T7	Q902T7 xenopus lae
20	90.5	7.5	241	10	Q9XHR9	Q9XHR9 nicotiana s
21	90	7.5	2315	5	Q95ZK3	Q95ZK3 caenorhabdi
22	90	7.5	2396	5	Q23081	Q23081 caenorhabdi
23	89	7.4	212	10	Q7XBN6	Q7XBN6 antirrhinum
24	89	7.4	237	10	Q7XSS6	Q7XSS6 oryza sativ
25	89	7.4	242	10	Q8LLR0	Q8LLR0 vitis vinif
26	89	7.4	242	10	Q38733	Q38733 antirrhinum
27	89	7.4	738	4	Q9P2P8	Q9P2P8 homo sapien
28	89	7.4	1360	5	Q9TYK4	Q9TYK4 caenorhabdi
29	88.5	7.3	617	17	Q8PUY5	Q8PUY5 methanosarc
30	88.5	7.3	2439	5	Q9VMS2	Q9VMS2 drosophila
31	88	7.3	283	16	Q9JX61	Q9JX61 neisseria m
32	88	7.3	524	13	Q8JGL7	Q8JGL7 xenopus lae
33	88	7.3	777	12	Q7TFN7	Q7TFN7 rhesus cyto
34	88	7.3	1049	4	Q8WYL5	Q8WYL5 homo sapien
35	88	7.3	1135	13	Q9YHD3	Q9YHD3 xenopus lae
36	88	7.3	1762	2	Q9KWC9	Q9KWC9 agrobacteri
37	87.5	7.3	288	4	Q8N5S3	Q8N5S3 homo sapien
38	87.5	7.3	340	5	Q9XW80	Q9XW80 caenorhabdi
39	87.5	7.3	386	6	Q9N2H6	Q9N2H6 bos taurus
40	87.5	7.3	665	16	Q87JP9	Q87JP9 vibrio para
41	87.5	7.3	1844	4	Q86QE3	Q86QE3 homo sapien
42	87	7.2	147	10	Q22831	Q22831 arabidopsis
43	87	7.2	1205	12	Q56300	Q56300 human herpe
44	87	7.2	1205	12	Q69513	Q69513 human herpe
45	86.5	7.2	210	10	Q7XBM3	Q7XBM3 lycopersico

#### ALIGNMENTS

#### RESULT 1

Q8JHU4	Q8JHU4	PRELIMINARY;	PRT;	584 AA.
AC	Q8JHU4;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Protein kinase RICK.			
GN	RICK.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,			
RA	Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.;			
RT	"PKC mediates Bcl10-independent NF-kappa B activation induced by phorbol ester.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
DR	EMBL; AF487540; AAM76920.1;			
DR	GO; GO:0005622; C:intracellular;			
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006915; P:apoptosis; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR000719; Prot_Kinase.			



OC Ephydroidea; Drosophilidae; Drosophila.  
 RN NCBI\_TaxID=7227;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Dorsett V., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J., Andrews-Frankoch C., Balwin D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Balwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Chert J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jaldali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.F., Wasarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Seearle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celnik S.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003728; AAN13815.1; -;  
 DR EMBL; BT004903; AAO47881.1; -;  
 DR FlyBase; FBgn0021776; mira;  
 DR GO; GO:0045180; C:basal cortex; NAS;  
 DR GO; GO:0008105; P:asymmetric protein localization; IGI;  
 DR GO; GO:0008105; P:asymmetric protein localization; IGI;  
 SQ SEQUENCE 799 AA; 89816 MW; AE00B9F2C7F654B6 CRC64;  
 Query Match 8.1%; Score 98; DB 5; Length 799;  
 Best Local Similarity 21.3%; Pred No. 3.3;  
 Matches 44; Conservative 39; Mismatches 78; Indels 46; Gaps 8;  
 QY 12 AIHLCKKRMELSLNIPVNHGPGESCGSSQLHNSGSPETSRSLPAPQDNFLSRKAQD 71  
 Db 64 AVRPASSKEAKEPAIP---KEDKSKGLRLFRTPSLPQRLRPRTPTSDTATGSG-- 117  
 QY 72 CYFMKLHCPGHNHSDSTISSQRAAFCDHKTTCPSSAIINPLSTAGNSERLQPGIAQW 131  
 Db 118 -----SGASTAA-----STPLHSAATTPVKEAKSASRLKGEALQY 153  
 QY 132 -IQSKREDIVNQTEA-CLNOSLDALLSRDLIMKEDYELVSTKPTKSVROLLDTTDIQ 189  
 Db 154 EIRHNKELIESQLSDVLRHVDQKEAKLREHEHLATSK---TDRLIEALTSNLIS 210  
 QY 190 GEEFAKIVQKLNKQNGQLQPYPEIL 216  
 Db 211 HKAL-----NEQMG-QEHADLL 226  
 RESULT 5  
 Q9VDR7 PRELIMINARY; PRT; 829 AA.  
 ID Q9VDR7;  
 AC Q9VDR7;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE CG12249 protein.  
 GN MIRA OR CG12249.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Balwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,



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ID Q04224 PRELIMINARY; PRT; 830 AA.
AC Q04224;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MIRANDA.
GN MIRA OR CG12249.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=98065952; PubMed=9403694;
RA Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.Q.,
RA Matsuzaki F.;
RT "Miranda directs Prospero to a daughter cell during Drosophila
RT asymmetric divisions.";
RL Nature 390:625-629(1997).
DR EMBL; AB05661; BAA24111.1; -.
DR PIR; T00029; T00029.
DR FlyBase; FBgn0021776; mira.
DR GO; GO:0045180; C:basal cortex; NAS.
DR GO; GO:0008105; P:asymmetric protein localization; IGI.
SQ SEQUENCE 830 AA; 93171 MW; F7AD159AA58F178A CRC64;

Query Match 8.1%; Score 98; DB 5; Length 830;
Best Local Similarity 21.3%; Pred.No.3.5; Indels 46; Gaps 8;
Matches 44; Conservative 39; Mismatches 78;

QY 12 AIHLCDKKMELSLINIPVNHGPOEESCGSQLHENSGETSRSLPAPQNDFLSRKAQD 71
DB 64 AVTFASSKKEAKFAIP-----KEDKSKGLRLFTPSLPQELRFRPTSHDTATGSG-- 117
QY 72 CYPMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAINPLSTAGNSERLQPGIAQQW 131
DB 118 -----SCASTAA-----STPLHSAATTPVKEAKSASRLKGKEALQY 153
QY 132 -IQSKREDIVNOMTEA-CLNQSLDALSLRDLIMKEDYELVSTKPTRSKVRLQDLDTDIO 189
DB 154 EIRHKNELIESQLDVLRRHVQDLKEAKUREEHATSK---TDRUEALTSENLS 210
QY 190 GEEFAKVIQKLDKNQKMGQPYPEIL 216
DB 211 HKAL-----NEQMG-QEHADLL 226

RESULT 8
Q9FTV4 PRELIMINARY; PRT; 869 AA.
ID Q9FTV4
AC Q9FTV4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0407B12.26 protein.
GN P0407B12.26.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RA clone: P0407B12.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002843; BAB17189.1; -.
DR Gramene; Q9FTV4; -.
SQ SEQUENCE 869 AA; 97064 MW; E2E59640E0BE63B2 CRC64;

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Query Match      8.1%; Score 97.5; DB 10; Length 869;
Best Local Similarity 23.0%; Pred. No. 4.1;
Matches 54; Conservative 35; Mismatches 71; Indels 75; Gaps 13;

Qy      24 SLNIPVNHGPOEESCGSS---QLHNSG---SPETSRLPAPQNDNFLSKAQCDFMKL 77
Db      330 SVSSSHDRTKGCSSRSIQ-KTDGLLSPSRSGDIESPK--DILCERDAEC----- 381
Qy      78 HHCPGHNHSDSTISGQRAAFCDHKHTPCS-----SAINPLSTA---GNSERLOFGIAQ- 129
Db      382 -----QVEPSDARVSPCVLEDKLVDFLCSQEKDNNSDL--GWANI 422
Qy      130 QWTQSKREDIVNOMTEACLNQSL-----DALLSRDLI-----MKED----- 165
Db      423 SDVNCCKGEKHVDDDDGSLSMGSEQRKCEDESLVDNSMCKTHEQKSKDDHSSPEDVSK 482
Qy      166 -VELVTKPTRTSKV-----RQLLDTDTIQEEFAKVIQKLDKNQOMGLQ 210
Db      483 THFDFSTKONISSAVDGNKEHFEPSKDDTNSLEGEKSLNKEHKEQSKEDNSGLE 537

RESULT 9
Q8JFU4 PRELIMINARY; PRT; 285 AA.
ID AC Q8JFU4
AC Q8JFU4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SI:d257F23.2 (Novel protein) (Fragment).
GN SI:D257F23.2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxId=7955;
CX [1]
RN R
RP SEQUENCE FROM N.A.
RA Kimberley A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL603786; CAD3437.1; -.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000159; RA_domain.
DR Pfam; PF00788; RA; 1.
DR SMART; SM00314; RA; 1.
DR PROSITE; PS50200; RA; 1.
FT NON_TER
FT TER
SQ SEQUENCE 285 AA; 33269 MW; D757B6A7D1046693 CRC64;

Query Match      8.0%; Score 97; DB 13; Length 285;
Best Local Similarity 23.8%; Pred. No. 1.1;
Matches 68; Conservative 41; Mismatches 93; Indels 84; Gaps 14;

Qy      4 LQIQSVSSAIHLCDKKKM-----ELSLNIPVNHGPOEESCGSQ-----LH-----ENSGS 49
Db      16 LQIQ-----DEKQIFNESSVSKSPDIPSLGNKRGMTWGEFDNLHIALEBAGS 66
Qy      50 PET-----SRSLPAPQNDNFLSKAQCDFMKLH-----HCFGNHSD 87
Db      67 PENPTEDIYVETWTLRPSRTMGINEDSSYLIRMTSDASLVKRVKSKMIESQKNRHR 126
Qy      88 STISGQRAAFCDHKT---TPCSSAI---INPLSTAGNSERLQPGIAQWQIQSKREDIV 140
Db      127 FSINGH-----FNYKTSVFTPSFGATTNVHNSMTT-----QEVITQLLHKFKVNSP 176
Qy      141 NQMTTEACLNQSLD--ALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTDTIQEEFA---- 194
Db      177 NEFSLVCIHQTKGRRLSSDDLPL---WERVLOGPSNFIMKFMFLMDTDE---EBISLDA 230
Qy      195 -----KVIVOKLKNQKQGLQDPYELIVVSRSPSLNLLQNK 230
Db      231 QYLNLEMPILKVTLQKLEENIEORIKAKYOKERSLLLOCLRKK 276

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Query Match      8.0%; Score 97; DB 13; Length 285;
Best Local Similarity 23.0%; Pred. No. 1.;
Matches          68; Conservative 41; Mismatches 93; Indels 84; Gaps 14;

Qy    4   LQLQSVSIAHLCDKKM---ELSLAIPVNHQEESSCGSSQ-----LH-----ENSGS 49
       |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    16  LQIQ-----DEKQIFSNESSVKSPDPISPLGNKRGMTRWGEFDNLNHAIELEAGS 66
       ::::::::::::-SRLPAPONDFLSKAQDCYFKMLH-----HCFGNSWD 87
Qy    50  PET-----
       |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    67  PENPTEDIYETWTURPSRMTQINEDSSYLIRTMDSALVKRVKSKKMIESQKNRHR 126
       ::::::::::::-TPCSSAI-----INPLSTAGNSERLPQGAQQIWIOQSKREDIV 140
Qy    88  STTSGSORAAFCDHKT-----FYNKYTSVFTPSGATTNVHINSRWTT-----QEVIQTLLHKFEVNSP 176
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    127 FSINGH-----
       ::::::::::::-ALLSRDLIMKEDYEIUVSTKPRTSTKVROLDDTTDIQGEFA---- 194
Qy    141 NQWTEACLNQSLD-----WVRVLQGPSNFIMKMFILMDTDE---EBISLDVA '230
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    177 NEFSLYCIHTGKBKRLSSDLPL-----KVIVOKLKONQGLQPYPEILVVSRSPSNILOXK 230
       ::::::::::::-KVIVOKLKONQGLQPYPEILVVSRSPSNILOXK 230
Qy    195 -----
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    231 QYLINLEMPILKVTLQKEEENLEIORIKAKYOKERSLLOCLQRKK 276

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RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AB016928; AAO75816.1; -.
DR InterPro; IPR001364; Hemagglutn.
DR ProDom; PD000225; Hemagglutn; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 791 AA; 8843 MW; 7C72011D0CD93232 CRC64;

Query Match 7.9%; Score 95.5; DB 16; Length 791;
Best Local Similarity 19.4%; Pred. No. 5.6;
Matches 48; Conservative 36; Mismatches 80; Indels 83; Gaps 9;

QY 2 YSLQLQSSSAIHLCDKKXWELSLNIP-----VNHGPQESCG 39
Db 452 YTLSLQAI-----RKNTAATNLPDEPEKLAFLIPADISRAQLTHLINQSCS 503

QY 40 SSQIHNSSPETSRLPAPQNDFLSRKAQDCYFMKLHHCPCGNH-----SWDSTISG 92
Db 504 SLLTSTEASSVSTARNQDYGHFDILCKAFEHLELISSYKINGRHPKLVPEYPSLSAFLTG 563

QY 93 SQRAAFCDHKHTPCSSAIINPLSTAG-----NSERL-----OPGIAQOWIQSKREDIVN 141
Db 564 -----TPSSLLIFIPMETGLYVNRFLINTFLPAWQDVFAEKVRA--DDLFN 610

QY 142 QMTEACINQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDPTTDIOGEEPAKVIVQKL 201
Db 611 ELSMRFQOMAL-----FLKDSPT-----VKLTDQKFEFNRVFTQLL 648

QY 202 KDNKQMG 208
Db 649 KDTDLG 655

RESULT 12
Q80TB4 PRELIMINARY; PRT; 2063 AA.
AC Q80TB4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MKIA1606 protein (Fragment).
GN MKIA1606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
DR EMBL; AK122531; BAC65813.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR003822; PAH-.
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
SQ SEQUENCE 2063 AA; 227819 MW; 8AA6E1AA113B3899 CRC64;

Query Match 7.9%; Score 95.5; DB 11; Length 2063;
Best Local Similarity 21.2%; Pred. No. 19;
Matches 43; Conservative 35; Mismatches 84; Indels 41; Gaps 7;

QY 25 LNIPVNHGPQESCGSSQLHNSSGSPETSRLPAPQNDFLSRKAQDCYFMKLHHCPCGNH 84

RESULT 10
Q7ZAJ1 PRELIMINARY; PRT; 1169 AA.
AC Q7ZAJ1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA translocase stage III sporulation prot.
GN S21414.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren Y., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016748; AAO05013.1; -.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 1.
DR PROSITE; PS50901; FtsK_SpoIIIE; 1.
KW Complete proteome.
SQ SEQUENCE 1169 AA; 133548 MW; 320DC7EDAA48E2C8 CRC64;

Query Match 8.0%; Score 96; DB 16; Length 1169;
Best Local Similarity 16.2%; Pred. No. 8.3;
Matches 49; Conservative 57; Mismatches 93; Indels 104; Gaps 10;

QY 17 DKKQM-----ELSLNIP-----VNHGPQESCGSSQLHE----- 45
Db 559 DKRMQDNHKKVSPPELKPEKQANANHRKDSSEKFEKQINTNETDSNYESNGIE 618

QY 46 ---NSGSPETSRLPAPQNDFLSRKAQDCYFMKLHHCPCGNHSD-----STISGQRAAF 98
Db 619 HDMNSSDEHVYTPSPQDEQIQKQDDPHFENAHAKINNSNETGNQSNISHSKRSQY 678

QY 99 CDHKHTPCSSAIINPLSTAGNSERLQPG-----IAQOWIQSKREDI- 139
Db 579 STNESKNIDQTSNNSSTNSQNFQIRKGNPKLPYSQYLLPEAPHEKDDQWIDNKKQELN 738

QY 140 -----VNQMTAC-----LNQSLDALLSRDLIMKED----- 165
Db 739 DALYFNVPAEVKNVTEGSPVTRFELSVKGVKVSRTALQDDIKMALAAKDIRIEAIP 798

QY 166 -----YELVSTKPTRTSKVRQLDPTTDIOGEEPAKVIVQKLKDNKQMGLOPYPEILVVS 219
Db 799 GTSLVGIEVFNQNPKNV-LRSIIESPKFNKTESKLTVMAGYRINNE-----PLLMEDIA 851

QY 220 RSP 222
Db 852 KTP 854

RESULT 11
Q8A9V6 PRELIMINARY; PRT; 791 AA.
AC Q8A9V6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN B70709.
OC Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
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Db 1026 LTLFVTSIPEDKAQVKLDVAEGKNAPQNPESKLPQELTPL-----CTTVFSKEEP--K 1077
QY 85 SWDSTISGSGRAAFCDHKTTTPCSSALINPLSTAGNSERLQ-----PG 126
Db 1078 SHWSSADTGSQAFSE--SSACSWAUVKTESQSGSEKACGVTWVKTTEDGGHVEPLPQ 1135
QY 127 IAQWITQSKREDIVNQ-----TRACL-----NQSLDALLSRDLIMKEDYELVSTKPTR 175
Db 1136 NLQDSLSPSSKOLLNVMKMEADCMVEISSNLPKQDIGBEVKESMELDSESPQEKPSR 1195
QY 176 TSKV--RLQDITDIQGEFAKV 196
Db 1196 ASEMSKQTVLQREDTOAAKSPSV 1218

RESULT 13
Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF190020; AAF04585.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
Apoptosis Protein 1, 2, and 3 Genes.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF183431; AAG22971.1; -.
DR HSSP; Q13490; IQBH.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 589 AA; 66777 MW; E6812FPE3EA34142 CRC64;

Query Match 7.8%; Score 94.5; DB 11; Length 589;
Best Local Similarity 25.5%; Pred. No. 4.7;
Matches 28; Conservative 21; Mismatches 48; Indels 13; Gaps 2;

QY 132 IQSKREDIVNQTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLDITDIQGE 191
Db 432 IRKNRMALFQQLT--CVIPILDLLEASVLTKEHDIIRQKQIPIQARELIDITLVKGN 489
QY 192 EFAKIVQKLKD-----NKGMLQPYPEILVSVSRPSLNLLQNK 230
Db 490 AAASVFKNSLKEVDSTLYEHLFVETKMKYIPTEDVSGLSLEQLRLQEE 539

RESULT 15
Q91XIO PRELIMINARY; PRT; 896 AA.
AC Q91XIO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Leu M., Ehler B., Perriard J.-C.;
RT "Cloning of an unknown protein.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040842; AAK84686.1; -.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 896 AA; 97422 MW; 7F2DFD53500B5A4 CRC64;

Query Match 7.8%; Score 94.5; DB 11; Length 896;
Best Local Similarity 21.2%; Pred. No. 8.1;
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Db	436	LTLPTVTSIPEDKAQVKLDVAEGKNAPONPESKLPQELTPEL-----CTTVFPKKEP--K	487		
Qy	85	SWDSTTSGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ-----PG	126		
Db	488	SWHSSADTGSQEAFFE--SSACSWAVVVKTESQESSEKSACGWTVVVKTEGGHVEPLPQ	545		
Qy	127	IAQQWIOSKREDIVNQ-----TEACL-----NQSLDALLSRDLIMKEDYELVSTKPTR	175		
Db	546	NLQDSLSSPSKDLLNMVMEAECDMVEISSNLPKQDIGBEVKEECSELDSESPQKPSR	605		
Qy	176	TSKV--RQLLDTTDIQEEPAKV	196		
Db	606	ASEMSKQTVLQREDTQAAKSPSV	628		

Search completed: March 29, 2004, 14:09:37  
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:09:03 ; Search time 105 Seconds  
(without alignments)  
1226.177 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVSRSPSLNLQKSM 232

Scoring table:  
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Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 20

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh  
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-DB=Issued\_Patents\_NA -QFMT=fastap -SURFIX=ol120p2n.rni -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=quality -THR MIN=20  
-ALIGN=15 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
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5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	97.8	2501	4	US-09-920-663-3
2	227	97.8	2502	4	US-09-069-023-2
3	185	79.7	1060	4	US-09-023-655-684
4	128	55.2	1820	4	US-09-099-041A-3
5	128	55.2	1820	4	US-09-245-281-3
6	128	55.2	1620	4	US-09-207-359B-3
7	128	55.2	1620	4	US-09-340-620A-3
8	128	55.2	1620	4	US-09-865-364-3
9	128	55.2	1931	3	US-09-019-942-2
10	128	55.2	1931	4	US-09-099-041A-1
11	128	55.2	1931	4	US-09-245-281-1
12	128	55.2	1931	4	US-09-470-271-2

13	128	55.2	1931	4	US-09-207-359B-1	Sequence 1, Appli
14	128	55.2	1931	4	US-09-340-620A-1	Sequence 1, Appli
15	128	55.2	1931	4	US-09-865-364-1	Sequence 1, Appli
16	128	55.2	1931	4	US-09-748-537-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Alignment Scores:  
Pred. No.: 2.61e-231 Length: 2501  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-920-663-3 (1-2501)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
DB 1164 TTACAGAGTGTTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTCTG 1223

QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1224 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1283

QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
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QY 66 SerAspGlyAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
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QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
DB 1404 TGGGATAGCACCATTCTGGTTCTCAAGGGCTGCATTCTGTGATCACAAGACCCTCCA 1463

QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
DB 1464 TGCTCTTCAGCAATAATAATCACTCACTCACTGAGGAACTCAGAACGCTCTGCAGCCT 1523

QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
DB 1524 GGTATAGCCACAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATGACAGAA 1583

QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
DB 1584 GCCTGCCTTAACCACTCGCTAGATGCCCTTCTGTCAGGAGCTTGTATCATGAAGAGGAC 1643

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185

Db 1644 TATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 1703  
Qy 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
Db 1704 ACTGACATCCAGGAGGAAGATTGCGCAAGTTATAGTACAAATAATGGAAGATAACAAA 1763  
Qy 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1764 CAAATGGGTCTTCAGCCTTACCGGAAATACCTTGTTCTAGATCACCATCTTTAAT 1823  
Qy 226 LeuLeuGlnAsnLysSerMet 232  
Db 1824 TTACTTCAAAATAAAAGCATG 1844  
RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-2  
Alignment Scores:  
Pred. No.: 2,61e-231 Length: 2502  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.84% Indels: 0  
DB: 4 Gaps: 0  
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Qy 6 LeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
Db 1165 TTACAGAGTGTTCAGAGTGCCTTACCTATGTGACAAAGAAATGGAAATATCTCTG 1224  
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
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Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1285 AATAGTGGTTCCTCGTAAACTTCAAGTCCCTCAGCTCCTCTCAAGCAATGATTTTAA 1344  
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisLysCysProGlyAsnHisSer 85  
Db 1345 TCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCTACTGTCTCTGGAATCAGT 1404  
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrPro 105  
Db 1405 TGGGATAGCACCATTCTGGTTCTCAAGGGCTGCTTCTGTGATCAAGAGCCTCCA 1464  
Qy 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlnSerGluArgLeuGlnPro 125  
Db 1465 TGCTCTTCAGCAATAATAATCCACTCTCACTCGAGGAACCTCAGAACTGTCGACCT 1524  
Qy 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
Db 1525 GGTATAGCCCGAGCTGATCCAGGCAAAAGGAGGAGACATTGTGACCAATGACAGAA 1584

Qy 146 AlaCysLysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
Db 1585 GCCTGCTTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGGAC 1644  
Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
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Db 1705 ACTGACATCCAGGAGGAAGATTGCGCAAGTTATAGTACAAATAATGGAAGATAACAAA 1764  
Qy 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1765 CAAATGGGTCTTCAGCCTTACCGGAAATACCTTGTTCTAGATCACCATCTTTAAT 1824  
Qy 226 LeuLeuGlnAsnLysSerMet 232  
Db 1825 TTACTTCAAAATAAAAGCATG 1845  
RESULT 3  
US-09-023-655-684  
; Sequence 684, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 684:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1060 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: MPHGN0703  
; CLONE: 445186  
US-09-023-655-684  
Alignment Scores:  
Pred. No.: 4.57e-187 Length: 1060  
Score: 185.00 Matches: 226  
Percent Similarity: 98.69% Conservative: 0

Best Local Similarity: 98.69% Mismatches: 1  
Query Match: 79.74% Indels: 3  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-023-655-684 (1-1060)

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QY	26	AniLeProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
416	AACTACCTGT	AAATCATGGTCCCAAGAGGATCATGTGATCTCTCAGCTCCATGAA	475
QY	46	AsnSer--GlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheL	65
476	AATAG-GTG	GTTCCTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT	534
QY	65	eusSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	85
535	TATCTAGAAAGCT	CAAGACTGTTATTTATGAAGCTGCATCACTGTCTTGGAAATCACA	594
QY	85	eTrtAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrP	105
595	GTGGATAGC	ACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAAGCCACTC	654
QY	105	roCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnP	125
655	CATGCTTTCAGCA	TATATAATCACTCTCACTGAGGAACTCAGACGCTCTGCAGC	714
QY	125	roGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG	145
715	CTGTATAGCC	CAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAG	774
QY	145	luAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGluA	165
775	AGCCCTGCCTT	AACAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAGG	834
QY	165	spTyrgLluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspT	185
835	ACTATGAACTT	GTAGTACCAAGCTCAGAGCTCAAAAGTCAGACATTAATAGACA	894
QY	185	hTrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnL	205
895	CTACTGACAT	CCAAGAGAAATTTGCCAAAGTTATAGTACAAAAATGGAAGATAACA	954
QY	205	ysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuA	225
955	AACAAATGGGT	CTCAGCCTTACCCGGAATACCTTGTGTTTCTAGATCACCATCTTTAA	1014
QY	225	snLeuLeuGlnAsnLysSerMet	232
1015	ATTACTTCAAA	TATAAAGCATG	1037

RESULT 4  
US-09-099-041A-3  
; Sequence 3, Application US/0909041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-099-041A-3  
Alignment Scores:  
Pred. No.: 2,35e-126 Length: 1620  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-099-041A-3 (1-1620)

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QY	26	AniLeProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
1000	AACTACCTGT	AAATCATGGTCCCAAGAGGATCATGTGATCTCTCAGCTCCATGAA	1059
QY	46	AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
1060	AATAGTGTTC	CTCCTGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT	1119
QY	66	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	85
1120	TCTAGAAAGCT	CAAGACTGTTATTTATGAAGCTGCATCACTGTCTTGGAAATCACAGT	1179
QY	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrP	105
1180	TGGATAGC	ACCATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAAGCCAT-TCC	1238
QY	105	oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnP	125
1239	ATGCTTTCAGCA	TATATAATCACTCTCACTGAGGAACTCAGACGCTCTGCAGCC	1298
QY	125	oGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG	145
1299	TGGTATAGCC	CAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACAGA	1358
QY	145	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGluAs	165
1359	AGCCCTGCCTT	AACAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAGGA	1418
QY	165	pTyrgLluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh	185
1419	CTATGAACTT	GTAGTACCAAGCTCAGAGCTCAAAAGTCAGACATTAATAGACAC	1478
QY	185	rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsnL	205
1479	TACTGACAT	CCAAGAGAAATTTGCCAAAGTTATAGTACAAAAATGGAAGATAACA	1538
QY	205	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225
1539	ACAAATGGGT	CTTACCCGGAATACCTTGTGTTTCTAGATCACCATCTTTAA	1598
QY	225	nLeuLeuGlnAsnLysSerMet	232
1599	TTTACTTCAAA	TATAAAGCATG	1620

RESULT 5  
US-09-245-281-3  
; Sequence 3, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08



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Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 7
US-09-340-620A-3
; Sequence 3, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-340-620A-3

Alignment Scores:
Pred. No.: 2,35e-126 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-340-620A-3 (1-1620)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLeuMetGluLeuSerLeu 25
Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 999
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlySerSerGlnLeuHisGlu 45
Db 1000 AACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1059
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTTATA 1119
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGGAATCACAGT 1179
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105
Db 1180 TGGGATAGCACCATTCTCGAATCTCAAGGGCTGATCTTGATCACAAGACCAT-TCC 1238
Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db 1239 ATGCTCTTCAGCAATAATAATCACTCTCACTGCAGGAACCTCAGAACGTCGCGCC 1298
Qy 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db 1299 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTCAACCAATGACAGA 1358
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1359 AGCCTGCCTTAACAGTCGCTAGATGCCCTCTGTCCAGGGACTTGATCATGAAAGAGA 1418
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Qy 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1419 CTATGAACCTTGTGTAGTACCAAGCCTCAAGAGACCTCAAAAGCTCAGACAATTTACTAGACAC 1478
Qy 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
Db 1479 TACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAA 1538
Qy 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db 1539 ACAAATGGTCTTCAGCCTTACCCGGAATACTTTGTGGTTCTAGATCACCATCTTTAA 1598
Qy 225 nLeuLeuGlnAsnLysSerMet 232
Db 1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 8
US-09-865-364-3
; Sequence 3, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-865-364-3

Alignment Scores:
Pred. No.: 2,35e-126 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-865-364-3 (1-1620)

Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLeuMetGluLeuSerLeu 25
Db 940 TTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTATCTCTG 999
Qy 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlySerSerGlnLeuHisGlu 45
Db 1000 AACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1059
Qy 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1060 AATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGGAATTTTATA 1119
Qy 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db 1120 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGGAATCACAGT 1179
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105
Db 1180 TGGGATAGCACCATTCTCGAATCTCAAGGGCTGATCTTGATCACAAGACCAT-TCC 1238
Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
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Db 1239 ATGCTCTTCAGCAATAATAATCACTCACTCACTGACAGGAACTCAGAACGCTTCGAGCC 1298  
Qy 125 oGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
Db 1299 TGGTATAGCCACGAGTGGATCCAGACAAAGGGAAGACATTTGTGAACCAATGACAGA 1358  
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
Db 1359 AGCTGCTTTAAACAGTCGCTAGATGCTTCTGTCCAGGAGCTTGTATCATGAAGAGGA 1418  
Qy 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
Db 1419 CTATGAACCTTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAAGACAAATTTACTAGCAC 1478  
Qy 185 rThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspLeuLy 205  
Db 1479 TACTGACATCCAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1538  
Qy 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValValSerArgSerProSerLeuAs 225  
Db 1539 ACAAAATGGGTCTTCAGGCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTAAA 1598  
Qy 225 nLeuLeuGlnAsnLysSerMet 232  
Db 1599 TTTACTTCAAAATAAAAGCATG 1620  
RESULT 9  
US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-09-019-942-2  
Alignment Scores: 2,78e-126 Length: 1931  
Pred. No.: 128.00 Matches: 226  
Score:

Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 3 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)  
Qy 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
Db 1153 TTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAAATGGAATTTATCTCTG 1212  
Qy 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
Db 1213 AACATACCTGTAAATCATGTCACCAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
Qy 46 AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1273 AATAGTGGTTCCTCGAACTTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTTAA 1332  
Qy 66 SerArgLysAlaGlnAspCysTyrgluMetLysLeuHisHisCysProGlyAsnHisSer 85  
Db 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGTCTGGAATCACAGT 1392  
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr-Pr 105  
Db 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAATTCCTGTGATCACAAGACCAT-TCC 1451  
Qy 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
Db 1452 ATGCTCTTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGACCTGTGAGCC 1511  
Qy 125 oGlylleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
Db 1512 TGGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGA 1571  
Qy 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
Db 1572 AGCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGAGGA 1631  
Qy 165 pTyrgluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
Db 1632 CTATGAACCTTGTAGTACCAAGCTCAAGACCTCAAAAGTCAGACAAATTTACTAGCAC 1691  
Qy 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspLeuLy 205  
Db 1692 TACTGACATCCAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAA 1751  
Qy 205 sGlnMetGlyLeuGlnProTyrgluIleLeuValValSerArgSerProSerLeuAs 225  
Db 1752 ACAAAATGGGTCTTCAGCCTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811  
Qy 225 nLeuLeuGlnAsnLysSerMet 232  
Db 1812 TTTACTTCAAAATAAAAGCATG 1833  
RESULT 10  
US-09-099-041A-1  
; Sequence 1, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA



; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)....(1833)  
US-09-099-041A-1

## Alignment Scores:

Pred. No.: 2,78e-126 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-099-041A-1 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
DB 1153 TTACAGAGTGTTCAGTGCCCAATTCACCTATGTGCAAGAGAAATGGAATTTATCTCTG 1212  
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGAATACACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
DB 1393 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTCTGATCACAAAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
DB 1452 ATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAAAGCTTCGAGCC 1511  
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
DB 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571  
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAs 165  
DB 1572 AGCCTGCCTTACCACTGCTAGATGCCCTTCTGTCCAGGACTGATCATGAAAGAGGA 1631  
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
DB 1632 CTATGAACCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691  
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
DB 1692 TACTGACATCCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACA 1751  
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
DB 1752 ACAATGGGTCTTCAGCCCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCTTTAA 1811  
QY 225 nLeuLeuGlnAsnLysSerMet 232  
DB 1812 TTATCTTCAAAATAAAGCATG 1833

## RESULT 11

US-09-245-281-1  
; Sequence 1, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/118001

; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)....(1833)  
US-09-245-281-1

## Alignment Scores:

Pred. No.: 2,78e-126 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservative: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-245-281-1 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
DB 1153 TTACAGAGTGTTCAGTGCCCAATTCACCTATGTGCAAGAGAAATGGAATTTATCTCTG 1212  
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
DB 1213 AACATACCTGTAAATCATGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
DB 1273 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332  
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
DB 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGAATACACAGT 1392  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
DB 1393 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTCTGATCACAAAGACCAT-TCC 1451  
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
DB 1452 ATGCTCTTCAGCAATAATAATCAACTCTCAACTGCAGGAACTCAGAAAGCTTCGAGCC 1511  
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
DB 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571  
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAs 165  
DB 1572 AGCCTGCCTTACCACTGCTAGATGCCCTTCTGTCCAGGACTGATCATGAAAGAGGA 1631  
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
DB 1632 CTATGAACCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691  
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
DB 1692 TACTGACATCCCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACA 1751  
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225  
DB 1752 ACAATGGGTCTTCAGCCCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCTTTAA 1811

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QY 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 12
US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Alignment Scores:
Pred. No.: 2,78e-126 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-470-271-2 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 1153 TTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCTCTG 1212

QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1213 AACATACCTGTAAATCATGTGTCCACAGAGAAATCATGTGCATCTCTAGCTCCATGAA 1272

QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1273 AATAGTGGTCTCTGTAAGCTTCAAGGTCCCTGACAGTCCCTCAAGACAATGATTTTAA 1332

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1333 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATACAGT 1392
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QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105
Db 1393 TGGGATAGCACCATTCTGGAICTCAAGGGCTGCATTCTGTGATCACAAGACCAT-TCC 1451

QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db 1452 ATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTCTGCAGCC 1511

QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATATGACAGA 1571

QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db 1572 AGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGGA 1631

QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db 1632 CTATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTTACTAGAC 1691

QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
Db 1692 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATACAA 1751

QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225
Db 1752 ACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAA 1811

QY 225 nLeuLeuGlnAsnLysSerMet 232
Db 1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 13
US-09-207-359B-1
; Sequence 1, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-207-359B-1

Alignment Scores:
Pred. No.: 2,78e-126 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-207-359B-1 (1-1931)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db 1153 TTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCTCTG 1212

QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 1213 AACATACCTGTAAATCATGTGTCCACAGAGAAATCATGTGCATCTCTAGCTCCATGAA 1272

QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 1273 AATAGTGGTCTCTGTAAGCTTCAAGGTCCCTGACAGTCCCTCAAGACAATGATTTTAA 1332

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db 1333 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATACAGT 1392
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QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1213 AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1273 AATAGTGGTCTCTCGAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAAATGATTTTAA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 Db 1393 TGGGATAGCACCATTTCTGAACTTCAAGGGCTGCATCTCTGATCACAAGACCAT-TCC 1451  
 QY 105 OCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1452 ATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTTCTGAGCC 1511  
 QY 125 OGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1572 AGCCTGCCTTAAACCAAGTCGTAGTCCCTTCTGCTCCAGGAGCTTGCATCATGAAAGAGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1632 CTATGAACCTTGTAGTACCAAGCTTACAAAGGACCTCAAAAGTCAGACAAATTTACTAGACAC 1691  
 QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205  
 Db 1692 TACTGACATCCCAAGAGAAATTTGCCAAAGCTTATAGTACAAAATTTGAAAGATAACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAs 225  
 Db 1752 ACAATGGGTCTTACGCTTACCGGAAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1812 TTTACTTCAAAATAAAGCATG 1833  
 RESULT 14  
 ; US-09-340-620A-1  
 ; Sequence 1, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/340,620A  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)...(1833)  
 ; US-09-340-620A-1

Alignment Scores:  
 Pred. No.: 2,786-126 Length: 1931  
 Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservative: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 4 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-09-340-620A-1 (1-1931)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysValLysMetGluLeuSerLeu 25  
 Db 1153 TTACAGAGTGTTCAGTGCCTTCCATTCATGTGCAAGAAGAAATGGAATTAATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1213 AACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1273 AATAGTGGTCTCTCGAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAAATGATTTTAA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 Db 1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGAAATCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105  
 Db 1393 TGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATCTCTGTGATCACAAGACCAT-TCC 1451  
 QY 105 OCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1452 ATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTTCTGAGCC 1511  
 QY 125 OGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145  
 Db 1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1572 AGCCTGCCTTAAACCAAGTCGTAGTCCCTTCTGCTCCAGGAGCTTGCATCATGAAAGAGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1632 CTATGAACCTTGTAGTACCAAGCTTACAAAGGACCTCAAAAGTCAGACAAATTTACTAGACAC 1691  
 QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205  
 Db 1692 TACTGACATCCCAAGAGAAATTTGCCAAAGCTTATAGTACAAAATTTGAAAGATAACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProTyProGluIleLeuValSerArgSerProSerLeuAs 225  
 Db 1752 ACAATGGGTCTTACGCTTACCGGAAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1812 TTTACTTCAAAATAAAGCATG 1833  
 RESULT 15  
 ; US-09-865-364-1  
 ; Sequence 1, Application US/09865364  
 ; Patent No. 6613521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/865,364  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17

Job time : 116 secs

;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (214)...(1833)  
US-09-865-364-1

Alignment Scores:  
Pred. No.: 2,78e-126 Length: 1931  
Score: 128.00 Matches: 226  
Percent Similarity: 99.12% Conservatives: 0  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 55.17% Indels: 2  
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-865-364-1 (1-1931)

Qy	6	LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu	25
Db	1153	TTACAGAGTCTTTCAAGTGCATTACCTATGTGACAAAGAGAAATGGAATTATCTCTG	1212
Qy	26	AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu	45
Db	1213	AACATCCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCATGAA	1272
Qy	46	AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu	65
Db	1273	AATAGTGGTCTCTCGAACTTCAAGCTCCCTGCCAGCTCCTCAAGACAATGATTTTAA	1332
Qy	66	SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer	85
Db	1333	TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGAAATCACAGT	1392
Qy	86	TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	105
Db	1393	TGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTATCACAAGACCAT-TCC	1451
Qy	105	OCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr	125
Db	1452	ATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGCTCGCAGCC	1511
Qy	125	oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl	145
Db	1512	TGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAACCAATGACAGA	1571
Qy	145	uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs	165
Db	1572	AGCTGCCTTACAGTCGGTAGTGCCTTCTGTCCAGGACTTGATCATGAAGAGGA	1631
Qy	165	pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuAspThr	185
Db	1632	CTATGAACCTGTTAGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAAATTACTAGACAC	1691
Qy	185	rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy	205
Db	1692	TACTGACATCCAAGGAGAAGAAATTGGCCAAAGTTATAGTACAAAATTGAAAGATACAA	1751
Qy	205	sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs	225
Db	1752	ACAAATGGGTCTTCAGGCTTACCCGGAATACTTGTGGTTCTTAGATCACCACTTTTAA	1811
Qy	225	nLeuLeuGlnAsnLysSerMet	232
Db	1812	TTTACTTCAAAATAAAAGCATG	1833

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:50:59 ; Search time 417 Seconds  
(without alignments)  
2080.611 Million cell updates/sec

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Perfect score: 232  
Sequence: 1 MYSLOQSVSSAIHLCDKKK.....PEILVVSRSPLNLQKSM 232

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 2465228 seqs, 1869859620 residues

Word size: 20

Total number of hits satisfying chosen parameters: 15

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLAB=200 -THR SCORE=quality -THR MIN=20  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:
- 2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:
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- 9: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:
- 10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:
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- 18: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	232	100.0	1669	9	US-09-771-161A-2	Sequence 2, Appli
2	227	97.8	1623	12	US-10-342-887-957	Sequence 957, App
3	227	97.8	2501	10	US-09-981-397A-13	Sequence 13, Appl
4	227	97.8	2709	9	US-09-925-301-173	Sequence 173, Appl
5	128	55.2	1620	9	US-09-728-721-3	Sequence 3, Appli
6	128	55.2	1620	13	US-10-105-931-3	Sequence 3, Appli
7	128	55.2	1620	13	US-10-118-984-3	Sequence 3, Appli
8	128	55.2	1620	14	US-10-235-981-3	Sequence 3, Appli
9	128	55.2	1931	9	US-09-748-537-2	Sequence 2, Appli
10	128	55.2	1931	9	US-09-728-721-1	Sequence 1, Appli
11	128	55.2	1931	13	US-10-133-780-2	Sequence 2, Appli
12	128	55.2	1931	13	US-10-105-931-1	Sequence 1, Appli
13	128	55.2	1931	13	US-10-118-984-1	Sequence 1, Appli
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15	120	51.7	491	10	US-09-918-995-20565	Sequence 20565, A

ALIGNMENTS

RESULT 1  
US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

Alignment Scores:  
Pred. No.: 8.03e-227 Length: 1669  
Score: 232.00 Matches: 232  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-771-161A-2 (1-1669)

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DB	320	ATGTATTTCATTACAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAA	379
QY	21	MetGluLeuSerLeuAsnIleProValAnHisGlyProGlnGluSerCysGlySer	40
DB	380	ATGGAATTATCTCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGGATCC	439
QY	41	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln	60
DB	440	TCTCAGCTCCATGAAATAGTGGTTCTCTCTGAAACTCAAGGTCCCTCCAGCTCTCAA	499
QY	61	AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCys	80
DB	500	GACAAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGT	559

QY 81 ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp 100  
Db 560 CTTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGGAT 619  
QY 101 HisIysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSer 120  
Db 620 CACAAGACCACTCCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAAATCA 679  
QY 121 GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleVal 140  
Db 680 GAAGCTGTGAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATGTG 739  
QY 141 AsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeu 160  
Db 740 AACCAATGACAGAGCTGCCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTG 799  
QY 161 IleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArg 180  
Db 800 ATCATGAAGAGGACTATGAATGTTAGTACCAAGCCTACAAAGGACCTCAAAAGTCAGA 859  
QY 181 GlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 200  
Db 860 CAATTACTAGACACTACTGATCCAGAGGAGAAATTTGCCAAAGTTATAGTACAAAA 919  
QY 201 LeuLysAspHisGlnMetGlyLeuGlnProTyrProGluLeuValValSerArg 220  
Db 920 TTCAAGATACAAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGA 979  
QY 221 SerProSerLeuAsnLeuGlnAsnLysSerMet 232  
Db 980 TCACCATCTTTAAATTTACTTCAAAATAAAAGCATG 1015

## RESULT 2

US-10-342-887-957  
; Sequence 957, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yungue  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna  
; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 957  
; LENGTH: 1623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-957

## Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.84%	Indels:	0
DB:	12	Gaps:	0

US-09-771-161A-93 (1-232) x US-10-342-887-957 (1-1623)

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Db 940 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAAAATGGAATTTATCTCTG 999  
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45  
Db 1000 ACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 1059  
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
Db 1060 AATAGTGGTTCCTCTCAAACTTCAAGTCCCTGCGAGCTCCTCAAGACAATGATTTTTTA 1119  
QY 66 SerArgGlyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
Db 1120 TCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTGTCTCTGGAATCAAGT 1179  
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
Db 1180 TGGGACAGACCACTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCCTCCA 1239  
QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
Db 1240 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTGCGAGCCT 1299  
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
Db 1300 GGTATAGCCAGCAGTGGATCCAGACAAAAGGGAAGACATTGTGAACCAAAATGACAGAA 1359  
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
Db 1360 GCCTGCTTAAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAAGGAC 1419  
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
Db 1420 TATGAACCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAGACAAATTACTAGACACT 1479  
QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsnLys 205  
Db 1480 ACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1539  
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn 225  
Db 1540 CAAATGGGTCTTCAGCCTTACCCGGAATAACTTGTGTTTCTAGATCACCATCTTTAAT 1599  
QY 226 LeuLeuGlnAsnLysSerMet 232  
Db 1600 TTACTTTCAAAATAAAAGCATG 1620

## RESULT 3

US-09-981-397A-13  
; Sequence 13, Application US/09981397A  
; Publication No. US20030082519A1  
; GENERAL INFORMATION:  
; APPLICANT: Axxima Pharmaceuticals AG  
; APPLICANT: Schubart, Daniel  
; APPLICANT: Habenberger, Peter  
; APPLICANT: Stein-Gerlach, Matthias  
; APPLICANT: Bevec, Dorian  
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
; TITLE OF INVENTION: Inhibition  
; FILE REFERENCE: AXM-004.1 US  
; CURRENT APPLICATION NUMBER: US/09/981,397A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/240,750  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-397A-13

Alignment Scores:

```
Pred. No.: 1.47e-221 Length: 2501
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-981-397A-13 (1-2501)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
DB 1164 TTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGAATATCTCTG 1223
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1224 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1283
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1284 AATAGTGGTTCCTCGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAATGATTTTGA 1343
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysAspProGlyAsnHisSer 85
DB 1344 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTGGAATCACAGT 1403
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 105
DB 1404 TGGGATAGCACCATTTCTGGTTCTCAAGGGCTGCATTCGTGATCACAAGACCCTCCA 1463
QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
DB 1464 TGTCTTTCAGCAATTAATAATCACTCTCACTGAGGAACTCAGAGAGCTCTGAGGCT 1523
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
DB 1524 GGTATAGCCACAGCTGGATCCAGAGCAAAAGGAGACATTTGTGAACAATGACAGNA 1583
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
DB 1584 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAGAGGAC 1643
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
DB 1644 TATGAACCTTGTATGACCAAGCTCAAGGAGCTCAAGAGCTCAAAAGTCAGACAAATTA 1703
QY 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
DB 1704 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAA 1763
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
DB 1764 CAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTTAGATCACCATCTTTAA 1823
QY 226 LeuLeuGlnAsnLysSerMet 232
DB 1824 TTACTTCAAAATAAAGCATG 1844

RESULT 4
US-09-925-301-173
; Sequence 173, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 173
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2622)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2659)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2670)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-301-173

Alignment Scores:
Pred. No.: 1.58e-221 Length: 2709
Score: 227.00 Matches: 227
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.84% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-925-301-173 (1-2709)

QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
DB 1206 TTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGAATATCTCTG 1265
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1266 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1325
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1326 AATAGTGGTTCCTCGAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTTTGA 1385
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysAspProGlyAsnHisSer 85
DB 1386 TCTAGAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTGGAATCACAGT 1445
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrPro 105
DB 1446 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAAGACCCTCCA 1505
QY 106 CysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
DB 1506 TGTCTTTCAGCAATTAATAATCACTCTCACTGAGGAACTCAGAGCTCTGAGGCT 1565
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
DB 1566 GGTATAGCCACAGCTGGATCCAGAGCAAAAGGAGACATTTGTGAACAATGACAGNA 1625
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
DB 1626 GCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAGAGGAC 1685
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
DB 1686 TATGAACCTTGTATGACCAAGCTCAAGGAGCTCAAAAGTCAGACAAATTACTAGACACT 1745
QY 186 ThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
DB 1746 ACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATACAAA 1805
QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225
DB 1806 CAAATGGGTCTTCAGCCTTACCCTGGAATATCTGTGGTTCTTAGATCACCATCTTTAA 1865
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Db      1299 TGGTATAGCCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGA 1358
Qy      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db      1359 AGCCTGCCTTACCAGTCGCTAGATGCCCTCTGTCCAGGAGCTTCATCATGAAGAGGA 1418
Qy      165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db      1419 CTATGAACCTTGTAGTACCAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1478
Qy      185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsnLys 205
Db      1479 TACTGACATCCAAAGGAGAAGATTTCGCAAGATTATAGTACAAAATTGAAAGATAACAA 1538
Qy      205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db      1539 ACAATGGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1598
Qy      225 nLeuLeuGlnAsnLysSerMet 232
Db      1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 7
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3

Alignment Scores:
Pred. No.: 1,07e-120 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-118-984-3 (1-1620)

Qy      6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db      940 TTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTCTG 999
Qy      26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db      1000 AACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGTCCATGAA 1059
Qy      46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      1060 AATAGTGGTTCCTCGAAATCTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTTAA 1119
Qy      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85

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Db      1120 TCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCACTGCTCTCGAANAATCACAGT 1179
Qy      86 TrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr-Pr 105
Db      1180 TGGGATAGACCAATTTCTGGATCTCAAAAGGGCTGCATCTCTGTGATCACAAGACCAT-TCC 1238
Qy      105 cCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db      1239 ATGCTCTTTCAGCAATAATAATCCACTCTCAACTCAGGAAACTCAGAACGCTCTGCAGCC 1298
Qy      125 cGlyIleAlaGlnGlnTPIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db      1299 TGGTATAGCCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGA 1358
Qy      145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
Db      1359 AGCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAGAGGA 1418
Qy      165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db      1419 CTATGAACCTTGTAGTACCAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1478
Qy      185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsnLys 205
Db      1479 TACTGACATCCAAAGGAGAAGATTTCGCAAGATTATAGTACAAAATTGAAAGATAACAA 1538
Qy      205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db      1539 ACAATGGGTCTTCAGCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAA 1598
Qy      225 nLeuLeuGlnAsnLysSerMet 232
Db      1599 TTTACTTCAAAATAAAAGCATG 1620

RESULT 8
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3

Alignment Scores:
Pred. No.: 1,07e-120 Length: 1620
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-295-981-3 (1-1620)

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QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 940 TTACAGAGTGTTCACAGTCCATTACCTATGTGACAGAGAAATGGAAATATCTCTG 999  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1000 AACATACCTGTAATCATGTGTCCACAAGAGGAATCATGTGATCCTCTCAGCTCCATGAA 1059  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProGlnAspAsnAspPheLeu 65  
 Db 1060 AATAGTGGTTCCTCTGAACTTCAAGGTCCCTGCCAGTCTCTCAAGCAATGATTTTAA 1119  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 Db 1120 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCCTCTCTGGAATCACAGT 1179  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105  
 Db 1180 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGACCAT-TCC 1238  
 QY 105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1239 ATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTCTGCAGCC 1298  
 QY 125 oGlyIleAlaGlnIleTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 Db 1299 TGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGACAGA 1358  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1359 AGCCTGCTTTAAACAGTTCGTAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAGGA 1418  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1419 CTATGAACCTTGTATGACCAAGCTTCAAGAGCTCAAGAGCTCAAGAGTACAGCAATTTACTAGACAC 1478  
 QY 185 rThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 Db 1479 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 1538  
 QY 205 sGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAs 225  
 Db 1539 ACAAAATGGGTCTTCAGCCTTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1598  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1599 TTTACTTCAAAATAAAGCATG 1620  
 RESULT 9  
 US-09-748-537-2  
 ; Sequence 2, Application US/09748537  
 ; Patent No. US20020061833A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-748-537-2  
 Alignment Scores:  
 Pred. No.: 1.25e-120 Length: 1931

Score: 128.00 Matches: 226  
 Percent Similarity: 99.12% Conservativity: 0  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 55.17% Indels: 2  
 DB: 9 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)  
 QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25  
 Db 1153 TTACAGAGTGTTCACAGTCCATTACCTATGTGACAGAGAAATGGAAATATCTCTG 1212  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 Db 1213 AACATACCTGTAATCATGTGTCCACAAGAGGAATCATGTGATCCTCTCAGCTCCATGAA 1272  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 Db 1273 AATAGTGGTTCCTCTGAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTTTAA 1332  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 Db 1333 TCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCCTCTCTGGAATCACAGT 1392  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr-Pr 105  
 Db 1393 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGACCAT-TCC 1451  
 QY 105 oCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125  
 Db 1452 ATGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTCTGCAGCC 1511  
 QY 125 oGlyIleAlaGlnIleTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrG1 145  
 Db 1512 TGGTATAGCCACAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGACAGA 1571  
 QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165  
 Db 1572 AGCCTGCTTTAAACAGTTCGTAGTGCCTTCTGTCCAGGACTTGTATCATGAAGAGGA 1631  
 QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185  
 Db 1632 CTATGAACCTTGTATGACCAAGCTTCAAGAGCTTCAAGAGCTCAAGAGTACAGCAATTTACTAGACAC 1691  
 QY 185 rThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205  
 Db 1692 TACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAACAA 1751  
 QY 205 sGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeuAs 225  
 Db 1752 ACAAAATGGGTCTTCAGCCTTTACCGGAAATACTTGTGGTTTCTAGATCACCATCTTTAAA 1811  
 QY 225 nLeuLeuGlnAsnLysSerMet 232  
 Db 1812 TTTACTTCAAAATAAAGCATG 1833  
 RESULT 10  
 US-09-728-721-1  
 ; Sequence 1, Application US/09728721  
 ; Patent No. US20020061845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/728,721  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 09/340,620  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942

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; PRIORITY FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-728-721-1

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTCCCAATCACCATTGTGACAGAGAAATGAATATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1213 AACATACCTGTAATCAATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACTGTATTATTAAGAGCTGCATCACTGTCTGGAATACACAGT 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
DB 1393 TGGGATAGCACCATTTCTGATCTCAAGGGCTGCATCTGTGATCACAAGACCAT-TCC 1451
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCAGCC 1511
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
DB 1572 AGCCTGGCTTACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGGA 1631
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValaGlnLeuLeuAspThr 185
DB 1632 CTATGAACCTGTGTAGTACCAGCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
DB 1692 TACTGACATCCCAAGGAGAGAATTGGCCAAAGTTATAGTACAAAATTTAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225
DB 1752 ACAATGGGTCTTCAGCCTTACCGGAATATCTTGGTTCCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
DB 1812 TTACTTCAAAATAAAGCATG 1833

RESULT 11
US-10-133-780-2
; Sequence 2, Application US/10133780
```

```
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meikiejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-133-780-2

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-133-780-2 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTCCCAATCACCATTGTGACAGAGAAATGAATATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1213 AACATACCTGTAATCAATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACTGTATTATTAAGAGCTGCATCACTGTCTGGAATACACAGT 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
DB 1393 TGGGATAGCACCATTTCTGATCTCAAGGGCTGCATCTGTGATCACAAGACCAT-TCC 1451
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB 1452 ATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCCTGCAGCC 1511
QY 125 oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAs 165
DB 1572 AGCCTGGCTTACCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGGA 1631
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValaGlnLeuLeuAspThr 185
DB 1632 CTATGAACCTGTGTAGTACCAGCTACAAGGACCTCAAAAGTCAGACAATTACTAGACAC 1691
QY 185 rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnly 205
DB 1692 TACTGACATCCCAAGGAGAGAATTGGCCAAAGTTATAGTACAAAATTTAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAs 225
DB 1752 ACAATGGGTCTTCAGCCTTACCGGAATATCTTGGTTCCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
DB 1812 TTACTTCAAAATAAAGCATG 1833

RESULT 11
US-10-133-780-2
; Sequence 2, Application US/10133780
```

```

Db      1452 ATGCTCTTTCAGCAATTAATTAATCCATCTCACTGAGGAACTCAGAACGCTGCAGCC 1511
QY      125  oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db      1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGA 1571
QY      145  uAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAs 165
Db      1572 AGCCTGCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGA 1631
QY      165  pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db      1632 CTATGAACTTTAGTACCAAGCTCACAAGACCTCAAAAGTCAGACAATTTACTAGACAC 1691
QY      185  rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
Db      1692 TACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAA 1751
QY      205  sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db      1752 ACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811
QY      225  nLeuLeuGlnAsnLysSerMet 232
Db      1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 12
US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 05/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-105-931-1 (1-1931)

QY      6  LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeu 25
Db      1153 TTACAGATGTTTCAAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTCTG 1212
QY      26  AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db      1213 AACATACCTGTAATCATGGTCCACAGAGAAATCATGTGGATCCTCTCAGCTCCATGAA 1272
QY      46  AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPheLeu 65

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Db      1273 AATAGTGGTTCTCTGAAACCTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 1332
QY      66  SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db      1333 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCACAGT 1392
QY      86  TrpAspSerThrIleSerGlySerGlnArgAlaLalaPheCysAspHisLysThrThr-Pr 105
Db      1393 TGGGATAGCACCATTTCTGGATCTCAAAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451
QY      105  cCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
Db      1452 ATGCTCTTTCAGCAATTAATTAATCCATCTCAACTCCAGGAACTCAGAACGCTGCAGCC 1511
QY      125  oGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGl 145
Db      1512 TGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGA 1571
QY      145  uAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAs 165
Db      1572 AGCCTGCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAGA 1631
QY      165  pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
Db      1632 CTATGAACTTTAGTACCAAGCTCACAAGACCTCAAAAGTCAGACAATTTACTAGACAC 1691
QY      185  rThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205
Db      1692 TACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAA 1751
QY      205  sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
Db      1752 ACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTTAA 1811
QY      225  nLeuLeuGlnAsnLysSerMet 232
Db      1812 TTTACTTCAAAATAAAAGCATG 1833

RESULT 13
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Alignment Scores:
Pred. No.: 1.25e-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1

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Query Match: 55.17% Indels: 2
DB: 13 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-118-984-1 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGAATTAATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1213 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTCTCCTGAAATCTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCAAGACAATGATTTTAA 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
DB 1393 TGGGATAGCACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB 1452 ATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1511
QY 125 oGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCGAGCTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuLeuMetLysGluAs 165
DB 1572 AGCCTGCCTTAACCAAGTACAGTGCCTTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1631
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
DB 1632 CTATGAACCTTGTATGACCAAGCTTACAGGACCTCAAGAGCTGTGAACCAATGACACA 1691
QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
DB 1692 TACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
DB 1752 ACAATGGTCTTCAGCTTACCGGAATACTTGTGGTTTCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
DB 1812 TTTACTTCAAAATAAAGCATG 1833
RESULT 14
US-10-295-981-1
; Sequence 1, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-295-981-1
Alignment Scores:
Pred. No.: 1,258-120 Length: 1931
Score: 128.00 Matches: 226
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 55.17% Indels: 2
DB: 14 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-295-981-1 (1-1931)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
DB 1153 TTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGAATTAATCTCTG 1212
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
DB 1213 AACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 1272
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
DB 1273 AATAGTGGTCTCCTGAAATCTCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTTAA 1332
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
DB 1333 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCAAGACAATGATTTTAA 1392
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPr 105
DB 1393 TGGGATAGCACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT-TCC 1451
QY 105 oCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPr 125
DB 1452 ATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1511
QY 125 oGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThrCl 145
DB 1512 TGGTATAGCCCGAGCTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGACAGA 1571
QY 145 uAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuLeuMetLysGluAs 165
DB 1572 AGCCTGCCTTAACCAAGTACAGTGCCTTCTCAACTGCAGGAACTCAGAAGCTCTGCAGCC 1631
QY 165 pTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspTh 185
DB 1632 CTATGAACCTTGTATGACCAAGCTTACAGGACCTCAAGAGCTGTGAACCAATGACACA 1691
QY 185 rThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsnLy 205
DB 1692 TACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAA 1751
QY 205 sGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAs 225
DB 1752 ACAATGGTCTTCAGCTTACCGGAATACTTGTGGTTTCTAGATCACCATCTTTAA 1811
QY 225 nLeuLeuGlnAsnLysSerMet 232
DB 1812 TTTACTTCAAAATAAAGCATG 1833
RESULT 15
US-09-918-995-20565
; Sequence 20565, Application US/09918995
; Publication No. US20030073623A1
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Thu Apr 1 15:53:02 2004

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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20565
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-20565

Alignment Scores:
Pred. No.:      5.24e-113      Length:      491
Score:          120.00         Matches:    120
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:      51.72%        Indels:     0
DB:               10           Gaps:       0

US-09-771-161A-93 (1-232) x US-09-918-995-20565 (1-491)

Qy      6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db      131 TTACAGAGTGTTCACAGTGCCTATTCACCTATGTGACAAAGAGAAATGGAATTTATCTCTG 190

Qy      26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db      191 AACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 250

Qy      46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db      251 AATAGTGTTCCTCGAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTAA 310

Qy      66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85
Db      311 TCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGTCTCTGGAAATCACAGT 370

Qy      86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105
Db      371 TGGGATAGACCACTTTCTGGATCTCAAAGGCTGCATTTCTGTGATCAAGACCACTCCA 430

Qy      106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
Db      431 TGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAAACTCAGAACGTCGTGAGCCT 490

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Search completed: April 1, 2004, 14:59:43  
Job time : 426 secs

GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 12:07:21 ; Search time 2694 Seconds  
(without alignments)  
2571.650 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 232  
Sequence: 1 MSLQLQSVSSAIHLCDKKK.....PEILVVSRSPLNLLQKSM 232

Scoring table:  
OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 20

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh  
-O=/cn2.1/USPTO.spool/SUP9771161/runat.29032004.124851.19870/app.query.fasta\_1.391  
-DB=EST\_QFMT=fastap -SUFFIX=oli20p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=quality -THR MIN=20 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161@CN 1 1 1906 @runat.29032004.124851.19870 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsl1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	204	87.9	883	12	BG393551	BG393551 602411943
2	195	84.1	883	14	CB852764	CB852764 UI-CF-FNO
3	186	80.2	938	13	BQ670832	BQ670832 AGENCOURT
4	184	79.3	656	12	BM973770	BM973770 UI-CF-ECL
5	184	79.3	660	12	BM840808	BM840808 K-EST0117
6	184	79.3	715	14	CB851847	CB851847 UI-CF-FNO
7	184	79.3	734	12	BQ008463	BQ008463 UI-H-ED1-
8	181	78.0	592	9	AI745575	AI745575 WC34112.X
9	178	76.7	852	12	BG757422	BG757422 602711061
10	175	75.4	811	12	BG170405	BG170405 602322736
11	167	72.0	667	13	BQ773811	BQ773811 UI-H-E21-
12	167	72.0	721	13	BQ774940	BQ774940 UI-H-FHO-
13	167	72.0	744	14	CD365404	CD365404 UI-H-FH2-
14	165	71.1	672	14	CA314123	CA314123 UI-CF-FNO
15	165	71.1	709	14	CA413941	CA413941 UI-H-E20-
16	165	71.1	1623	29	AY415527	AY415527 Homo sapi
17	161	66.4	647	10	AW960501	AW960501 EST372572
18	154	66.4	1623	29	AY415528	AY415528 Pan trogl
19	153	65.9	636	10	BE551615	BE551615 7A43G06.X
20	153	65.9	812	12	BE1257472	BE1257472 602367861
21	153	65.9	870	10	BE877822	BE877822 601486392
22	147	63.4	564	12	BM796243	BM796243 K-EST0078
23	145	62.5	606	9	AW085560	AW085560 wy67G04.X
24	144	62.1	479	12	BM855477	BM855477 K-EST0138
25	144	62.1	505	13	EX280487	EX280487 BX280487
26	138	59.5	610	13	BQ623654	BQ623654 UI-H-FGI-
27	137	59.1	423	9	AA574167	AA574167 nl78501.S
28	137	59.1	483	9	A1343247	A1343247 tb94A04.X
29	137	59.1	624	14	CD368863	CD368863 UI-H-FH1-
30	136	58.6	476	14	CF528565	CF528565 UI-H-BG1-
31	133	57.3	455	9	A1343850	A1343850 qp07401.X
32	130	56.0	828	10	BE875947	BE875947 601486423
33	129	55.6	476	9	AA913804	AA913804 ol35G11.S
34	129	55.6	499	12	BQ011550	BQ011550 UI-1-BC1P
35	128	55.2	496	12	BQ011702	BQ011702 UI-1-BC1P
36	126	54.3	628	12	BQ000991	BQ000991 UI-H-DH1-
37	116	50.0	350	10	BF754627	BF754627 QV3-CT055
38	116	50.0	432	9	AA723533	AA723533 zg73G08.S
39	114	49.1	400	9	AA826052	AA826052 od60S09.S
40	113	48.7	346	10	BF825562	BF825562 CM1-HN001
41	112	48.3	738	14	CD356485	CD356485 AGENCOURT
42	109	47.0	423	10	BF062840	BF062840 7h70G03.X
43	108	46.6	615	9	A1801150	A1801150 t085H04.X
44	107	46.1	518	10	AW593657	AW593657 xl94d07.X
45	107	46.1	546	12	BQ013098	BQ013098 UI-1-BC1P

ALIGNMENTS

RESULT 1  
BG393551  
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DEFINITION mRNA sequence.  
ACCESSION BG393551  
VERSION BG393551.1 GI:13286999  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 883)

AUTHORS NTH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10471 row: e column: 12  
 High quality sequence stop: 767.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4540787"  
 /tissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_92"  
 /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,78e-193 Length: 883  
 Score: 204.00 Matches: 204  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 87.93% Indels: 0  
 DB: 12 Gaps: 0  
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 QY 29 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 48  
 DB 2 GTAAATCATGGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAGTAAGAAATAGTGGT 61  
 QY 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68  
 DB 62 TCTCTGAACACTCAAGTCTCCCTGCCAGCTCCTCAGACATGATTTTATCTAGAAA 121  
 QY 69 AlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSer 88  
 DB 122 GCTCAGACCTGTATTTATGAAGCTGCATCACTGTCTCGAATACACAGTGGGATAGC 181  
 QY 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108  
 DB 182 ACCATTTCTGGATCTCAAGAGGCTGCATCTGTGATCACAGACCACTCCATGCTCTTCA 241  
 QY 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128  
 DB 242 GCAATATAATCACTCTCACTGCAGAGAACTCAGACGCTGCAGCTGGTATAGCC 301  
 QY 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
 DB 302 CAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGACAGAGGCTGCTT 361  
 QY 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
 DB 362 AACGAGTCGCTAGATGCCCTTCTGTCAGGACTTGTATGAAGAGGACTATGAACCT 421  
 QY 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188  
 DB 422 GTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAACTTACTAGACACTACTGACATC 481  
 QY 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208

Db 482 CAAGGAGAAGAATTTCGCAAGTTATAGTACAAAAATTGAAGATACAAACAAATGGGT 541  
 QY 209 LeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuGln 228  
 Db 542 CTTGAGCCTTACCCGGAATACCTTGGTTCCTAGATCACCATCTTTAAATTTACTTCAA 601  
 QY 229 AsnLysSerMet 232  
 Db 602 AATAAAGCATG 613  
 RESULT 2  
 CB852764/c  
 LOCUS CB852764.1  
 DEFINITION UI-CF-FNO-aex-p-08-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
 ACCESSION CB852764.1 GI:30047800  
 VERSION CB852764.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 683)  
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 Location/Qualifiers  
 1..683  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-FNO-aex-p-08-0-UI"  
 /tissue\_type="Human Lung Epithelial cells"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-FNO"  
 /notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu  
 TAG\_SEQ=None found"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,42e-184 Length: 683  
 Score: 195.00 Matches: 195  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 84.05% Indels: 0  
 DB: 14 Gaps: 0



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US-09-771-161A-93 (1-232) x CB852764 (1-683)
QY 24 SerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeu 43
Db 661 TCTCTGAACATACCTGTAATCATGGTCACAAAGAGGAATCATGTGGATCTCTCAGCTC 602
QY 44 HisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsn 63
Db 601 CATGAAATAGTGGTTCTCCTGAACTTCAAGGTCCTCCAGCTCCTCAAGACAATGAT 542
QY 64 PheLeuSerArgGlyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsn 83
Db 541 TTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTGGAAT 482
QY 84 HisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 103
Db 481 CACAGTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACC 422
QY 104 ThrProCysSerSerAlaIleIleLeuProLeuSerThrAlaGlyAsnSerGluArgLeu 123
Db 421 ACTCCATGCTCTCTAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACGTTTG 362
QY 124 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 143
Db 361 CAGCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATG 302
QY 144 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLys 163
Db 301 ACAGAAGCTGCTTAACCAAGTCGTAGATGCCCTCTCTGCCAGGACTTGATCATGAA 242
QY 164 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeu 183
Db 241 GAGGACTATGAATGTTAGTACCAGGCTCAAGAGCCTCAAAAGTCAGACAATTACTA 182
QY 184 AspThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 203
Db 181 GACACTACTGATCCAGGGAAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAAGAT 122
QY 204 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValVal 218
Db 121 AACAACAATGGCTTTCAGCTTACCCTGCGAAATACTTGTGTT 77

RESULT 3
LOCUS BM973770.1
DEFINITION AGENCOURT_8191703 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257019
5', mRNA sequence.
ACCESSION BM973770
VERSION BM973770.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLCM2410 row: k column: 04
High quality sequence stop: 659.
Location/Qualifiers
i. .938
/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6257019"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 102"
/notes="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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## ORIGIN

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Alignment Scores:
Pred. No.: 1,998-175 Length: 938
Score: 186.00 Matches: 199
Percent Similarity: 99.50% Conservative: 0
Best Local Similarity: 99.50% Mismatches: 0
Query Match: 80.17% Indels: 1
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ670832 (1-938)
QY 6 LeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeu 25
Db 139 TTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAGAAATGAAATATCTCTG 198
QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45
Db 199 AACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 258
QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65
Db 259 AATAGTGGTTCTCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAAATGATTTTAA 318
QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85
Db 319 TCTAGAAAAGCTCAAGACTGTTATTTTAAAGCTGCATCTCTCTGGAATCACAGT 378
QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105
Db 379 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCCTCA 438
QY 106 CysSerSerAlaIleAlaAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125
Db 439 TGCTCTTCAAGCAATTAATATCCATCTCACTGCAGGAACTCAGAACTCTGAGCCT 498
QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145
Db 499 GGTATAGCCAGCAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAA 558
QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165
Db 559 GCCTGCTTAAACAGCTCGTAGATCCCTTCTGTCCAGGAGCTTGCATCATGAAAGAGGAC 618
QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185
Db 619 TATGAATCTGTGTAGTACCAGCTCAAGAGCTCAAAAGTCAAGACAAATATTAGTACACT 678
QY 186 ThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 679 ACTGACATCCAGGAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 736

RESULT 4
BM973770/c
LOCUS BM973770.1
DEFINITION UI-CF-EC1-ach-1-07-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-ach-1-07-0-UI 3', mRNA sequence.
ACCESSION BM973770
VERSION BM973770.1
GI:19591361
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES             Location/Qualifiers
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        /dev_stage="Adult and Fetal"
        /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
        /clone_lib="UI-CF-EC1"
        /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
        modified polylinker; Site 1: EcoR I; Site 2: Not I;
        UI-CF-EC1 is a normalized CDNA library containing the
        following tissue(s): Normal lung from adult and from fetal
        day 64, day 87, week 19 and week 42. The library was
        constructed according to Bonaldo, Lennon and Soares,
        Genome Research, 6:791-806, 1996. First strand cDNA
        synthesis was primed with an oligo-dT primer containing a
        Not I site. Double stranded cDNA was ligated to an EcoR I
        adaptor, digested with Not I, and cloned directionally
        into pT7T3-Pac vector. The oligonucleotide used to prime
        the synthesis of first-strand cDNA contains a library tag
        sequence that is located between the Not I site and the
        (dT)18 tail. The sequence tag for this library is
        AAGTGCCTTAC."
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCCTTAC"

ORIGIN
Alignment Scores:
Pred. No.: 1..41e-173 Length: 656
Score: 184.00 Matches: 184
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BM973770 (1-656)

Qy 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgIlys 68
Db 625 TCTCTGGAACCTTCNAGGTCCTGCCAGCTCTCTCAAGACATGATTTTATCTAGAAA 566

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Qy 69 AlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSer 88
Db 565 GCTCAAGACTGTTATTTATGAACTGTCATCACTGCTCTGGAAATCACAGTTGGGATAGC 506
Qy 89 ThrIleSerGlySerGlnArgAlaIalalpheCysAspHisLysThrThrProCysSerSer 108
Db 505 ACCATTTCGATCTCAAAGGGCTGCTTCTGTGATCAAGACCACCTCCATGCTCTTCA 446
Qy 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128
Db 445 GCATATATTAATCCACTCTCAACTGCAGAAACTCAGAACGCTGCAGCCTGGTATAGCC 386
Qy 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148
Db 385 CAGCAGTGCATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCGCTGCCTT 326
Qy 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168
Db 325 AACCAAGTCGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAGACTATGAACCT 266
Qy 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188
Db 265 GTTAGTACCACGCTCAAGAGACCTCAAAGTCAGACAACTACTAGACACTACTGACATC 206
Qy 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208
Db 205 CAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAAGATAACAAACAAATGGGT 146
Qy 209 LeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuLeuGln 228
Db 145 CTTCAAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 86
Qy 229 AsnLysSerMet 232
Db 85 AATAAAGCATG 74

RESULT 5
BM840808
LOCUS K-EST0117952 S12SNU216 Homo sapiens cDNA clone S12SNU216-38-G08 5',
DEFINITION mRNA sequence.
ACCESSION BM840808.1 GI:19197217
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 660)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 38 row: G column: 08
High quality sequence stop: 660.
FEATURES             Location/Qualifiers
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     1..660
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="S12SNU216-38-G08"
        /sex="F"
        /tissue_type="Lymph node"
        /cell_type="Epithelial"
        /cell_line="SNU-216"

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/lab\_host="Top10P"  
 /clone\_lib="S12NU216"  
 /note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including EcoR  
 I site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10P, by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.42e-173 Length: 660  
 Score: 184.00 Matches: 184  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 79.31% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BM840808 (1-660)

QY 6 LeuGlnSerValSerSerSerlalleHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 67 TTACAGAGTGTTCAGTGCCCTTACCTATGTCAGAGAGAAATGGAATATCTCTG 126  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 127 AACATACCTGTAAATCATGGTCCAGAGGAATCATGTGGATCTCTCAGCTCCATGAA 186  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 187 ATATGTTGTTCTCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTTGA 246  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 DB 247 TCTAGAAAGCTCAAGACTGTATTATTATGAAGCTGCATCACTGTCTCGAAATCACAGT 306  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
 DB 307 TGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGACCCTCCA 366  
 QY 106 CysSerSerAlaIleleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 367 TGCTCTTCAGCAATAATAATCCACTCTCACTGAGGAACTCAGAGCTCTGAGCT 426  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 427 GGTATAGCCAGCAGTGGATCCAGACAAAGGAAGACATTGTCAACCAATGACAGAA 486  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 487 GCCTGCTTAAACAGTCGGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAAGAGGAC 546  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 DB 547 TATGAACTGTGTATGACCAAGCTACAGGACTCAAGGTACAGCAATATTACTAGACT 606  
 QY 186 ThrAspIleGln 189  
 DB 607 ACTGACATCCAA 618  
 RESULT 6  
 CB851847/c  
 LOCUS CB851847 715 bp mRNA linear EST 22-APR-2003

## DEFINITION

UI-CF-FNO-aem-o-20-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
 UI-CF-FNO-aem-o-20-0-UI 3', mRNA sequence.

ACCESSION CB851847  
 VERSION CB851847.1 GI:30046667

KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 715)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.

## AUTHORS

Normalization and subtraction: two approaches to facilitate gene

## TITLE

discovery

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## MEDLINE

97044477

## PUBMED

8889548

## COMMENT

Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.reagen.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

sequence: 1-24, >AT rich#Low\_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1..715

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-FNO-aem-o-20-0-UI"

/tissue\_type="Human Lung Epithelial cells"

/lab\_host="DH10B (life technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-FNO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoR I; Site 2: Not I;

UI-CF-FNO is a subtracted cDNA library derived from two

normalized Human lung epithelial cell libraries (EN1 and

DUI) The library was subtracted according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. For additional information, contact:

bento-soares@uiowa.edu

TAG\_SEQ=None found"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.53e-173 Length: 715  
 Score: 184.00 Matches: 208  
 Percent Similarity: 99.52% Conservative: 0  
 Best Local Similarity: 99.52% Mismatches: 1  
 Query Match: 79.31% Indels: 1  
 DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CB851847 (1-715)

QY 24 SerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeu 43

DB 691 TCTCTGAACATACCTGTAAATCATGGTCCACAGGAATCATGTGGATCTCTCAGCTC 632

QY 44 HisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsn 63

DB 631 CATGAAATAGTGT-TCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGAT 573

QY 64 PheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAan 83

```

Db 572 TTTTATCTAGAAAGCTCAAGACTGTATTTATGAAGCTGATCACTGTCTCGAAAT 513
QY 84 HisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 103
Db 512 CACAGTTGGATAGCACCATTCTGGATCTCAAGAGGCTGCATCTGTGATCAAGACC 453
QY 104 ThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 123
Db 452 ACTCCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACCTCAGAACGCTG 393
QY 124 GlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMet 143
Db 392 CAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATG 333
QY 144 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLys 163
Db 332 ACAGAAGCCTGCTTAAACCAAGTCGTAGTGCCTCTCTGTCAGGACCTTGATCATGAA 273
QY 164 GluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 183
Db 272 GAGGACTATGAATGTTAGTACCAAGCCTTCAAGGACCTCAAAAGTCAGACAATTACTA 213
QY 184 AspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 203
Db 212 GACACTACTGACATCCAAAGAGAGAAGATTTGCCAAAGTTATAGTACAAAAATTTGAAAGAT 153
QY 204 AsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSer 223
Db 152 AACAAACAATAGGCTCTTACGCTTACCCGGAATATCTTGTGTTTCTAGATCACCATCT 93
QY 224 LeuAsnLeuLeuGlnAsnLysSerMet 232
Db 92 TTTAAATTTACTTCAAAATAAAGCATG 66

RESULT 7
BQ008463/c
LOCUS
DEFINITION
BQ008463 734 bp mRNA linear EST 26-MAR-2002
IMAGE:5840010 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1..734
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5840010"
/tissue type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac"

FEATURES
source
1..734

```

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(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=Chondrosarcoma
TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"

ORIGIN
Alignment Scores:
Pred. No.: 1.57e-173 Length: 734
Score: 184.00 Matches: 184
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.31% Indels: 0
DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BQ008463 (1-734)
QY 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68
Db 681 TCTCCTGGAACCTTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTTTTTATCTAGAAA 622
QY 69 AlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSer 88
Db 621 GCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAATCACAGTTGGGATAGC 562
QY 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108
Db 561 ACCATTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCCTCCATGCTCTTCA 502
QY 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128
Db 501 GCATTAATAAATCCATCTCACTGAGGAACTCAGACCTGTCAGCTGCTGATAGCC 442
QY 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148
Db 441 CAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTCAACCAATGACAGAAGCTGCTT 382
QY 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168
Db 381 AACCACTGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAAGAGGACTATGAACCT 322
QY 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188
Db 321 GTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTACTAGACTACTGACATC 262
QY 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208
Db 261 CAAGGAGAAGAAATTTCCAAAGATTAGTACAAAAATTTGAAGATAACAAACAAATGGGT 202
QY 209 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGln 228
Db 201 CTTTCAGCCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 142
QY 229 AsnLysSerMet 232
Db 141 AATAAAGCATG 130

RESULT 8
AI745575/c
LOCUS
DEFINITION
AI745575 592 bp mRNA linear EST 17-DEC-1999
wc34f12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2317103 3'
similar to TR:Q43353 SERINE/THREONINE KINASE RICK. ; mRNA

```

```

sequence.
AI745575
VERSION AI745575.1 GI:5113863
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 673 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
FEATURES
source
1..592
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2317103"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Pr28"
/note="Organ: prostate; Vector: pTT3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 1,29e-170 Length: 592
Score: 181.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.02% Indels: 0
DB: 9 Gaps: 0
US-09-771-161A-93 (1-232) x AI745575 (1-592)
QY 52 ThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLyAlaGlnAap 71
Db ATTTCAAGTCTCTGCCAGCTCTCTCAAGCAATGATTTTATCTAGAAAAGCTCAAGAC 533
QY 72 CysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSer 91
Db TGTATTATTAAGAGTGCATCACTGCTCTGGAATACAGTTGGATAGCACCATTCT 473
QY 92 GlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIle 111
Db GGATCTCAAGGGTGCATCTCTGTGATCAACAGACCATCTTCATCTTCAACAATAA 413
QY 112 AsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnTrp 131
Db ATTCACCTCTCACTGCAGAAACTCAGAACGCTCTGCAGCCTGGTATATGCCAGCATGG 353
sequence.
132 IleGlnSerLysArgGluAspIleValaAsnGlnMetThrGluAlaCysLeuAsnGlnSer 151
Db ATCCAGAGCAAAAGGGAAGACATTTGAACCAAAATGACAGAAAGCCTTACCCAGTCG 293
QY 152 LeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThr 171
Db CTAGATGCGCTTCTCTCCAGGACTTGATCATGAAGAGGACTATGAATCTTTAGTACC 233
QY 172 LysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGly 191
Db AAGCCTACAGGACCTCAAAAGTCAGACAAATTTACTAGACACTTACTGACATCCAA 173
QY 192 GluPheAlaLysValIleValGlnLysLysLeuAspAsnLysGlnMetGlyLeuGlnPro 211
Db GAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAAACAAATGGGTCTTCAG 113
QY 212 TyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLys 231
Db TACCCGGAATACTTGTGTTTCTAGATCACCATCTTTAAATTTTACTTCAAAATAAAG 53
QY 232 Met 232
Db 52 ATG 50
RESULT 9
BG757422 852 bp mRNA linear EST 15-MAY-2001
LOCUS 602711061F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851542 5';
DEFINITION mRNA sequence.
ACCESSION BG757422
VERSION BG757422.1 GI:14068075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 852)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1694 row: i column: 15
High quality sequence stop: 814.
FEATURES
source
1..852
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851542"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOT7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1.85e-167 Length: 852

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Score: 178.00 Matches: 178  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 76.72% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG757422 (1-852)

QY 6 LeuGlnSerValSerSerAlaLeuHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 121 TTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAAAGAAATGGAATATCTCTG 180  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 181 AACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGCTCCATGAA 240  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 241 AATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCTCTCAAGACCAATGATTTTAA 300  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 301 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCCTCTCTGGAATCAGT 360  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 361 TGGATAGACCACTTCTGGATCTCAAAGGCTGCACTTCTGTATCACAAGACCACTCCA 420  
 QY 106 CysSerSerAlaLeuLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 421 TGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGAAACTCAGAACCTCTGCAGCCT 480  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 481 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACAGAA 540  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 541 GCCTGCCTTAACAGTCGTAGATGCCCTTCTGTCCAGGACCTGATCATGAAAGAGGAC 600  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeu 183  
 DB 601 TATGAACCTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGACAAATTA 654

RESULT 10  
 BG170405 811 bp mRNA linear EST 06-FEB-2001  
 LOCUS 60232736F1 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:4426016 5',  
 DEFINITION mRNA sequence.

ACCESSION BG170405  
 VERSION BG170405.1 GI:12677108  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 811)

NTH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNALibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10172 row: g column: 09

High quality sequence stop: 721.

Location/Qualifiers

1..811

FEATURES  
 source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4426016"  
 /tissue\_type="hypernephroma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_89"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.3 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC library."

# ORIGIN

## Alignment Scores:

Pred. No.: 1-78e-164 Length: 811  
 Score: 175.00 Matches: 175  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 75.43% Indels: 0  
 DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG170405 (1-811)

QY 6 LeuGlnSerValSerSerAlaLeuHisLeuCysAspLysLysMetGluLeuSerLeu 25  
 DB 168 TTACAGAGTGTTCCTCAAGTGCCTTACCTATGTGACAAAGAAATGGAATATCTCTG 227  
 QY 26 AsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGlu 45  
 DB 228 AACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGCTCCATGAA 287  
 QY 46 AsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeu 65  
 DB 288 AATAGTGGTTCCTCTGAACTTCAAGTCCCTGCCAGCTCTCTCAAGACCAATGATTTTAA 347  
 QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
 DB 348 TCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCCTCTCTGGAATCAGT 407  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrPro 105  
 DB 408 TGGATAGACCACTTCTGGATCTCAAAGGCTGCACTTCTGTATCACAAGACCACTCCA 467  
 QY 106 CysSerSerAlaLeuLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 DB 468 TGCTCTTTCAGCAATAATAATCACTCTCAACTGCAGAAACTCAGAACCTCTGCAGCCT 527  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 DB 528 GGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACAGAA 587  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 DB 588 GCCTGCCTTAACAGTCGTAGATGCCCTTCTGTCCAGGACCTGATCATGAAAGAGGAC 647  
 QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArg 180  
 DB 648 TATGAACCTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGATCAGA 692

## RESULT 11

BQ773811/c

LOCUS

DEFINITION

UI-H-EZ1-bbz-f-10-0-UI.s1 NCI\_CGAP\_Ch2 Homo sapiens cDNA clone

UI-H-EZ1-bbz-f-10-0-UI 3', mRNA sequence.

ACCESSION BQ773811

VERSION BQ773811.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

667 bp mRNA linear EST 26-JUL-2002

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of Orthopedics  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

**FEATURES** Location/Qualifiers  
 1..667  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-E21-bbz-f-10-0-UI"  
 /tissue\_type="Chondrosarcoma Grade II"  
 /dev\_stage="Adult"  
 /lab\_host="DH108 (Life Technologies)"  
 /clone\_lib="NCI\_CGAP Ch2"  
 /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCCAGCT.  
 TAG\_TISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=UI-H-E21  
 TAG\_SEQ=ATCTAATATG"

**ORIGIN**

Alignment Scores:  
 Pred. No.: 1..5e-156 Length: 667  
 Score: 167.00 Matches: 167  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.98% Indels: 0  
 DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x BQ773811 (1-667)

QY 66 SerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSer 85  
 |||||  
 Db 630 TCTAGAAAAGCTCAGACTGTTATTATTATGAAGCTGCATCTGCTCTGGAATCAGACT 571  
 |||||  
 QY 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
 |||||  
 Db 570 TGGATAGCACCATTCTCGATCTCAAGGGCTGCATCTTGATCACAAGACCCTCCA 511  
 |||||  
 QY 106 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
 |||||  
 Db 510 TGCCTCTCAGCAATATAATCACTCTCACTGACGAGAACTCAGAACTCTGCAGCT 451  
 |||||  
 QY 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
 |||||  
 Db 450 GGTATAGCCAGCAGTGGATCCAGACAAAAGGAACATTGTGTAACCAATGACAGAA 391  
 |||||  
 QY 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
 |||||  
 Db 390 GCCTGCTTTAAACGATCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAGAGGAC 331  
 |||||

QY 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
 |||||  
 Db 330 TATGAACCTTGTGTAGTACCAAGCCTACAAAGGAGCTCAAAAGTCAAGCAATTACTAGCACT 271  
 |||||  
 QY 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
 |||||  
 Db 270 ACTGACATCCAAAGGAGAAGATTTCCTCAAGTTATAGTACAAAATTTGAAGATACAAA 211  
 |||||  
 QY 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
 |||||  
 Db 210 CAAATGGGCTCTCAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 151  
 |||||  
 QY 226 LeuLeuGlnAsnLysSerMet 232  
 |||||  
 Db 150 TTACTTCAAAATAAAGCATG 130  
 |||||

**RESULT 12**  
 BQ774940/c  
 BQ774940/c  
**LOCUS** BQ774940  
**DEFINITION** UI-H-FHO-bcd-1-20-0-UI.s1 NCI CGAP FHO Homo sapiens cDNA clone  
 UI-H-FHO-bcd-1-20-0-UI 3', mRNA sequence.  
**ACCESSION** BQ774940  
**VERSION** BQ774940.1 GI:21983416  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** 1 (bases 1 to 721)  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: James Martin  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA sequence: 1-22, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

**FEATURES** Location/Qualifiers  
 1..721  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FHO-bcd-1-20-0-UI"  
 /tissue\_type="Human Chondrosarcoma Cell Line"  
 /dev\_stage="Adult"  
 /lab\_host="DH108 (Life Technologies)"  
 /clone\_lib="NCI\_CGAP FHO"  
 /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGCG. The cell line was provided by Dr. James Martin from University of Iowa  
 TAG\_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1 Chondrosarcoma

TAG\_LIB=UI-H-FHO  
TAG\_SEQ=AGAAATCCGGC

ORIGIN

Alignment Scores: 1.62e-156 Length: 721  
Pred. No.: 167.00 Matches: 167  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 71.98% Gaps: 0  
DB: 13

US-09-771-161A-93 (1-232) x BQ774940 (1-721)

Qy 66 SerArglyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSer 85  
Db 612 TCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTCGAATCAAGT 553  
Qy 86 TrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrPro 105  
Db 552 TGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGACCACTCCA 493  
Qy 106 CysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 125  
Db 492 TGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGAACTCAGAACTCTGCAGCCT 433  
Qy 126 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 145  
Db 432 GGTATAGCCAGCAGTGGATCCAGAGAAAAGGAGACATTGTGAACCAAAATGACAGAA 373  
Qy 146 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAsp 165  
Db 372 GCCTGGCTTACCAAGTGCAGTACGCTCTCTGTCAGAGGACTGATCATGAAAGAGGAC 313  
Qy 166 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 185  
Db 312 TATGAACCTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAAGACAAATTAAGACACT 253  
Qy 186 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 205  
Db 252 ACTGACATCCCAAGAGAGAATTTGCCAAGATTATAGTACMAAAATTTGAAGATAACAAA 193  
Qy 206 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 225  
Db 192 CAATGGGTCTCAGCCCTTACCGGAATACTTGTGGTTCTAGATCACCATCTTTAAAT 133  
Qy 226 LeuLeuGlnAsnLysSerMet 232  
Db 132 TTACTTCAAAATAAAAGCATG 112

RESULT 13  
CD365404/c  
LOCUS  
DEFINITION  
UI-H-FR2-bj1-h-03-0-UI-s1 NCI-CGAP\_F12 Homo sapiens CDNA clone  
UI-H-FR2-bj1-h-03-0-UI 3', mRNA sequence.

ACCESSION  
CD365404  
VERSION  
CD365404.1 GI:31149494  
KEYWORDS  
EST.  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 744)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

JOURNAL  
COMMENT  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/cgap.html  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

1..744  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FR2-bj1-h-03-0-UI"  
/tissue\_type="Aveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI-CGAP\_F12"  
/note="Organ: Lung; Vector: pVT3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP F12 is a subcloned CDNA library constructed from  
a pool of 81 RNA samples from Alveolar Macrophages  
challenged with different treatments. The library was  
subtracted according to Bonaldo, Lennon and Soares, Genome  
Research, 6:791-806, 1996. The tissue was provided by Dr.  
Gary W. Hunninghake of the University of Iowa.  
TAG\_TISSUE=Human Lung Aveolar Macrophage  
TAG\_LIB=UI-H-FR2  
TAG\_SEQ=GGCAATGCCG"

ORIGIN

Alignment Scores: 1.67e-156 Length: 744  
Pred. No.: 167.00 Matches: 208  
Score: 99.05% Conservative: 0  
Percent Similarity: 99.05% Mismatches: 1  
Best Local Similarity: 71.98% Indels: 2  
Query Match: 14 Gaps: 0  
DB: 14

US-09-771-161A-93 (1-232) x CD365404 (1-744)

Qy 24 SerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeu 43  
Db 662 TCTCTGAAACATACCTGTAAATCATGTCACAAAGGAGTAATCATGTGGATCTCTCAGCTC 603  
Qy 44 HisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAsp 63  
Db 602 CATGAAAATAGTGGTCTCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGAT 543  
Qy 64 -PheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAs 83  
Db 542 TTTTNA-TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAAA 484  
Qy 83 nHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysTh 103  
Db 483 TCACAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCACAAGAC 424  
Qy 103 rThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLe 123  
Db 423 CACTCCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGTCT 364  
Qy 123 uGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMe 143  
Db 363 GCAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAACCAAT 304  
Qy 143 tThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLy 163  
Db 303 GACAGAACCTTGCTTAACAGTCCGATAGTGCCTTCTGTCCAGGGACTTGATCATGAA 244  
Qy 163 sGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeu 183  
Db 243 AGAGGACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTTCAGAAATTAAT 184  
Qy 183 uAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAs 203  
Db 183 AGACACTACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGA 124



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QY 203 pAnlysGlnMetGlyLeuGlnProTyPrOgLuileuValSerArgSerProSe 223
Db 123 TAACAACAAATGGGCTTACCCGAAATACTTGTGGTTCTAGATCACCATC 64
QY 223 rLeuAenLeuGlnAenLysSerMet 232
Db 63 TTAAATTTACTTCAAATATAAAGCATG 36

RESULT 14
CA314123/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 672)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
CONTACT: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .672
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-aes-o-11-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (ENI and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN
Alignment Scores:
Pred. No.: 1.52e-154 Length: 672
Score: 165.00 Matches: 165
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.12% Indels: 0
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CA314123 (1-672)
QY 68 LysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAsp 87
Db 546 AAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTGGAAATCACAGTTGGGAT 487
QY 88 SerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSer 107
Db 486 AGCACCATTTCTGGATCTCAAGAGGCTCATTTCTGTGATCAACAAGACCATCCATGCTCT 427
QY 108 SerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIle 127
Db 426 TCAGCAATATATATATCCACTCTCACTCAGAGAACTCAGAACGCTGCGAGCTGGTATA 367
QY 128 AlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCys 147
Db 366 GCCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCCTGC 307
QY 148 LeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGluAspTyrGlu 167
Db 306 CTTAACCAGTCGTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGACTATGAA 247
QY 168 LeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAsp 187
Db 246 CTTGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACTACTGAC 187
QY 188 IleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMet 207
Db 186 ATCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAATG 127
QY 208 GlyLeuGlnProTyPrOgLuileuValSerArgSerProSerLeuAsnLeuLeu 227
Db 126 GGTCTTCAGCCTTACCCCGAAATACTTGTGGTTTCTAGATCACCATCTCTTAAATTTACTT 67
QY 228 GlnAsnLysSerMet 232
Db 66 CAAATATAAAGCATG 52

RESULT 15
CA413941/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-64, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
1. .709
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="UI-H-EZO-bau-f-07-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/notes="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZO
TAG_SEQ=ATCTAATATG"

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ORIGIN

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Alignment Scores:
Pred. No.: 1.6e-154 Length: 709
Score: 165.00 Matches: 165
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.12% Indels: 0
DB: 14 Gaps: 0

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US-09-771-161A-93 (1-232) x CA413941 (1-709)

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Qy 68 LysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAsp 87
Db 708 AAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAAATCACAGTTGGAT 649
Qy 88 SerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSer 107
Db 648 AGCACCAATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAGACCCTCCATGCTCT 589
Qy 108 SerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIle 127
Db 588 TCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACTGTCTGCAGCCTGGTATA 529
Qy 128 AlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCys 147
Db 528 GCCCAGCAGTGGATCCAGAGAAAAGGGAAGACATTGTGAACCAATGACAGAACCTGC 469
Qy 148 LeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGlu 167
Db 468 CTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAAGAGACTATGAA 409
Qy 168 LeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrAsp 187
Db 408 CTTGTTAGTACCAGCCTACAGGACCTCAAAAGTTCAGACAATTACTAGACACTACTGAC 349
Qy 188 IleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMet 207
Db 348 ATCCAAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATACAAACAATG 289
Qy 208 GlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsnLeuLeu 227
Db 288 GGTCTTCAGCCTTACCCGGAATATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTT 229
Qy 228 GlnAsnLysSerMet 232
Db 228 CAAATAAAGCATG 214

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Search completed: April 1, 2004, 14:50:52  
Job time : 2712 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 08:35:52 ; Search time 4002 Seconds  
(without alignments)  
2512.640 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-O=/cgn2.1/USPTO spool/US09771161/runat\_29032004.124819.19493/app query fasta\_1.391  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1.1.2496 @runat\_29032004.124819.19493 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

RESULT 1

ALIGNMENTS

Result No.	Score	Query Match %	Length	DB ID	Description
1	1182	98.0	1623	9	AF078530 Homo sapi
2	1182	98.0	1623	12	AY335645 Synthetic
3	1182	98.0	1886	9	AY358813 Homo sapi
4	1182	98.0	1889	9	BC004553 Homo sapi
5	1182	98.0	1902	9	AF064824 Homo sapi
6	1182	98.0	2024	6	BD251808 Phosphory
7	1182	98.0	2033	6	BD127583 Primer fo
8	1182	98.0	2033	9	AK075213 Homo sapi
9	1182	98.0	2098	6	A82777 Sequence 2
10	1182	98.0	2098	6	BD106658 Modulator
11	1182	98.0	2501	6	AR221453 Sequence
12	1182	98.0	2501	6	AX429236 Sequence
13	1182	98.0	2501	9	AF027706 Homo sapi
14	1182	98.0	2502	6	AR194318 Sequence
15	1182	98.0	2521	9	AY358814 Homo sapi
16	1176	97.5	1620	6	AR183235 Sequence
17	1176	97.5	1620	6	AR205635 Sequence
18	1176	97.5	1620	6	AR241237 Sequence
19	1176	97.5	1620	6	AR256253 Sequence
20	1176	97.5	1620	6	AR391600 Sequence
21	1176	97.5	1620	6	AX082201 Sequence
22	1176	97.5	1620	6	BD123999 Novel mol
23	1176	97.5	1931	6	AR183234 Sequence
24	1176	97.5	1931	6	AR205634 Sequence
25	1176	97.5	1931	6	AR216112 Sequence
26	1176	97.5	1931	6	AR241236 Sequence
27	1176	97.5	1931	6	AR256252 Sequence
28	1176	97.5	1931	6	AR391599 Sequence
29	1176	97.5	1931	6	AX082199 Sequence
30	1176	97.5	1931	6	BD123998 Novel mol
31	1165	96.6	1060	6	AR380139 Sequence
32	839.5	69.6	1620	10	AF461040 Mus muscu
33	839.5	69.6	1620	10	AF487539 Mus muscu
34	726	60.2	116650	9	AC004003 Homo sapi
35	726	60.2	320187	9	AF117829 Homo sapi
36	569.5	47.2	173259	2	AC117336 Rattus no
37	514.5	42.7	186519	10	AL807379 Mouse DNA
38	417.5	34.6	575	6	BD126039 Primer fo
39	371	30.8	61099	2	AC139421 Homo sapi
40	335	27.8	1755	5	AF487540 Danio rer
41	125	10.4	1400	6	AR205645 Sequence
42	125	10.4	1400	6	AR241247 Sequence
43	125	10.4	1400	6	AR256263 Sequence
44	125	10.4	1400	6	AR391610 Sequence
45	125	10.4	1400	6	AX082238 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29: em.vi.\*  
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31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rtd.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Not loaded

AF078530	AF078530	1623 bp	mRNA	linear	PRI 28-JUL-1998
LOCUS	Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete				
DEFINITION					
ACCESSION	AF078530	1	GI:3342909		
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM					
REFERENCE					
AUTHORS	McCarthy, J.V., Ni, J. and Dixit, V.M.				
TITLE	RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase				
JOURNAL	J. Biol. Chem. 273 (27), 16968-16975 (1998)				
MEDLINE	98307936				
PUBMED	9642260				
REFERENCE	2 (bases 1 to 1623)				
AUTHORS	McCarthy, J.V., Ni, J. and Dixit, V.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-JUL-1998) Molecular Oncology, Genentech Inc, 1 DNA Way, South San Francisco, CA 94080, USA				
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	/function="activates NF-kappaB"				
	/function="induces cell death"				
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Percent Similarity:	100.00%	Conservative:	1		
Best Local Similarity:	99.56%	Mismatches:	0		
Query Match:	98.01%	Indels:	0		
DB:	9	Gaps:	0		
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QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64		
Db	1057	GAATAAGTGTCTCTCTGAACTTCAAGTCCCTGACGCTCTCTCAAGCAATGATTTT	1116		
QY	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84		
Db	1117	TTATCTAGAAAAGCTCAAGACTGTATTATTATTAAGCTGATCCTGCTGGAATCAC	1176		
QY	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrThr	104		
Db	1177	AGTTGGGACAGCACCATTTCTGGATCTCAAGGGCTGCAATTCGTGATCACAGACCAT	1236		
QY	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124		
Db	1237	CCANGCTCTTCAGCAATAATAATCACTCTCACTGCGAGAACTCAGAACGCTGCGAG	1296		
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Db	1297	CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	1356		
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164		
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QY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184		
Db	1417	GACTATGAATCTGTGTAGTACCAAGCTCAGAGCACTCAAAAGTCAAGCAATTTACTAGAC	1476		
QY	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204		
Db	1477	ACTACTGACATCCAGGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAAC	1536		
QY	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	224		
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LOCUS	AY335645	1623 bp	mRNA	linear	SYN 15-OCT-2003
DEFINITION	Synthetic construct Homo sapiens serine-threonine kinase 2 (RIPK2) mRNA, partial cds.				
ACCESSION	AY335645				
VERSION	AY335645.1	GI:33303916			
KEYWORDS	FLI CDNA.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 1623)				
AUTHORS	Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jenson, D., Harlow, E., LaBaer, J., and Brizuela, L.				
TITLE	Cloning of human full-length CDS FLEXGene kinases in recombinational vector system				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1623)				
AUTHORS	Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jenson, D., Harlow, E., LaBaer, J., and Brizuela, L.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA				
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last 'codon' and before HindIII site to maintain reading frame.				
FEATURES	Location/Qualifiers				
source	1..1623				

1886  
227

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Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	98.01%	Indels:	0
DB:	9	Gaps:	0
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QY	25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44
DB	1068	CTGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGGATCCTCTCAGCTCCAT	1127
QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
DB	1128	GAATATAGTGTCTCTGTAACCTTCAGGTCTCCAGCTCCTCAAGCAATGATTTT	1187
QY	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	84
DB	1188	TTATCTAGAAAGCTCAAGACTGTATTTATGAAAGTGCATCACTGTCTCGAAATCAC	1247
QY	85	SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104
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QY	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1308	CCATGCTCTTCAGCAATATAATCACTCTCACTGCAGGAACATCAAGACGCTGCAG	1367
QY	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
DB	1368	CCTGTTATAGCCAGCAGTGGATCCAGAGCAAGAAAGGAGACATTGTGAACCAATGAC	1427
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
DB	1428	GAGAGCTCGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACATGATCATGAAG	1487
QY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
DB	1488	GACTATGAATCTGTAGTACAGCCCTACAGGACCTCAAAAGTCAGCAATTTACTAGAC	1547
QY	185	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
DB	1548	ACTACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC	1607
QY	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
DB	1608	AAACAAATGGTCTTACGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA	1667
QY	225	AsnLeuLeuGlnAsnLysSerMet	232
DB	1668	AATTACTTCAATAATAAAGCATG	1691
RESULT 4			
BC004553			
LOCUS			
DEFINITION	1889 bp mRNA linear PRI 03-OCT-2003		
DESCRIPTION	Homo sapiens receptor-interacting serine-threonine kinase 2, mRNA		
ACCESSION	BC004553		
VERSION	BC004553.2		
KEYWORDS	GI:33871163		
SOURCE	MGC.		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1 (bases 1 to 1889)		
	Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,		
	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,		
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,		
	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,		

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahsey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257  
12477932  
2 (bases 1 to 1889)  
Strausberg, R.  
Direct Submission  
Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:13528713.  
Contact: MGC help desk  
Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 15 Row: n Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127435.

FEATURES	Location/Qualifiers
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gene	1..1889 /gene="RIPK2" /note="synonyms: RICK, RIP2, CARDIAK, CARD3" /db_xref="LocusID:8767" /db_xref="MIM:603455" 203..1825 /codon_start=1 /product="receptor-interacting serine-threonine kinase 2" /protein_id="AAH04553.1" /db_xref="GI:13528714" /db_xref="LocusID:8767" /translation="MNNEAICSGALPTIPYKHLADLYLSRGASGTVSSARHARWVQV"
CDS	



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QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 1359 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGAAAATCAC 1418
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1419 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAGACCACT 1478
QY 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1479 CCATGCTCTTACGAATTAATAATCACTCTCACTGCAGGAACCTCAGACCTCTGCAG 1538
QY 125 ProGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
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QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1659 GACTATGAATCTGTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTAGAC 1718
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaIleValIleValGlnLysLeuLysAspAsn 204
Db 1719 ACTACTGACATCCAAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1778
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1779 AACAATATGGGTCTTACAGCTTACCCGGAATATCTTGTTGTTCTAGATCACCATCTTTA 1838
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1839 AATTACTTCAAAATAAAAGCATG 1862

RESULT 6
BD251808 2024 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Phosphorylation effectors.
ACCESSION BD251808
VERSION BD251808.1 GI:33061578
KEYWORDS JP 2002526035-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2024)
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A.,
Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L.
Phosphorylation effectors
Patent: JP 2002526035-A 6 20-AUG-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002526035-A/6
PD 20-AUG-2002
PF 28-JUL-1999 JP.2000562510
PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR
14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR
19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR
12-JAN-1999 US 60/155233
PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J
```

```
PI GUEGLER,
PI MARIAH R BAUGHN, CHANDRA PATTERSON, OLGA BANDMAN, JANICE AU
YOUNG.
PI GINA A GORGONE, HENRY YUE, YALDA AZIMZAI, ROOPA REDDY, DYUNG AINA
PI M LU,
PI LEO L SHIH
PC C12N15/09, A61K38/00, A61K45/00, A61P1/04, A61P1/16, A61P3/10 PC
,A61P5/14, A61P5/38,
PC A61P7/00, A61P9/10, A61P11/00, A61P17/00, A61P19/02, A61P19/06, PC
A61P21/04,
PC A61P25/00, A61P25/08, A61P25/14, A61P25/16, A61P25/18, A61P25/28,
PC A61P31/04,
PC A61P31/10, A61P31/12, A61P31/18, A61P33/00, A61P35/00, A61P35/02,
PC A61P37/00,
PC A61P37/08, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/
PC 12, C12N9/16,
PC C12Q1/68, G01N33/50, G01N33/566, C12N15/00, C12N5/00, A61K37/02 CC
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FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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1..2024
Location/Qualifiers
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Score: 100.00% Conservative: 1
Percent Similarity: 99.56% Mismatches: 0
Best Local Similarity: 98.01% Indels: 0
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US-09-771-161A-93 (1-232) x BD251808 (1-2024)
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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
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QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1259 GAAAAATAGTGGTCTCTCTGAACTTCAAGTCTCCGCCAGCTCTCAAGACATGATTTT 1318
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
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QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
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QY 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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QY 125 ProGlyIleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
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QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164
Db 1559 GAAGCCTGCTTAAACAGTCGTAGATGCCCTCTCTGTCAGGGACTTGATCATGAAGAG 1618
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAen 204
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RESULT 7
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LOCUS BD127583 2033 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127583
VERSION BD127583.1 GI:23222528
KEYWORDS JP 2002017375-A/3014.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 202017375-A 3014 22-JAN-2002;
COMMENT HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 202017375-A/3014
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
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Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
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US-09-771-161A-93 (1-232) x BD127583 (1-2033)
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QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
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QY 225 AsnLeuLeuGlnAsnLysSerMet 232
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LOCUS AK075213 2033 bp mRNA linear PRI 03-SEP-2002
DEFINITION Homo sapiens cDNA FLJ90732 fis, clone PLACE1010081, highly similar
to Homo sapiens serine/threonine kinase RICK (RICK) mRNA.
ACCESSION AK075213
VERSION AK075213.1 GI:22761157
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotaka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2033)
Isogai,T. and Otsuki,T.
JOURNAL Direct Submission
COMMENT Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).

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		/tissue_type="placenta"		MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS	
		/clone_lib="PLACE1"		Patent: WO 9855507-A 2 10-DEC-1998;	
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Pred. No.:		1182.00		Matches: 227	
Score:		100.00%		Conservative: 1	
Percent Similarity:		99.56%		Mismatches: 0	
Best Local Similarity:		98.01%		Indels: 0	
Query Match:		6		Gaps: 0	
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DB		1316 GAAATAGTGGTTCCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT		1375	
QY		65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis		84	
DB		1376 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTGTGATCAAGACCCT		1435	
QY		85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr		104	
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DB		1616 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTCTCTGTCAGGAGACTTGATCATGAAGAG		1675	
QY		165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp		184	
DB		1676 GACTATGAATGTTGTAGTACCAAGACCTCAAGACCTCAAAAGTCAAGCAATTACTAGAC		1735	
QY		185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn		204	
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QY		205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu		224	
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		/tissue_type="placenta"		MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL SURVIVAL PATHWAYS	
		/clone_lib="PLACE1"		Patent: WO 9855507-A 2 10-DEC-1998;	
		/note="cloning vector: pME18SFL3"		BOLDIN MARK (IL); WALLACH DAVID (IL)	
ORIGIN		Location/Qualifiers		1..2098	
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Pred. No.:		1182.00		Matches: 227	
Score:		100.00%		Conservative: 1	
Percent Similarity:		99.56%		Mismatches: 0	
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DB		1215 CTGAACATACCTGTAATCATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT		1274	
QY		45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe		64	
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QY		65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis		84	
DB		1335 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTGGAATCAC		1394	
QY		85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr		104	
DB		1395 AGTTGGGATAGCACCACTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCCT		1454	
QY		105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln		124	
DB		1455 CCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGCAG		1514	
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QY		145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu		164	
DB		1575 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG		1634	
QY		165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp		184	
DB		1635 GACTATGAATGTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC		1694	
QY		185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn		204	
DB		1695 ACTACTGACATCCAGGAGAGAAATTTGCTAAAGTTATAGTACAAAATTTGAAGATAAC		1754	
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QY		225 AsnLeuLeuGlnAsnLysSerMet		232	
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DEFINITION							

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QY 225 AsnLeuGlnAsnLysSerMet 232
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RESULT 10
LOCUS BD106658
DEFINITION Modulators of intracellular inflammation, cell death and cell survival pathways.
ACCESSION BD106658
VERSION BD106658.1 GI:23201476
KEYWORDS JP 2002502258-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2098)
AUTHORS Wallach,D., Boldin,M. and Malinin,N.
TITLE Modulators of intracellular inflammation, cell death and cell survival pathways
JOURNAL Patent: JP 2002502258-A 1 22-JAN-2002;
COMMENT YEDA RESEARCH AND DEVELOPMENT CO LTD
PN JP 2002502258-A/1
PD 22-JAN-2002
PF 01-JUN-1998 JP 1999501993
PR 03-JUN-1997 IL 121011,30-JUN-1997 IL 121199 PR
11-SEP-1997 IL 121746
PI DAVID WALLACH,MARK BOLDIN,NIKOLAI MALININ
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FH Key Location/Qualifiers.
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Alignment Scores:
Pred. No.: 6.84e-104 Length: 2098
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
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US-09-771-161A-93 (1-232) x BD106658 (1-2098)

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QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
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QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIlysrThrThr 104
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QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1496 CCATGCTCTTCAGCAATAATAATCACTCTCACTGACAGGAACATCAGAAGCTCTGCAG 1555

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DB 1736 ACTACTGCATCCAAAGGAGAAGATTTGCCAAGTTATAGTACAAAAATTTGAAAGATAAC 1795
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RESULT 11
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DEFINITION Sequence 3 from patent US 6426221.
ACCESSION AR221453
VERSION AR221453.1 GI:23328503
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2501)
AUTHORS Ward,D.T. and Cowsett,L.M.
TITLE Patent: US 6426221-A 3 30-JUL-2002;
JOURNAL Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 8.52e-104 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x AR221453 (1-2501)

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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1221 CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCCCTCAGCTCCAT 1280

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
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QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
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QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIlysrThrThr 104
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LOCUS
DEFINITION Sequence 13 from Patent EP1201765.
ACCESSION AX429236
VERSION AX429236.1 GI:21540548
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SOURCE
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synthetic construct
synthetic construct
artificial sequences.
REFERENCE
AUTHORS Schubart,D., Habenberger,P., Stein-Cerlach,M. and Bevec,D.
TITLE Cellular kinases involved in cytomegalovirus infection and their inhibition
JOURNAL Patent: EP 1201765-A 13 02-MAY-2002;
Axixma Pharmaceuticals Aktiengesellschaft (DE)
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Location/Qualifiers
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LOCUS
DEFINITION Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
ACCESSION AF027706
VERSION AF027706.1 GI:3123886
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
TITLE RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis
JOURNAL J. Biol. Chem. 273 (20), 12296-12300 (1998)
MEDLINE 98241596
PUBMED 9575181
REFERENCE
AUTHORS Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor, MI 48109, USA
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Alignment Scores:
Pred. No.: 8,52e-104 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 9 Gaps: 0

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Db : : : : :
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ACCESSION ARI94318
VERSION ARI94318.1 GI:20240910
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2502)
AUTHORS Nunez, G., Inohara, N. and Koseki, T.
TITLE Compositions and methods for identifying apoptosis signaling
pathway inhibitors and activators
JOURNAL Patent: US 6348573-A 2 19-FEB-2002;
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DEFINITION Homo sapiens clone DNA43305 RIPK2 (UNQ277) mRNA, complete cds.
ACCESSION AY358814
VERSION AY358814.1 GI:37182745
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2521)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J.S., Grimaldi,C., Gu,Q., Hass,P.E.,
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Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 2521)
AUTHORS Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Pred. No.: 8 61e-104 Length: 2521  
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Percent Similarity: 100.00% Conservative: 1  
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US-09-771-161A-93 (1-232) x AY358814 (1-2521)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: April 1, 2004, 06:43:21 ; Search time 473 Seconds  
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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9: geneseqn2003cs:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1182	98.0	2501	6 AAD45172	Aad45172 Human rec
6	1182	98.0	2502	3 AAZ48762	Aaz48762 Human RIC
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8	1176	97.5	1620	7 ABX75870	Abx75870 Human Cas

9	1176	97.5	1931	2 AAZ09246	Aaz09246 Human CAR
10	1176	97.5	1931	4 AAF30001	Aaf30001 Human CAR
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15	1149	95.3	1619	6 AAL40753	Aal40753 DNA of hu
16	1027	85.2	1959	9 ADC99131	Adc99131 Human KPP
17	650	53.9	491	8 ACH33353	Ach33353 Human end
18	436	36.2	762	7 ACD96414	Acd96414 Human col
19	417.5	34.6	575	4 AAK93010	Aak93010 Human cDN
20	125	10.4	1400	2 AAZ09250	Aaz09250 Human CAR
21	125	10.4	1400	4 AAF30005	Aaf30005 Human CAR
22	125	10.4	1400	6 ABK89283	Abk89283 Human cDN
23	125	10.4	1400	6 AAL40763	Aal40763 cDNA of h
24	125	10.4	1400	7 ABX75880	Abx75880 Human cDN
25	125	10.4	1400	8 ABT44225	Abt44225 Human nuc
26	125	10.4	3382	4 AAF30002	Aaf30002 Human CAR
27	125	10.4	3382	6 ABK89281	Abk89281 Human cDN
28	125	10.4	3382	6 AAL40754	Aal40754 cDNA of h
29	125	10.4	3382	7 ABX75871	Abx75871 Human cDN
30	125	10.4	4302	2 AAZ09249	Aaz09249 Human CAR
31	125	10.4	4302	4 AAF30004	Aaf30004 Human CAR
32	125	10.4	4302	6 ABK89282	Abk89282 Human cDN
33	125	10.4	4302	6 AAL40762	Aal40762 cDNA of h
34	125	10.4	4302	7 ABX75879	Abx75879 Human cDN
35	125	10.4	4302	8 ABT44224	Abt44224 Human nuc
36	125	10.4	4390	8 ABT44133	Abt44133 DNA of th
37	125	10.4	4415	3 AAA95791	Aaa95791 Apoptosis
38	125	10.4	4570	4 AAK51622	Aak51622 Human pol
39	125	10.4	4610	4 AHI18313	Ahi18313 Human cDN
40	125	10.4	4610	8 ABT44141	Abt44141 Human nuc
41	125	10.4	5250	4 AAK52606	Aak52606 Human pol
42	122.5	10.2	2859	6 AAL40755	Aal40755 DNA of hu
43	122.5	10.2	2859	7 ABX75872	Abx75872 Human Cas
44	122.5	10.2	3789	3 AAA95798	Aaa95798 Apoptosis
45	122.5	10.2	3893	4 AAH34994	Aah34994 Human col

ALIGNMENTS

RESULT 1  
AAZ46143  
ID AAZ46143 standard; cDNA; 2024 BP.  
XX  
AC AAZ46143;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE cDNA sequence encoding a human phosphorylation effector PHSP-6.  
XX  
KW Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 203..1825  
FT /tag= a  
FT /product= "phosphorylation effector"

PN WO200006728-A2.  
XX  
PD 10-FEB-2000.  
XX

XX 28-JUL-1999; 99WO-US017132.  
PF  
XX 28-JUL-1998; 98US-0155213P.  
PR  
XX 14-SEP-1998; 98US-0155196P.  
PR  
XX 14-OCT-1998; 98US-0155239P.  
PR  
XX 03-NOV-1998; 98US-0106889P.  
PR  
XX 19-NOV-1998; 98US-0109093P.  
PR  
XX 22-DEC-1998; 98US-0113796P.  
PR

PR	12-JAN-1999;	99US-0155233P.	
XX	(INCY-)	INCYTE PHARM INC.	
PA	Hillman JL,	Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;	
XX	Patterson C,	Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;	
PI	Reddy R,	Lu DAM, Shih LJ;	
PI	WPI;	2000-183125/16.	
XX	P-PSDB;	AAV68774.	
DR	New human phosphorylation effectors useful for the diagnosis, treatment		
DR	and prevention of proliferative, immune and neuronal disorders.		
XX	Claim 9;	Page 121-122; 142pp; English.	
PS	AAZ46138-246168	encode human phosphorylation effectors (PHSP), designated	
XX	PHSP1-PHSP31	(the protein sequence for PHSP28 is not given in the	
CC	specification). The sequences were isolated from cDNA libraries prepared		
CC	from various human tissues. The PHSP proteins are useful for the		
CC	diagnosis, treatment and prevention of proliferative disorders, immune		
CC	disorders and neuronal disorders. The PHSP proteins form pharmaceutical		
CC	compositions which useful for treating or preventing disorders associated		
CC	with decreased PHSP expression/activity. PHSP antagonists are useful for		
CC	treating or preventing disorders associated with increased PHSP		
CC	expression/activity		
XX	Sequence 2024 BP; 612 A; 445 C; 434 G; 533 T; 0 U; 0 Other;		
SQ			
Alignment Scores:			
Pred. No.:	1.79e-108	Length:	2024
Score:	1182.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	98.01%	Indels:	0
DB:	3	Gaps:	0
US-09-771-161a-93 (1-232) x AAZ46143 (1-2024)			
QY	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	24
DB	1139	AAAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAAATTAATCT	1198
QY	25	LeuSerIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44
DB	1199	CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCAT	1258
QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
DB	1259	GAAATAGTGTTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT	1318
QY	65	LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis	84
DB	1319	TTATCTAGAAAGCTCAAGACGTGTATTTATGAAGCTGCATCATCTCTCGGAATCAC	1378
QY	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104
DB	1379	AGTTGGATAGACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACT	1438
QY	105	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1439	CCATGCTCTTACGAATAATAATCACTCTCAACTGCAGGAAACTCAGAAGCTGTGCAG	1498
QY	125	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
DB	1499	CTGTGTATAGCCAGAGTGGATCAGAGCAAAAGGAGACATTTGTGAACCAATGACA	1558
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
DB	1559	GAAGCTGCTTAACACGATCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG	1618
QY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184

1619

GACTATGAACCTTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCACACAATTA

1678

185

ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn

204

1679

ACTACTGCATCCCAAGGAGAAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC

1738

205

LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu

224

1739

AAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA

1798

225

AsnLeuLeuGlnAsnLysSerMet

232

1799

AATTTACTTCAAAATAAAAGCATG

1822

RESULT 2

AAK94554

ID

AAK94554

standard; cDNA; 2033 BP.

AC

AAK94554;

DT

06-NOV-2001

(first entry)

XX

Human full-length cDNA, SEQ ID NO: 3453.

DE

Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

KW

Human sapiens.

OS

Homo sapiens.

PN

EP1130094-A2.

XX

05-SEP-2001.

XX

07-JUL-2000; 2000EP-00114089.

PF

08-JUL-1999; 99JP-00194486.

XX

11-JAN-2000; 2000JP-00118774.

PR

02-MAY-2000; 2000JP-00183765.

PR

(HELI-) HELIX RES INST.

XX

Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI

Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

WPI; 2001-524255/58.

DR

P-PSDB; AAM93621.

XX

830 Primers useful for synthesizing full length cDNA clones and their use

DR

in genetic manipulation.

PT

Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.

PS

The invention relates to primers for synthesising full length cDNA

XX

clones. 830 cDNA molecules encoding a human protein have been isolated

CC

and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have

CC

been determined. Primers for synthesising the full length cDNA are useful

CC

for clarifying the function of the protein encoded by the cDNA. The full

CC

length clones were obtained by construction of full length enriched cDNA

CC

libraries that were synthesised by the oligo-capping method. The primers

CC

enable the production of the full length cDNA easily without any special

CC

methods. The present sequence is a full length human cDNA of the

CC

invention. Note: The sequence data for this patent did not form part of

CC

the printed specification, but was obtained in CD-ROM format directly

CC

from EPO

XX

Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

1.8e-108

1182.00

100.00%

99.56%

98.01%

4

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

2033

227

1

0

0

4



```
US-09-771-161A-93 (1-232) x AAX94554 (1-2033)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1155 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAAGAAATGAATATCT 1214
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
Db 1215 CTGAACATACCTGTAAATCATGTGCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1274
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1275 GAAATAGTGGTTCCTGGAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1334
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1335 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCCTCTCGGAATACAC 1394
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisThrThr 104
Db 1395 AGTTGGGATAGACCACTTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 1454
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1455 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCCAGGAACCTCAGAACGCTCTGCAG 1514
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1515 CTGGTATAGCCAGCAGTGGATCCAGACCAAAAGGGAAGACATTTGTGAACCAATGACA 1574
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164
Db 1575 GAAGCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 1634
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1635 GACTATGAACCTTGTAGTACCAGGCTCAAGAGACCTCAAAAGTCAGACAAATTACTAGAC 1694
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1695 ACTACTGACATCCAGGAGAGAAATTTGCTAAGTTATAGTACAAAATTTGAAGATAAC 1754
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1755 AAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTCTAGATCACCATCTTTA 1814
QY 225 AsnLeuGlnAsnLysSerMet 232
Db 1815 AATTACTTCAAAATAAAAGCATG 1838

RESULT 3
AAX02558
ID AAX02558 standard; cDNA; 2098 BP.
XX AC AAX02558;
XX DT 07-MAY-1999 (first entry)
XX DE Human B1 cDNA.
XX KW B1 protein; intracellular mediator; modulator; inflammation; cell death;
XX KW cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
XX OS Homo sapiens.
XX PN WO9855507-A2.
XX PD 10-DEC-1998.
XX PF 01-JUN-1998; 98WO-IL000255.
XX PR 05-JUN-1997; 97IL-00121011.

PR 30-JUN-1997; 97IL-00121199.
PR 11-SEP-1997; 97IL-00121746.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Wallach D, Boldin M, Malinin N;
XX WPI; 1999-070258/06.
XX P-PSDB; AAW92795.
PT New B1 protein regulates cell death and cell survival pathways -
PT derivatives, DNA and antibodies, also regulate intracellular inflammation
PT ; for treating AIDS, cancer.
XX Claim 4; Fig 3B; 90pp; English.
XX This invention describes the isolation of a novel human B1 protein which
CC can interact with, intracellular mediators or modulators of inflammation,
CC cell death and/or cell survival pathways, directly or indirectly. Cells
CC can be modulated or mediated in inflammation, cell death or cell survival
CC pathways or another intracellular signalling activity using B1.
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,
CC oligonucleotides and ribozymes can also be used to regulate the above
CC pathways
XX Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;

Alignment Scores:
Pred. No.: 1,898-108 Length: 2098
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 2 Gaps: 0

US-09-771-161A-93 (1-232) x AAX02558 (1-2098)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1196 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAAGAAATGAATATCT 1255
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
Db 1256 CTGAACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1315
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1316 GAAATAGTGGTTCCTCTGAAACCTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1375
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 1376 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTGTCTCGAAATCAC 1435
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisThrThr 104
Db 1436 AGTTGGGATAGACCACTTTCTGGATCTCAAGGGCTGCATCTCTGTGATCACAAGACCACT 1495
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1496 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCGAGGAATCTCAGAACTCTGCAG 1555
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1556 CTGGTATAGCCAGCAGTGGATCCAGACAAAAGGGAAGACATTTGTGAACCAATGACA 1615
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164
Db 1616 GAAGCTGCTTAAACCAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG 1675
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1676 GACTATGAACCTTGTAGTACCAGGCTCAAGAGACCTCAAAAGTCAGACAAATTACTAGAC 1735
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QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 Db 1736 ACTACTGACATCCAGAGAGAGAAATTTGCCAAGTTATAGTACAAATAATGGAAGTAAAC 1795  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 Db 1796 AAACAAATGGTCTTCAGCCTTACCGGAATACTTGTGGTCTTAGATCACCATCTTTA 1855  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1856 AATTACTTCAAAATAAAGCATG 1879  
 RESULT 4  
 ABK51169  
 ID ABK51169 standard; cDNA; 2501 BP.  
 AC ABK51169;  
 DT 30-JUL-2002 (first entry)  
 DE cDNA encoding human cellular kinase RICK protein.  
 XX Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;  
 KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human cellular kinase RICK"  
 PN EPI201765-A2.  
 XX 02-MAY-2002.  
 XX 15-OCT-2001; 2001EP-00124604.  
 XX 16-OCT-2000; 2000US-0240750P.  
 XX (AXXI-) AXXIMA PHARM AG.  
 XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;  
 XX WPI; 2002-373930/41.  
 DR P-PSDB; AAU80369.  
 XX Identifying agents for treatment or prevention of cytomegalovirus  
 PT infection, comprises contacting test compound with cellular kinase and  
 PT detecting change in cellular kinase activity.  
 XX Disclosure; Page 20-23; 49pp; English.  
 XX The present invention relates to a new method for identifying compounds  
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or  
 CC related diseases. The method of the invention comprises contacting a test  
 CC compound with at least one of the cellular kinases RICK, RIP, Nck-  
 CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase  
 CC activity. The method of the invention can be used to treat and/or prevent  
 CC CMV infections and related diseases. Oligonucleotides that can detect the  
 CC specified kinases can also be used for diagnosis of infection. The  
 CC present nucleic acid sequence encodes the human cellular kinase RICK  
 CC protein of the invention, as described above  
 XX Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2.41e-108 Length: 2501  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 98.01% Indels: 0  
 DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x ABK51169 (1-2501)  
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
 Db 1161 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAATGAATTAICT 1220  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 Db 1221 CTGAACATACCTGTAATCATGTCTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1280  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 Db 1281 GAAATAAGTGGTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1340  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 Db 1341 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTCTCTGGAAATCAC 1400  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 Db 1401 AGTTGGATAGCACCATTTCTGTTCTCAAAGGGTGCATTCTGTGATCACAAGACCACT 1460  
 QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 Db 1461 CCATGCTCTTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACCTCAGAACGTCTGCAG 1520  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 Db 1521 CTGGTATAGCCAGCAGTGGATCCAGACCAAAAGGAAGACATTTGTGAACCAATGACA 1580  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 Db 1581 GAAGCTGCTTAAACCAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAG 1640  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 Db 1641 GACTATGAATCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTTACTAGAC 1700  
 QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 Db 1701 ACTACTGACATCCAGGAGAAGAAATTTGCCAAGTTATAGTACAAATAATGGAAGTAAAC 1760  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 Db 1761 AAACAAATGGTCTTTCAGCCTTACCGGAATACTTGTGGTCTTAGATCACCATCTTTA 1820  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1821 AATTACTTCAAAATAAAGCATG 1844  
 RESULT 5  
 AAD45172  
 ID AAD45172 standard; DNA; 2501 BP.  
 XX AAD45172;  
 AC AAD45172;  
 DT 27-DEC-2002 (first entry)  
 XX Human receptor interacting protein (RIP) 2 DNA.  
 DE Human; receptor interacting protein; RIP2; antisense; gene therapy; gene;  
 KW ds.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 225..1847  
 FT /\*tag= a  
 FT /product= "Human RIP2 protein"  
 XX US6426221-B1.

PD 30-JUL-2002.  
XX  
PF 01-AUG-2001; 2001US-00920663.  
XX  
PR 01-AUG-2001; 2001US-00920663.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ward DT, Cowser LM;  
XX WPI; 2002-673017/72.  
DR P-PSDB; AAE27882.  
XX  
XX New antisense oligonucleotide that targets regions of a nucleic acid  
PT encoding human receptor interacting protein (RIP)2, for treating diseases  
PT associated with RIP2 expression.  
XX  
XX Claim 1; Col 49-54; 35pp; English.  
PS  
CC The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding human receptor interacting protein (RIP)2 to inhibit its  
CC expression. Antisense compounds are used for treating diseases associated  
CC with RIP2 expression. They are also useful in antisense gene therapy. The  
CC present sequence is human RIP2 DNA  
XX  
SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 2, 41e-108 Length: 2501  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 6 Gaps: 0  
US-09-771-161A-93 (1-232) x AAD45172 (1-2501)  
QY 5 GlnLeuGlnSerValSerSerAlaLeuHisLeuCysAspLysLysMetGluLeuSer 24  
DB 1161 AAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 1220  
QY 25 LeuAenIleProValAenHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
DB 1221 CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCCCTCAGCTCCAT 1280  
QY 45 GluAenSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
DB 1281 GAAATAGTGTTCCTCAAGTGCATTCACCTGCTCCAGCTCCCTCAAGACATGATTTT 1340  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAenHis 84  
DB 1341 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCTCGAATATCAC 1400  
QY 85 SerTrpAspSerThrIleSerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
DB 1401 AGTTGGATAGCACCATTCTGTTCTCAAGGGCTGCATTCGTGATCACAAGACCAT 1460  
QY 105 ProCysSerSerAlaIleAenProLeuSerThrAlaGlyAenSerGluArgLeuGln 124  
DB 1461 CCATGCTCTTCAGCAATATATCACTCTCACTGAGGAACTCAGAACTGTGAG 1520  
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAenGlnMetThr 144  
DB 1521 CCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTGTGAACCAATGACA 1580  
QY 145 GluAlaCysLeuAenGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164  
DB 1581 GAAAGCTGCTTAACAGTCGTGTAGATGCCCTTCTGTCCAGGACATGATCATGAAAGAG 1640  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
DB 1641 GACTATGAACCTTGTAGTACCAGGCTTACAGACCTCAAGACCTCAAAAGTACAACTTACTAGAC 1700

QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
DB 1701 ACTACTGCATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1760  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
DB 1761 AAACAAATGGTCTTCAGCCTTACCAGGAAATACCTTGTGTTCTAGATCACCATCTTTA 1820  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
DB 1821 AATTACTTCAAAATAAAGCATG 1844  
RESULT 6  
AAZ48762  
ID AAZ48762 standard; cDNA; 2502 BP.  
XX  
AC AAZ48762;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DE Human RICK coding sequence.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO955134-A2.  
XX  
PD 04-NOV-1999.  
XX  
PF 27-APR-1999; 99WO-US009183.  
XX  
PR 27-APR-1999; 98US-00069023.  
XX  
PA (UNMI ) UNIV MICHIGAN.  
XX  
PI Nunez G, Inohara N, Koseki T;  
XX  
XX WPI; 2000-072163/06.  
DR P-PSDB; AAY59404.  
XX  
XX Compositions for identifying apoptosis signaling pathway inhibitors  
XX useful for treating diseases.  
PT  
PT  
PS Claim 8; Fig 7b; 93pp; English.  
XX  
XX This sequence encodes the human RICK (RIP-like interacting CLARP kinase)  
XX protein of the invention. The RICK protein acts as a positive regulator  
XX of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
XX during CD95 signalling. The invention provides methods for identifying  
XX apoptosis signalling pathway inhibitors and activators, and methods and  
XX compositions for screening compounds which will modulate the interactions  
XX of the various compositions identified: ARC, RICK, and the CIDE family of  
XX activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening  
XX assays for agents, useful in the diagnosis, prognosis or treatment of  
XX disease associated with excess cell growth and dysregulation of  
XX apoptosis. Complexes containing RICK and CLARP can be used in drug  
XX screening assays to identify inhibitor molecules blocking CD95-mediated  
XX apoptosis. Overexpression of ARC in an in vitro cell system can be used  
XX to identify inhibitors of the enzymatic activity of caspase-8.  
XX Identification of ARC-like inhibitory compounds may be useful for gene  
XX therapy treatment of disease with increased cell death in muscle tissue  
XX and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
XX treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
XX ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies  
XX can be used as reagents for the preparation or affinity chromatography  
XX media, and for diagnostically measuring RICK levels. A specific inhibitor  
XX of an essential step in the biochemistry of apoptosis is needed. RICK  
XX interaction with intracellular factors such as CLARP and FADD appears to

CC be essential for apoptosis, inhibitors of RICK binding to intracellular  
CC apoptosis factors are potential drug candidates  
XX  
XX  
SQ Sequence 2502 Bp; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	2.41e-108	Length: 2502
Score:	1182.00	Matches: 227
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	99.56%	Mismatches: 0
Query Match:	98.01%	Indels: 0
DB:	3	Gaps: 0

US-09-771-161A-93 (1-232) x AAZ48762 (1-2502)

Qy	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	24
Db	1162	AAAGTTACAGAGTGTTCCTCAAGTGCATTTCACCTATGTGACAAGAAGAAAATGGAATATATCT	1221
Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44
Db	1222	CTGACACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT	1281
Qy	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
Db	1282	GAAAAATAGTGGTTCCTCTGAAACTTCCAAGGTCCCTGCAGCTCCTCACAAGCAATGATTTT	1341
Qy	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisIshLsCysProGlyVAsnHis	84
Db	1342	TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCTGGAAATCAC	1401
Qy	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	104
Db	1402	AGTTGGGATAGCACCAATTTCTGGTTCTCAAAGGGCTGCATTTCTGTGATCACAAAGACCACT	1461
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
Db	1462	CCATGCTCTTCAGCAATAAATAATCCACTCTCAACTGCAGAAACTCAGAACGTCTCGAG	1521
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1522	CCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAGACATTTGTGAACCAAAATGACA	1581
Qy	145	GluAlaCysLeuAsnGlnSerLeuAspAlaIleLeuSerArgAspLeuIleMetLysGlu	164
Db	1582	GAAGCCCTGCCCTTAACCAAGTCGCTAGATGCCCTCTGTGCCAGGGACTTGATCATGAAAGAG	1641
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1642	GACTATGAACCTGTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCACACAATTTACTAGAC	1701
Qy	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
Db	1702	ACTACTGACATCCAAAGAGAGAAGAAATTTGCCAAAGTTTAGTACAAAAAATTTGAAAGATTAAC	1761
Qy	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
Db	1762	AAACAAATGGGTCTTCAGCCCTTACCCTGGAAATATCTTGTGGTTTCTAGATCACCAATCTTTA	1821
Qy	225	AsnLeuLeuGlnAsnLysSerMet	232
Db	1822	AAATTTACTTCAAAAATAAAGCATG	1845

## RESULT 7

AAC77779

ID AAC77779 standard; cDNA; 2709 BP.

AAC77779;

DT 08-FEB-2001 (first entry)

DE Human cancer associated gene sequence SEQ ID NO:173.

XX

KW	Human; cancer associated gene; cancer antigen; detection; cancer;
KW	diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
KW	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW	antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW	dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW	vasotropic; antiporiatic; antiangiogenic; gene therapy; inflammation
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW	allergic reaction; graft versus host disease; organ rejection;
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;
KW	neurological disease; drug screening; ss.
XX	
XX	Homo sapiens.
XX	
XX	WO2000055350-A1.
PN	
XX	
XX	21-SEP-2000.
PD	
XX	
XX	08-MAR-2000; 2000WO-US005882.
PF	
XX	
XX	12-MAR-1999; 99US-0124270P.
PR	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
XX	
PI	Rosen CA, Ruben SM;
XX	
XX	WPI; 2000-587533/55.
DR	P-PSDB; AAB43570.
XX	
XX	
XX	Novel isolated nucleic acids comprising sequences encoding peptides
PT	useful for treating or diagnosing e.g. cancer.
PT	

Sequence 2709 BP: 810 A; 580 C; 540 G; 769 T; 0 U; 10 Other;

Alignment Scores:					
Pred. No.:	2,698-108	Length:	2709		
Score:	1182.00	Matches:	227		
Percent Similarity:	100.00%	Conservative:	1		
Best Local Similarity:	99.56%	Mismatches:	0		
Query Match:	98.01%	Indels:	0		
DR:	3	Gaps:	0		

US-09-771-161A-93 (1-232) x AAC77779 (1-2709)

5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
...

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44



Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGACCAAGGGAAGACATTGTGACCAATGACA 1356  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164  
 Db 1357 GAAGCTGCTTAAACCAAGTCGTAGATGCCCTTCTGCCAGGACATTGATCAAGAGAG 1416  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 Db 1417 GACTATGAATCTTGTAGTACCAAGCCTACCAAGACCTCAAAAGTCAGACAAATTACTAGAC 1476  
 QY 185 ThrThrAspLeuGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 Db 1477 ACTACTGACATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAC 1536  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
 Db 1537 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1596  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1597 AATTACTTCAAAATAAAGCATG 1620

RESULT 9  
 AAZ09246  
 ID AAZ09246 standard; cDNA; 1931 BP.

AC AAZ09246;  
 XX  
 XX  
 XX 25-OCT-1999 (first entry)  
 XX Human CARD-3 cDNA.  
 XX CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
 KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
 KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
 KW human; ds.  
 XX  
 XX Homo sapiens.

Key Location/Qualifiers  
 CDS 214..1836  
 FT /\*tag= a  
 FT /product= "CARD-3"

XX WO9940102-A1.  
 XX 12-AUG-1999.  
 XX 05-FEB-1999; 99WO-US002544.  
 XX 06-FEB-1998; 98US-00019942.  
 XX 17-JUN-1998; 98US-00039041.  
 XX 08-DEC-1998; 98US-00207359.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Bertin J;  
 XX WPI; 1999-494269/41.  
 XX P-PSDB; AAY31140.  
 XX Novel CARD-3 and CARD-4 genes and polypeptides used or treating  
 PT regulation of cellular proliferation and differentiation and cell  
 PT survival.  
 XX

Example 2; Fig 1; 181pp; English.

PS This invention describes the isolation of novel human caspase recruitment  
 XX domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
 CC murine CARD-4L protein and genes. The genes and proteins of the invention  
 CC are involved in the regulation of caspase activation. The caspase  
 CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
 CC antibodies can be used in screening assays, detection assays, predictive  
 CC medicine and therapeutic and prophylactic methods of treatment. The  
 CC methods may be used to diagnose and treat patients which are suffering  
 CC from a disorder associated with abnormal level or rate of apoptotic cell  
 CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
 CC Diseases that may be treated include cancer (particularly follicular  
 CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
 CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
 CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
 CC CARD-3 protein interacts with other cellular proteins, and so can be used  
 CC for regulation of cellular proliferation and differentiation and cell  
 CC survival. The CARD proteins may also be used to for screen drugs or  
 CC compounds which modulate their activity. The CARD-4 gene can express a  
 CC long transcript that encodes CARD-4L, a short transcript that encodes  
 CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
 CC encodes the human CARD-3 protein described in the method of the invention  
 XX  
 SQ Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6,72e-108 Length: 1931  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 0  
 Query Match: 97.51% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAZ09246 (1-1931)  
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
 Db 1150 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAAATGGAATTATCT 1209  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
 Db 1210 CTGAACATACCTGTAATATGTCCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 Db 1270 GAAATAGTGGTTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 1329  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
 Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCAC 1389  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 Db 1390 AGTTGGGATAGCACCATTCTGGATCTCAAGAGGGCTGCATTCTGTGATCAAGACCAT 1449  
 QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 Db 1450 CCATGCTCTTCAGCAATATATATCCACTCTCACTGCAGGAAACTCAGAACGCTCTGCAG 1509  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 Db 1570 GAAGCCCTGCTTAAACCAAGTCGTAGATGCCCTTCTGTCCAGGACCTGATCATGAAAGAG 1629  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184

Db 1630 GACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTACAGAAATTACTAGAC 1689  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
Db 1750 AAACAATAGGGTCTTTCAGGCTTACCGGAAATACTTGTGGTTTCTAGATCACCATTCTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 10  
AAF30001  
ID AAF30001 standard; cDNA; 1931 BP.  
XX AAF30001;  
AC AAF30001;  
DT 23-APR-2001 (first entry)  
XX Human CARD-3 cDNA.  
XX CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 214..1826  
FT CDS /\*tag= a  
FT /note= "the open reading frame is also specifically  
FT claimed in Claim 1(a)"  
XX WO200100826-A2.  
XX 04-JAN-2001.  
XX 28-JUN-2000; 2000WO-US017691.  
XX 28-JUN-1999; 99US-00340620.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Bertin J;  
XX WPI; 2001-061973/07.  
XX P-PSDB; AAB20079.  
XX Isolated intracellular proteins predicted to be involved in regulating  
PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
PT viral infections, autoimmune diseases, neurological diseases and  
PT hematological disorders.  
XX Claim 1(a); Fig 1; 208pp; English.  
XX The present sequence is that of cDNA encoding human caspase recruitment  
CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
CC database search using known CARD sequences. Plasmid pXEL17A containing  
CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
CC protein predicted to be involved in regulating caspase activation. It is  
CC useful as a modulating agent in regulating cellular processes include  
CC cell growth and cell death. Methods of diagnosing and treating patients  
CC suffering from a disorder associated with an abnormal level or rate of  
CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
CC complex, abnormal activity of the tumour necrosis factor receptor complex  
CC or abnormal activity of a caspase involve administering a compound that  
CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
CC e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.

CC Such disorders include cancer, viral infection, autoimmune disorders,  
CC neurological diseases, haematological disorders, inflammatory disorders  
CC and immune disorders. CARD nucleic acids can be used to express CARD  
CC proteins in a host cell e.g. for gene therapy applications, to detect a  
CC genetic lesion and to modulate CARD activity  
XX Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 6,72e-108 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x AAF30001 (1-1931)  
Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
Db 1150 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAAAATGGAATATATCT 1209  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 1210 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1270 GAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 1330 TTATCTAGAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCATCTGTCTCGAAATCAC 1389  
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1390 AGTTGGGATAGACCATTTCTGGATCTCAAGGGGTCTGATCTGTGATCACAAGACCATT 1449  
Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1450 CCATGCTCTTCAGCAATAATAATCACTCTCACTCAGGAACTCAGAACGTCTGCAG 1509  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
Db 1570 GAAGCTCGCTTAACCATGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1630 GACTATGAACCTTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTAATAGAC 1689  
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
Db 1750 AAACAATAGGGTCTTTCAGGCTTACCGGAAATACTTGTGGTTTCTAGATCACCATTCTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 11  
ABK89280  
ID ABK89280 standard; cDNA; 1931 BP.  
XX  
AC ABK89280;  
XX DT 21-OCT-2002 (first entry)





XX OS Homo sapiens.  
 XX US6369196-B1.  
 XX PN  
 XX PD 09-APR-2002.  
 XX PF 05-FEB-1999; 99US-00245281.  
 XX PR 06-FEB-1998; 98US-00019942.  
 XX PR 17-JUN-1998; 98US-00099041.  
 XX PR 08-DEC-1998; 98US-00207359.  
 XX XX (MILL-) MILLENNIUM PHARM INC.  
 XX PA Bertin J;  
 XX PI  
 XX DR WPI: 2002-1391988/42.  
 XX DR N-PSDB; AAO221107, AAO221108, AAO221109, AAO221110.  
 XX XX  
 XX PT Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD  
 XX PT -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's  
 XX PT disease, cancers and viral infections.  
 XX PS Example 2; Fig 1; 116pp; English.  
 XX XX  
 XX XX The invention relates to novel isolated Caspase Recruitment Domain (CARD)  
 XX CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may  
 XX CC be used to treat disorders associated with decreased CARD expression by  
 XX CC supplementing the patient's own production of CARD. Disorders associated  
 XX CC with the expression and activity of CARD include cancers (particularly  
 XX CC follicular lymphomas, carcinomas associated with mutations in p53, and  
 XX CC hormone-dependent tumours such as breast cancer, prostate cancer, and  
 XX CC ovarian cancer), autoimmune disorders (such as systemic lupus  
 XX CC erythematosus, immune-mediated glomerulonephritis), viral infections  
 XX CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),  
 XX CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,  
 XX CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal  
 XX CC muscular atrophy, and various forms of cerebellar degeneration), anaemia  
 XX CC associated with chronic disease, aplastic anaemia, chronic neutropenia,  
 XX CC and the myelodysplastic syndromes. This polynucleotide sequence  
 XX CC represents the cDNA of a human CARD relating to the invention  
 XX SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6,72e-108 Length: 1931  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 97.51% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-771-161A-93 (1-232) x AAL40752 (1-1931)  
 QY 5 GinLeuGlnSerValSerSerAlaLeuHisLeuCysAspLysLysMetGluLeuSer 24  
 DB 1150 AAGTTACAGAGTGTTCAGAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCT 1209  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
 DB 1210 CTGAACATACCTGTAAATCATGGTCACAGAGGAATCATGTGGATCCCTCTCAGTCCAT 1269  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 DB 1270 GAATATAGTGGTTCCTCTGAATCTCAAGTCCCTGCCAGCTCTCTCAAGACATGATTTT 1329  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCAGTCTCTGGAAATCAC 1389  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
 DB 1390 AGTTGGGATAGCACCAATTTCTGGATCTCAAGGGCTGATCTCTGTGATCACAGACCATT 1449  
 QY 105 ProCysSerSerAlaIleAAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 DB 1450 CCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGAGGAACTCAGAACGCTCTGCAG 1509  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 DB 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 1569  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 DB 1570 GAAGCTGCTCTTAACCACTGCTAGATGCCCTCTCTGTCAGGGACTTGATCATGAAGAG 1629  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 DB 1630 GACTATGAACCTGTTAGTACCAAGCCTACAAGGCTCAAAAGTCAAGCAATTTACTAGAC 1689  
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204  
 DB 1690 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC 1749  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
 DB 1750 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTTA 1809  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 DB 1810 AATTTACTTCAAAATAAAAGCATG 1833  
 RESULT 13  
 ABX75869  
 ID ABX75869 standard; cDNA; 1931 BP.  
 XX AC ABX75869;  
 XX DT 30-APR-2003 (first entry)  
 XX DE Human cDNA encoding Caspase recruitment domain protein, CARD-3.  
 XX KW Human; ss; gene: caspase recruitment domain; CARD: CARD-3; CARD-4;  
 KW CARD-4L; CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS;  
 KW autoimmune disorder; systemic lupus erythematosus; viral infection;  
 KW immune related glomerulonephritis; acquired immunodeficiency syndrome;  
 KW neurologic lateral sclerosis; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular atrophy; cerebellar degeneration; haematological disease;  
 KW anaemia; neutropenia; myelodysplastic syndrome; myocardial infarction;  
 KW stroke; chromosome 7.  
 XX OS Homo sapiens.  
 XX PN US6469140-B1.  
 XX PD 22-OCT-2002.  
 XX PF 08-DEC-1998; 98US-00207359;  
 XX PR 06-FEB-1998; 98US-00019942.  
 XX PR 17-JUN-1998; 98US-00099041.  
 XX XX (MILL-) MILLENNIUM PHARM INC.  
 XX PA Bertin J;  
 XX PI  
 XX DR WPI: 2003-147109/14.  
 XX DR P-PSDB; ABUS6269.  
 XX XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
 XX PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
 XX PT detection assays, predictive medicine, and in therapeutic applications.  
 XX PS Example 2; Fig 1; 99pp; English.

XX CC The invention relates to an isolated polypeptide, comprising at least 25  
CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
CC polypeptide. Also included is an isolated fusion protein, comprising the  
CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
CC polypeptide. The CARD polypeptide is useful in screening assays,  
CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
CC prophylactic treatments (in diseases associated with apoptotic cell death  
CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
CC immune related glomerulonephritis), viral infections, AIDS (acquired  
CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
CC hematological diseases (e.g. anaemia, neutropenia and myelodysplastic  
CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
CC identify other proteins, which bind to or interact with other CARD  
CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
CC human CARD-4 is located on chromosome 7. The present sequence is a human  
CC CARD cDNA

Sequence 1931 BP: 613 A: 430 C: 416 G: 472 T: 0 U: 0 Other;

Alignment Scores:	6.72e-108	Length:	1931
Pred. No.:	1176.00	Matches:	226
Score:	99.58%	Conservative:	1
Percent Similarity:	99.13%	Mismatches:	1
Best Local Similarity:	99.51%	Indels:	0
Query Match:	7	Gaps:	0
DB:			

US-09-771-161A-93 (1-232) X ABX75869 (1-1931)

Qy	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysLysMetGluLeuSer	24
Db	1150	AAGTTACAGAGTGTTCACAGTGCCATTCACTATGTGCACAGAGAAAATGGAAATTA	1209
Qy	25	LeuAsnIleProValAsnHisGlyProGlnGlnGluSerCysGlySerSerGlnLeuHis	44
Db	1210	CTGAACATACCTGTAANAATCATGGTCCACAGAGAGAAATCATGTGGATCTCTCAGTCCAT	1269
Qy	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
Db	1270	GAAATAAGTGGTTCTCTCGAAATTCACAGGTCCTGCCAGCTCCTCAAGACAATGATTTT	1329
Qy	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84
Db	1330	TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCTGGAAATCAC	1389
Qy	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThr	104
Db	1390	AGTTGGGATACACCATTTCTGGATCTCAAAGGGCTGCATTCTCTGATCACAGACCATT	1449
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
Db	1450	CCATGCTCTTCAGCAATAAATACCATCTCAACTGCAGGAAACTCAGAACGTCGAC	1509
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1510	CCTGGTATAGCCAGCAGCTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	1569
Qy	145	GluAlaCysLeuAsnGlnSerIleuAspAlaLeuSerArgAspLeuIleMetLysGlu	164
Db	1570	GAAGCCTGCCTTAAACACGTCGTAGATGCCCTTCTGTCCAGGCACTTGATCATGAAAGAG	1629
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1630	GACTATGAACCTGTGTAGTACCAAGCCTCAAGGACCCTCAAAGGTGAGCAATTAATCTAGAC	1689
Qy	185	ThrThrAspIleGlnGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204

CC the binding of a polypeptide containing the CARD domain of CARD-3 to a  
 CC polypeptide comprising the death domain of p75 in the presence and  
 CC absence of the test compound, and determining if binding is altered. This  
 CC polynucleotide is the human CARD-3 cDNA sequence of the invention.

SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6,72e-108 Length: 1931  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 97.51% Indels: 0  
 DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x ADB81363 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLeuMetGluLeuSer 24  
 DB 1150 AAGTTACAGAGTGTTCAGATGCCATTACCTATGTGACAAAGAAATGGAATTATCT 1209  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 DB 1210 CTGAACATACCTGTAATCATGCTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 DB 1270 GAAATAGTGGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 DB 1330 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCTCTCTGGAATCAC 1389  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 DB 1390 AGTTGGATAGACCATCTTCGATCTCAAGGGCTGCACTTCTGTATCACAAAGACCAT 1449  
 QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCAG 1509  
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 DB 1510 CTTGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGTGAACCAATGACA 1569  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 DB 1570 GAAAGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 DB 1630 GACTATGAATCTGTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTAATCTAGAC 1689  
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 DB 1690 ACTACTGACATCCAAAGGAGAAATTTGCAAGATTTATAGTCAAAATTTGAAAGATATAC 1749  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 DB 1750 AAACAATGGGTCTTCAGCTTACCCTCGGAAATACTTGTGGTTTCTAGATCACCATCTTTA 1809  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 DB 1810 AATTTACTTCAAAATAAAGCATG 1833

## RESULT 15

AAAL40753

ID: AAL40753 standard; DNA; 1619 BP.

XX AC

XX AAL40753;

XX 27-SEP-2002 (first entry)

XX

DE DNA of human CARD-3 SEQ ID No 3.

KW Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's;  
 KW cerebroprotective; antiparkinsonian; antischlerotic; ophthalmological;  
 KW neotropic; antianaemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;  
 KW cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;  
 KW hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;  
 KW systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;  
 KW anaemia; neutropenia; myelodysplastic syndrome; human; ds.

OS Homo sapiens.

XX US6369196-B1.

XX 09-APR-2002.

XX 05-FEB-1999; 99US-00245281.

XX 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

PR 08-DEC-1998; 98US-00207359.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2002-391988/42.

DR N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.

XX Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD

PT -4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's

PT disease, cancers and viral infections.

XX Disclosure; Col 75-78; 116pp; English.

XX The invention relates to novel isolated Caspase Recruitment Domain (CARD)

CC polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may

CC be used to treat disorders associated with decreased CARD expression by

CC supplementing the patient's own production of CARD. Disorders associated

CC with the expression and activity of CARD include cancers (particularly

CC follicular lymphomas, carcinomas associated with mutations in p53, and

CC hormone-dependent tumours such as breast cancer, prostate cancer, and

CC ovarian cancer), autoimmune disorders (such as systemic lupus

CC erythematosus, immune-mediated glomerulonephritis), viral infections

CC (such as those caused by herpes viruses, poxviruses, and adenoviruses),

CC neurological diseases (such as Alzheimer's disease, Parkinson's disease,

CC amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal

CC muscular atrophy, and various forms of cerebellar degeneration), anaemia

CC associated with chronic disease, aplastic anaemia, chronic neutropenia,

CC and the myelodysplastic syndromes. This polynucleotide sequence

CC represents the DNA of a human CARD relating to the invention

XX SQ Sequence 1619 BP; 516 A; 360 C; 320 G; 423 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.69e-105 Length: 1619

Score: 1149.00 Matches: 225

Percent Similarity: 99.12% Conservative: 1

Best Local Similarity: 98.68% Mismatches: 2

Query Match: 95.27% Indels: 1

DB: 6 Gaps: 0

US-09-771-161A-93 (1-232) x AAL40753 (1-1619)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLeuMetGluLeuSer 24

DB 937 AAGTTACAGAGTGTTCAGATGCCATTACCTATGTGACAAAGAAATGGAATTATCT 996

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44

DB 997 CTGAACATACCTGTAATCATGCTCCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

Thu Apr 1 15:53:03 2004

us-09-771-161a-93.p2n.rng

Db	1057	GAATAAGTGGTTCTCTCTGAAGTTCAGGTCCTGCCAGCTCCTCAGACAAATGATTTT	1116
Qy	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84
Db	1117	TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTCATCACTGCTCTGGAATCAC	1176
Qy	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	104
Db	1177	AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATTCCTGTGATCACAAGACCATT	1236
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
Db	1237	CCATGCTCTTCAGCAATATATATCACTCTCACTGCAGGAACCTCAGAACGTCGTGCAG	1296
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1297	CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	1356
Qy	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
Db	1357	GAAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG	1416
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1417	GACTATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAAATTACTAGAC	1476
Qy	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
Db	1477	ACTACTGACATCCCAAGGAGAAGATTTCCTCAAGTTATAGTACAAAATTTGAAGATAAC	1536
Qy	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
Db	1537	AAACAAATGGGTCTTCAGCCTTACCCGGAATA-CTTGTGGTTTCTAGATCACCATCTTTA	1595
Qy	225	AsnLeuLeuGlnAsnLysSerMet	232
Db	1596	AATTTACTTCAAAATAAAAGCATG	1619

Search completed: April 1, 2004, 10:15:08  
Job time : 487 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 09:56:07 ; Search time 105 Seconds  
(without alignments)  
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Post-processing: Minimum Match 0%  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182	98.0	2501	4	US-09-920-663-3
2	1182	98.0	2502	4	US-09-069-023-2
3	1176	97.5	1620	4	US-09-099-041A-3
4	1176	97.5	1620	4	US-09-245-281-3
5	1176	97.5	1620	4	US-09-207-359B-3
6	1176	97.5	1620	4	US-09-340-620A-3
7	1176	97.5	1620	4	US-09-865-364-3
8	1176	97.5	1931	3	US-09-019-942-2
9	1176	97.5	1931	4	US-09-099-041A-1
10	1176	97.5	1931	4	US-09-245-281-1
11	1176	97.5	1931	4	US-09-470-271-2
12	1176	97.5	1931	4	US-09-207-359B-1

13	1176	97.5	1931	4	US-09-340-620A-1	Sequence 1, Appli
14	1176	97.5	1931	4	US-09-865-364-1	Sequence 1, Appli
15	1176	97.5	1931	4	US-09-748-537-2	Sequence 2, Appli
16	1165	96.6	1060	4	US-09-023-655-684	Sequence 684, Appl
17	125	10.4	1400	4	US-09-245-281-40	Sequence 40, Appl
18	125	10.4	1400	4	US-09-207-359B-40	Sequence 40, Appl
19	125	10.4	1400	4	US-09-340-620A-40	Sequence 40, Appl
20	125	10.4	1400	4	US-09-865-364-40	Sequence 40, Appl
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22	125	10.4	3382	4	US-09-245-281-7	Sequence 7, Appli
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25	125	10.4	3382	4	US-09-865-364-7	Sequence 7, Appli
26	125	10.4	4302	4	US-09-245-281-38	Sequence 38, Appl
27	125	10.4	4302	4	US-09-207-359B-38	Sequence 38, Appl
28	125	10.4	4302	4	US-09-340-620A-38	Sequence 38, Appl
29	125	10.4	4302	4	US-09-865-364-38	Sequence 38, Appl
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35	104.5	8.7	626	3	US-09-019-942-4	Sequence 4, Appli
36	104.5	8.7	626	4	US-09-470-271-4	Sequence 4, Appli
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38	104.5	8.7	1470	4	US-09-099-041A-27	Sequence 27, Appl
39	104.5	8.7	1470	4	US-09-245-281-27	Sequence 27, Appl
40	104.5	8.7	1470	4	US-09-207-359B-27	Sequence 27, Appl
41	104.5	8.7	1470	4	US-09-340-620A-27	Sequence 27, Appl
42	104.5	8.7	1470	4	US-09-865-364-27	Sequence 27, Appl
43	104.5	8.7	3080	4	US-09-099-041A-25	Sequence 25, Appl
44	104.5	8.7	3080	4	US-09-245-281-25	Sequence 25, Appl
45	104.5	8.7	3080	4	US-09-207-359B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Alignment Scores:			
Pred. No.:	3,11e-134	Length:	2501
Score:	1182.00	Matches:	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	98.01%	Indels:	0
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US-09-771-161A-93 (1-232) x US-09-920-663-3 (1-2501)

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Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44

Db 1221 CTGAACATACCTGTTAAATCATGTCACCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1280  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
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QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1641 GACTATGAACCTGTTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAAGACAAATTAAGTAC 1700  
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1701 ACTACTGACATCCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1760  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
Db 1761 AAACAATGGGCTCTCAGCCTTACCGGAAATACTTTGTGGTTCTAGATCACCATCTTTA 1820  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1821 AATTACTTCAAAATAAAAGCATG 1844

RESULT 2  
US-09-069-023-2  
; Sequence 2, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Nachiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-2  
Alignment Scores:  
Pred. No.: 3,12e-134 Length: 2502  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161a-93 (1-232) x US-09-069-023-2 (1-2502)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
Db 1162 AAGTTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 1221  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 1222 CTGAACATACCTGTTAAATCATGTCACCAAGAGGAATCATGTGGATCCTCTCAGTCCAT 1281  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1282 GAAAAATAGTGGTTCTCTGAACTTCAAGGTTCCTGCCAGCTCCTCAAGACAAATGATTTT 1341  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 1342 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCTGGAATAC 1401  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1402 AGTTGGGATAGCACCATTCTGTTCTCAAGAGGCTGCATCTCTGTGATCACAAGACCAT 1461  
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1462 CCATGCTCTTCAGCAATATAATCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1521  
QY 125 ProGlyIleAlaGlnIntrPileGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1522 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAAAATGACA 1581  
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1582 GAAGCCGCTCTTACCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 1641  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1642 GACTATGAACCTGTTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAAGACAAATTAAGTAC 1701  
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1702 ACTACTGACATCCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1761  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
Db 1762 AAACAATGGGCTCTCAGCCTTACCGGAAATACTTTGTGGTTCTAGATCACCATCTTTA 1821  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1822 AATTACTTCAAAATAAAAGCATG 1845

RESULT 3  
US-09-099-041A-3  
; Sequence 3, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-099-041A-3  
Alignment Scores:  
Pred. No.: 8,39e-134 Length: 1620  
Score: 1176.00 Matches: 226



FILE REFERENCE: 07334-112001  
CURRENT APPLICATION NUMBER: US/09/207,359B  
CURRENT FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 1620  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-207-359B-3

Alignment Scores:  
Pred. No.: 8.39e-134 Length: 1620  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
Gaps: 4

US-09-771-161A-93 (1-232) x US-09-207-359B-3 (1-1620)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
Db 937 AAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 996

Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 997 CTGAACATACCTGAATCATGCTCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056

Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 64  
Db 1057 GAAATAGTGTTCCTCTGAACTTCAAGTCCCTGCGAGCTCTCTCAAGCAATGATTTT 1116

Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db 1117 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCATCTCTCTGGAATCAC 1176

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
Db 1177 AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCAAGACCAT 1236

Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGAG 1296

Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1297 CCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1357 GAAGCCTGCTTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1416

Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1417 GACTATGAACCTGTGTAGTACCAGGCTTCAAGGACTCAAAAGTCAGACATTTACTAGAC 1476

Qy 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1477 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC 1536

Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
Db 1537 AAACAAATGGGTCTTCAGGCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATCTTTA 1596

Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1597 AATTTACTTCAAAATAAAGCATG 1620

RESULT 6  
US-09-340-620A-3  
Sequence 3, Application US/09340620A  
Patent No. 6482933  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-124001  
CURRENT APPLICATION NUMBER: US/09/340,620A  
CURRENT FILING DATE: 1999-06-28  
PRIOR APPLICATION NUMBER: US 09/245,281  
PRIOR FILING DATE: 1999-02-05  
PRIOR APPLICATION NUMBER: US 09/207,359  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: US 09/099,041  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: US 09/019,942  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 1620  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-340-620A-3

Alignment Scores:  
Pred. No.: 8.39e-134 Length: 1620  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 0  
Query Match: 97.51% Indels: 0  
Gaps: 4

US-09-771-161A-93 (1-232) x US-09-340-620A-3 (1-1620)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
Db 937 AAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATATCT 996

Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 997 CTGAACATACCTGTAATCATGCTCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056

Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 64  
Db 1057 GAAATAGTGTTCCTCTGAACTTCAAGTCCCTGCGAGCTCTCTCAAGCAATGATTTT 1116

Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db 1117 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCATCTCTCTGGAATCAC 1176

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104  
Db 1177 AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCAAGACCAT 1236

Qy 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGAG 1296

Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1297 CCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1357 GAAGCCTGCTTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1416

Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1417 GACTATGAACCTGTGTAGTACCAGGCTTCAAGGACTCAAAAGTCAGACATTTACTAGAC 1476

Qy 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204



Db 1477 ACTACTGACATCAGAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTGAAAGATAAC 1536  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGTCTTAGATCACCACATCTTTA 1596  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1597 AATTACTTCAAAATAAAGCATG 1620  
RESULT 7  
US-09-865-364-3  
; Sequence 3, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/865,364  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-865-364-3  
Alignment Scores:  
Pred. No.: 8,39e-134 Length: 1620  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-865-364-3 (1-1620)  
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24  
Db 937 AAGTTACAGAGTGTTCAGTCCCATTCACCTATGTGACAGAGAGAAATGGAATTAICT 996  
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 997 CTGAACATACCTGTAATCATGTCTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056  
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 1057 GAAATAGTAGGTCTCTCCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTT 1116  
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db 1117 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGTCTCTGGAATATC 1176  
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 1177 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGACCATTT 1236  
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1296  
QY 125 ProGlyIleAlaGlnGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 1297 CTGGTATAGCCAGCAGGTGGATCCAGACAAAGGGAAGACATTGTGAAACCAATGACA 1356

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164  
Db 1357 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1416  
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1417 GACTATGAACCTTGTGTAGTACCAAGCCTCAAGGACTCAAAAGTCAGACATTTACTAGAC 1476  
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
Db 1477 ACTACTGACATCCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATTGAAAGATAAC 1536  
QY 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACCTTGTGTCTTAGATCACCACATCTTTA 1596  
QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1597 AATTACTTCAAAATAAAGCATG 1620  
RESULT 8  
US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-019-942-2  
Alignment Scores:  
Pred. No.: 1.11e-133 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 97.51% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db	1150 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db	1210 CTGAACATACCTGTAATCATGTGTCACAAAGAGGATCATGTGGATCCTCTCAGCTCCAT 1269
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db	1270 GAAATAGTGGTTCCTCTGAAATTCAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	1330 TTATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTGCTCTGGAATCAG 1389
QY	85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db	1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	1450 CCATGCTCTTACCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 1509
QY	125 ProGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	1510 CCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGAGAGACATTGTGAACCAATGACA 1569
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	1570 GAAGCTGCTTAAACCAGTCGTAGATGCCCTTCTGTCAGGGACTTGTATCATGAAGAG 1629
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	1630 GACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAGACAATTACTAGAC 1689
QY	185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
Db	1690 ACTACTGACATCCACGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY	205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db	1750 AAACAAATGGTCTTCAGCCTTACCAGGAAATCTTGTGGTTCTAGATCACCATCTTTA 1809
QY	225 AsnLeuLeuGlnAsnLysSerMet 232
Db	1810 AATTTACTTCAAAATAAAGCATG 1833
RESULT 10	
US-09-245-281-1	
; Sequence 1, Application US/09245281	
; Patent No. 6369196	
; GENERAL INFORMATION:	
; APPLICANT: Bertin, John	
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY	
; TITLE OF INVENTION: AND USES THEREOF	
; FILE REFERENCE: 07334/118001	
; CURRENT APPLICATION NUMBER: US/09/245,281	
; CURRENT FILING DATE: 1998-02-05	
; EARLIER APPLICATION NUMBER: US 09/207,359	
; EARLIER FILING DATE: 1998-12-08	
; EARLIER APPLICATION NUMBER: US 09/099,041	

US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db	1150 AAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db	1210 CTGAACATACCTGTAATCATGTGTCACAAAGAGGATCATGTGGATCCTCTCAGCTCCAT 1269
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db	1270 GAAATAGTGGTTCCTCTGAAATTCAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	1330 TTATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCTGCTCTGGAATCAG 1389
QY	85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db	1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1449
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	1450 CCATGCTCTTACCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 1509
QY	125 ProGlyIleAlaGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	1510 CCTGGTATAGCCAGCAGTGGATCCAGCAAAAGGAGAGACATTGTGAACCAATGACA 1569
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	1570 GAAGCTGCTTAAACCAGTCGTAGATGCCCTTCTGTCAGGGACTTGTATCATGAAGAG 1629
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	1630 GACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTCAGACAATTACTAGAC 1689
QY	185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysAspAsn 204
Db	1690 ACTACTGACATCCACGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY	205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db	1750 AAACAAATGGTCTTCAGCCTTACCAGGAAATCTTGTGGTTCTAGATCACCATCTTTA 1809
QY	225 AsnLeuLeuGlnAsnLysSerMet 232
Db	1810 AATTTACTTCAAAATAAAGCATG 1833
RESULT 9	
US-09-099-041A-1	
; Sequence 1, Application US/09099041A	
; Patent No. 6340576	
; GENERAL INFORMATION:	
; APPLICANT: Bertin, John	
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED	
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF	
; FILE REFERENCE: 07334-076001	
; CURRENT APPLICATION NUMBER: US/09/099,041A	
; CURRENT FILING DATE: 1998-06-17	
; PRIOR APPLICATION NUMBER: 09/019,942	
; PRIOR FILING DATE: 1998-02-06	
; NUMBER OF SEQ ID NOS: 37	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 1	
; LENGTH: 1931	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (214)....(1833)	
; US-09-099-041A-1	

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; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-245-281-1

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-245-281-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATTATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAATAGTGGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATTATCT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTCATCAGTGTCTCGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCACAGACCATT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1510 CCTGGTATAGCCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCTGCTTTAACCAAGTCGCTAGATGCCCTTCTGTCTCAGGACCTTGATCATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTGTTAGTACCAAGCCCTACAGGACCTCAAAAGTCAGACAATTAAGTACAG 1689
QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGGCTTACCAGGAATATCTTGTGGTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATTAAGCATG 1833

RESULT 11
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US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-470-271-2 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATTATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAATAGTGGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATTATCT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTCATCAGTGTCTCGAATATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCACAGACCATT 1449
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105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
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125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
1510 CTTGGTATAGCCAGCAGTGGATCCAGACCAAAAGGAGACATTTGTGAACCAATGACA 1569  
145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
1570 GAAGCTGCTTAACACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629  
165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
1630 GACTATGAACCTTGTATGACCAAGCTTACAGGACCTCAAAAGTCAGACCAATTAAGAC 1689  
185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204  
1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1749  
205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
1750 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 1809  
225 AsnLeuLeuGlnAsnLysSerMet 232  
1810 AATTACTTCAAAATAAAGCATG 1833  
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US-09-207-359B-1  
; Sequence 1, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)....(1833)  
US-09-207-359B-1  
Alignment Scores:  
Pred. No.: 1,11e-133 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservativity: 1  
Best Local Similarity: 99.12% Mismatches: 0  
Query Match: 97.51% Indels: 0  
DB: 4 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-207-359B-1 (1-1931)  
5 GlnLeuGlnSerValSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuSer 24  
1150 AAGTTACAGAGTGTTCAGTGGCCATTCACCTATGTGACAGAAAGAAATGGAATTAATCT 1209  
25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
1210 CTGAACATACCTGTAATAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269  
45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

1270 GAAAAATAGTGGTCTCTCCTGAAATCTCAAGGTCCCTCCAGCTCCTCAAGACAATGATTT 1329  
65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
1330 TTATCTAGAAAAGCTCAAGACTGTATATTTATAGACTGTCATCACTCTCTGGAATCAC 1389  
85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
1390 AGTTGGGATAGCACCAATTTCTGGATCTCAAAAGGCTGCAATTTCTGTGATCAAGACCAT 1449  
105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
1450 CCATGCTCTTACGCAATAATAATCACTCTCAACTGCAGGAATCTCAGAACTGTGCAG 1509  
125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
1510 CTTGGTATAGCCAGCAGTGGATCCAGACCAAAAGGAGACATTTGTGAACCAATGACA 1569  
145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
1570 GAAGCTGCTTAACACAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1629  
165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
1630 GACTATGAACCTTGTATGACCAAGCTTACAGGACCTCAAAAGTCAGACCAATTAAGAC 1689  
185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204  
1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1749  
205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
1750 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 1809  
225 AsnLeuLeuGlnAsnLysSerMet 232  
1810 AATTACTTCAAAATAAAGCATG 1833  
RESULT 13  
US-09-340-620A-1  
; Sequence 1, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)....(1833)  
US-09-340-620A-1  
Alignment Scores:  
Pred. No.: 1,11e-133 Length: 1931  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservativity: 1  
Best Local Similarity: 99.12% Mismatches: 1

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Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
US-09-771-161A-93 (1-232) x US-09-340-620A-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLysAsp 144
DB 1510 CTGTGTATAGCCAGAGTGGATCCAGACCAAGAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1570 GAAGCTGCTGCTTAACCATGCTAGTGGCTTCTGTCCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAATGTTGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAATTTACTAGAC 1689
QY 185 ThrTrpAspIleGlnGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1690 ACTACTGACATCCAAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGCTTACCCGGAAATCTTGTGTTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
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RESULT 14
US-09-865-364-1
; Sequence 1, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214) ... (1833)
US-09-865-364-1
Alignment Scores:
Pred. No.: 1,11e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
US-09-771-161A-93 (1-232) x US-09-865-364-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCCTCGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLysAsp 144
DB 1510 CTGTGTATAGCCAGAGTGGATCCAGACCAAGAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1570 GAAGCTGCTGCTTAACCATGCTAGTGGCTTCTGTCCAGGACTTGTATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAATGTTGTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAATTTACTAGAC 1689
QY 185 ThrTrpAspIleGlnGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1690 ACTACTGACATCCAAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTCAGCTTACCCGGAAATCTTGTGTTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTTACTTCAAAATAAAAGCATG 1833

RESULT 15
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
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Job time : 117 secs

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-748-537-2

Alignment Scores:		Pred. No.:	1.11e-133	Length:	1931
Score:			1176.00	Matches:	226
Percent Similarity:			99.56%	Conservative:	1
Best Local Similarity:			99.12%	Mismatches:	1
Query Match:			97.51%	Indels:	0
DB:			4	Gaps:	0

US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)

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Qy	25	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis	44
Db	1210	CTGAACATACCTGTAAATCATGTGTCACAAAGAGGAATCATGTGGATCCTCTCAGCTCCAT	1269
Qy	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
Db	1270	GAATAATAGTGGTCTCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT	1329
Qy	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	84
Db	1330	TTATCTAGAAAGCTCAAGACTGTATTTATTTATGAGCTGCATCCTCTCTGGAAATCAC	1389
Qy	85	SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	104
Db	1390	AGTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTCCTGTGATCACAAGACCATT	1449
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
Db	1450	CCATGCTCTTCAGCAATAATAATCCACTCTCAACTCGAGGAAACTCAGAACGTCCTCAG	1509
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1510	CCTGGTATAGCCAGCAGTGTGATCCAGAGCAAAAGGGAGAGACATTTGTGAACCAATGACA	1569
Qy	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
Db	1570	GAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCTCAGGGACTTGATCATGAAAGAG	1629
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1630	GACTATGAACTTGTGTAGTACCAGCCTACAAGGACCTCAAAAGTCAGACAAATTTACTAGAC	1689
Qy	185	ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
Db	1690	ACTACTGACATCCAAAGGAGAGAATTTTGCCAAAGTTATAGTACAAAAATTGAAAGATAAC	1749
Qy	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
Db	1750	AAACAAATGGGTCTTTCAGCCTTTACCCGGAAATACCTTGTGGTTTCTAGATCACCATCTTTA	1809
Qy	225	AsnLeuLeuGlnAsnLysSerMet	232
Db	1810	AATTTACTTCAAAATAAAGCATG	1833

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 10:07:52 ; Search time 2506 Seconds  
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Maximum Match 100%

Lasting first 45 summaries

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- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1206	100.0	1669	9	US-09-771-161A-2	Sequence 2, Appli
2	1182	98.0	1623	12	US-10-342-887-957	Sequence 957, Appl
3	1182	98.0	2501	10	US-09-981-397A-13	Sequence 13, Appl
4	1182	98.0	2709	9	US-09-925-301-173	Sequence 173, Appl
5	1176	97.5	1620	9	US-09-728-721-3	Sequence 3, Appli
6	1176	97.5	1620	13	US-10-105-931-3	Sequence 3, Appli
7	1176	97.5	1620	13	US-10-118-984-3	Sequence 3, Appli
8	1176	97.5	1620	14	US-10-295-981-3	Sequence 3, Appli
9	1176	97.5	1931	9	US-09-748-537-2	Sequence 2, Appli
10	1176	97.5	1931	9	US-09-728-721-1	Sequence 1, Appli
11	1176	97.5	1931	13	US-10-133-780-2	Sequence 2, Appli
12	1176	97.5	1931	13	US-10-105-931-1	Sequence 1, Appli
13	1176	97.5	1931	13	US-10-118-984-1	Sequence 1, Appli
14	1176	97.5	1931	14	US-10-295-981-1	Sequence 1, Appli
15	650	53.9	491	10	US-09-918-995-20565	Sequence 20565, A
16	125	10.4	1400	9	US-09-728-721-40	Sequence 40, Appl
17	125	10.4	1400	13	US-10-118-984-40	Sequence 40, Appl
18	125	10.4	1400	14	US-10-006-883A-96	Sequence 96, Appl
19	125	10.4	1400	14	US-10-235-981-40	Sequence 40, Appl
20	125	10.4	3382	9	US-09-728-721-7	Sequence 7, Appli
21	125	10.4	3382	13	US-10-105-931-7	Sequence 7, Appli
22	125	10.4	3382	13	US-10-118-984-7	Sequence 7, Appli
23	125	10.4	3382	14	US-10-295-981-7	Sequence 2, Appli
24	125	10.4	4093	15	US-10-401-194-2	Sequence 38, Appl
25	125	10.4	4302	9	US-09-728-721-38	Sequence 38, Appl
26	125	10.4	4302	13	US-10-118-984-38	Sequence 95, Appl
27	125	10.4	4302	14	US-10-006-883A-95	Sequence 38, Appl
28	125	10.4	4302	14	US-10-295-981-38	Sequence 3, Appli
29	125	10.4	4390	14	US-10-006-883A-3	Sequence 3, Appli
30	125	10.4	4415	14	US-10-013-477-3	Sequence 11, Appl
31	125	10.4	4610	14	US-10-006-883A-11	Sequence 9, Appli
32	122.5	10.2	2859	9	US-09-728-721-9	Sequence 9, Appli
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35	122.5	10.2	2859	14	US-10-295-981-9	Sequence 10, Appl
36	122.5	10.2	3789	14	US-10-013-477-10	Sequence 2086, Ap
37	122.5	10.2	3893	14	US-10-106-698-2086	Sequence 13799, A
38	114	9.5	60	10	US-09-908-975-13799	Sequence 4, Appli
39	104.5	8.7	626	9	US-09-748-537-4	Sequence 4, Appli
40	104.5	8.7	626	13	US-10-133-780-4	Sequence 27, Appl
41	104.5	8.7	1470	9	US-09-728-721-27	Sequence 27, Appl
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43	104.5	8.7	1470	13	US-10-118-984-27	Sequence 27, Appl
44	104.5	8.7	1470	14	US-10-295-981-27	Sequence 25, Appl
45	104.5	8.7	3080	9	US-09-728-721-25	

ALIGNMENTS

RESULT 1  
US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -

Thu Apr 1 15:53:04 2004

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; LOCATION: (1)..(1669)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-2

Alignment Scores:
Pred. No.: 5.45e-140 Length: 1669
Score: 1206.00 Matches: 232
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 21 MetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySer 40
Db 380 ATGGAATTATCTCTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCC 439
QY 41 SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln 60
Db 440 TCTCAGCTCCATGAAATAGTGGTCTCTCTGAAATTCAGAGTCCCTGCCAGCTCCTCAA 499
QY 61 AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCys 80
Db 500 GACAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTATGAGCTGCATCACTGT 559
QY 81 ProGlnAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp 100
Db 560 CCTGGAATACATGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGAT 619
QY 101 HisLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSer 120
Db 620 CACAAGACCACTCCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCA 679
QY 121 GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleVal 140
Db 680 GAACGCTGCGAGCTGGTATAGCCAGAGTGGAATCCAGAGCAAAAGGAGACATTTGTG 739
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QY 221 SerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232
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RESULT 2
US-10-342-887-957
; Sequence 957, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
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Db 1597 AATTACTTCAAAATAAAAGCATG 1620  
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RESULT 3  
US-09-981-397A-13  
; Sequence 13, Application US/09981397A  
; Publication No. US20030082519A1  
; GENERAL INFORMATION:  
; APPLICANT: Axxima Pharmaceuticals AG  
; APPLICANT: Schubart, Daniel  
; APPLICANT: Habenberger, Peter  
; APPLICANT: Stein-Gerlach, Matthias  
; APPLICANT: Bevec, Dorian  
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
; TITLE OF INVENTION: Inhibition  
; FILE REFERENCE: AXM-004.1 US  
; CURRENT APPLICATION NUMBER: US/09/981,397A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: 60/240,750  
; PRIOR FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-397A-13  
Alignment Scores:  
Pred. No.: 9,87e-137 Length: 2501  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 10 Gaps: 0  
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QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
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QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
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QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
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QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
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; Sequence 173, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 2709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2595)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2622)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2659)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2670)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-173  
Alignment Scores:  
Pred. No.: 1.11e-136 Length: 2709  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 98.01% Indels: 0  
DB: 9 Gaps: 0  
US-09-771-161A-93 (1-232) x US-09-925-301-173 (1-2709)  
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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
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Db 1263 CTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1322  
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QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
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RESULT 5

US-09-728-721-3

Sequence 3, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 2000-12-01

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1620

TYPE: DNA

ORGANISM: Homo sapiens

US-09-728-721-3

Alignment Scores:

Pred. No.:2.88e-136Length:1620

Score:1176.00Matches:226

Percent Similarity:99.56%Conservative:1

Best Local Similarity:99.12%Indels:0

Query Match:97.51%Gaps:9

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US-09-771-161A-93 (1-232) x US-09-728-721-3 (1-1620)

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RESULT 6

US-10-105-931-3

Sequence 3, Application US/10105931

Publication No. US20020150987A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/10/105,931

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 09/099,041

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1620

TYPE: DNA

ORGANISM: Homo sapiens

US-10-105-931-3

Alignment Scores:

Pred. No.:2.88e-136Length:1620

Score:1176.00Matches:226

Percent Similarity:99.56%Conservative:1

Best Local Similarity:99.12%Indels:0

Query Match:97.51%Gaps:9

DB:

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Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0
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QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAAATCATGTCACAGAGGATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAAAATAGTGGTTCCTCGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGTCTCGAATACAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1177 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspLysValIleValGlnLysAspAsn 144
DB 1297 CCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1357 GAAGCTGCTTAAACAGCTCGTAGATGCCCTCTCTGTCAGGAGCTTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAATCTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAAGCAATTAATAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1477 ACTACTGACATCCAAAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AAACAATGGGTCTTCAGCTTACCCTGCGAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTTACTTCAAAATAAAAGCATG 1620
RESULT 7
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3
Alignment Scores:
Pred. No.: 2,88e-136 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0
US-09-771-161A-93 (1-232) x US-10-118-984-3 (1-1620)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLeuValSerMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGGAATATATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAAATCATGTCACAGAGGATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAAAATAGTGGTTCCTCGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTGTCTCGAATACAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1177 AGTTGGGATAGCACCATTCTCGAATCTCAAGGGCTGCATTCTGTGATCACAAGACCATT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspLysValIleValGlnLysAspAsn 144
DB 1297 CCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1357 GAAGCTGCTTAAACAGCTCGTAGATGCCCTCTCTGTCAGGAGCTTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAATCTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAAGCAATTAATAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1477 ACTACTGACATCCAAAGGAGAAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AAACAATGGGTCTTCAGCTTACCCTGCGAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTTACTTCAAAATAAAAGCATG 1620
RESULT 8
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
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; CURRENT APPLICATION NUMBER: US/10/295,981		; Sequence 2, Application US/09748537	
; CURRENT FILING DATE: 2002-11-15		; Patent No. US20020061833A1	
; PRIOR APPLICATION NUMBER: US/09/340,620		; GENERAL INFORMATION:	
; PRIOR FILING DATE: 1999-06-28		; APPLICANT: Bertin, John	
; PRIOR APPLICATION NUMBER: US 09/245,281		; APPLICANT: Chao, Moses V.	
; PRIOR FILING DATE: 1999-02-05		; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THEREOF	
; PRIOR APPLICATION NUMBER: US 09/207,359		; FILE REFERENCE: 07334-316001	
; PRIOR FILING DATE: 1998-12-08		; CURRENT APPLICATION NUMBER: US/09/748,537	
; PRIOR APPLICATION NUMBER: US 09/099,041		; CURRENT FILING DATE: 2000-12-26	
; PRIOR FILING DATE: 1998-06-17		; PRIOR APPLICATION NUMBER: US 09/099,041	
; PRIOR APPLICATION NUMBER: US 09/019,942		; PRIOR FILING DATE: 1998-06-17	
; NUMBER OF SEQ ID NOS: 71		; PRIOR APPLICATION NUMBER: US 09/019,942	
; SOFTWARE: FastSeq for Windows Version 4.0		; PRIOR FILING DATE: 1998-02-06	
; SEQ ID NO 3		; NUMBER OF SEQ ID NOS: 14	
; LENGTH: 1620		; SOFTWARE: FastSeq for Windows Version 4.0	
; TYPE: DNA		; SEQ ID NO 2	
; ORGANISM: Homo sapiens		; LENGTH: 1931	
US-10-295-981-3		; TYPE: DNA	
		; ORGANISM: Homo sapiens	
		US-09-748-537-2	
Alignment Scores:			
Pred. No.:	2,88e-136	Length:	1620
Score:	1176.00	Matches:	226
Percent Similarity:	99.56%	Conservative:	1
Best Local Similarity:	99.12%	Mismatches:	1
Query Match:	97.51%	Indels:	0
DB:	14	Gaps:	0
US-09-771-161A-93 (1-232) x US-10-295-981-3 (1-1620)			
QY	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	24
DB	937	AAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATATCT	996
QY	25	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	44
DB	997	CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT	1056
QY	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
DB	1057	GAAATAGTGGTCTCTGTAACACTTCAAGTTCCTGCCAGCTCTCTCAAGCAATGATTTT	1116
QY	65	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	84
DB	1117	TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCTCTGGAATATCAC	1176
QY	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104
DB	1177	AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCAAGACCAT	1236
QY	105	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	124
DB	1237	CCATGCTCTTCAGCAATTAATTAATCCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG	1296
QY	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
DB	1297	CCTGGTATAGCCAGCAGTGCATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACA	1356
QY	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	164
DB	1357	GAAGCCTGCCCTTAACCATGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG	1416
QY	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
DB	1417	GACTATGAATTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACATTTACTAGAC	1476
QY	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
DB	1477	ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAAGATAAC	1536
QY	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	224
DB	1537	AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACCATCTTTA	1596

QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnIleLysLeuLysAspAsn 204  
 Db 1690 ACTACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224  
 Db 1750 AAACAATGGGCTTCCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTA 1809  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1810 AATTACTTCAAAATAAAGCATG 1833  
 RESULT 10  
 US-09-728-721-1  
 ; Sequence 1, Application US/09728721  
 ; Patent No. US20020061845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT APPLICATION NUMBER: US/09/728,721  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 09/340,620  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)....(1833)  
 US-09-728-721-1  
 Alignment Scores:  
 Pred. No.: 3,75e-136 Length: 1931  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 97.51% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)  
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
 Db 1150 AGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAAATGAATATCT 1209  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44  
 Db 1210 CTGACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 Db 1270 GAAATAGTGGTTCTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 Db 1330 TTATCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCTCTCTGGAATAC 1389  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 Db 1390 AGTTGGATGACCACTTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1449  
 QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124

Db 1450 CCATGCTCTTCAGCAATAATAAATCCATCTCAACTGCAGGAAACTCAGAACGTCTGCAG 1509  
 QY 125 ProGlyIleAlaGlnGlnTriPileGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 Db 1510 CTTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGACCAATGACA 1569  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 Db 1570 GAAGCCTGCTTAACAGCTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 Db 1630 GACTATGAACCTTGTAGTACCAAGCCTCAAGAGCTCAAAAGTCAACAATTACTAGAC 1689  
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204  
 Db 1690 ACTACTGACATCCAGGAGAGAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749  
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224  
 Db 1750 AAACAATGGGCTTCCAGCCTTACCCGAAATACCTTGTGGTTCTAGATCACCATCTTTA 1809  
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232  
 Db 1810 AATTACTTCAAAATAAAGCATG 1833  
 RESULT 11  
 US-10-133-780-2  
 ; Sequence 2, Application US/10133780  
 ; Publication No. US20020123115A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/133,780  
 ; FILING DATE: 26-Apr-2002  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/019,942  
 ; FILING DATE: 06-FEB-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.  
 ; REGISTRATION NUMBER: 35,283  
 ; REFERENCE/DOCKET NUMBER: 07334/068001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1931 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-10-133-780-2

Alignment Scores:

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214) ... (1833)
US-10-105-931-1

Alignment Scores:
Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservatives: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-105-931-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTGGAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1390 AGTTGGATAGACCACTTCTGATCTCAAGGGCTGCATTCCTGTGATCACAAGACCA 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCAGCAGTGATCCAGACAAAAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCCTTAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGTATGATAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAATCTGTATGATCAAGACCTCAAGAGCCTCAAAAGCTCAAAAGCTACATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGGTCTTACCGGAAATATCTGTGGTTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 13
US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:

Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservatives: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-133-780-2 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCTCAAGACAAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCCTCTGGAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1390 AGTTGGATAGACCACTTCTGATCTCAAGGGCTGCATTCCTGTGATCACAAGACCA 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCAGCAGTGATCCAGACAAAAGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCCTTAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGTATGATAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAATCTGTATGATCAAGACCTCAAGAGCCTCAAAAGCTCAAAAGCTACATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLysLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGGTCTTACCGGAAATATCTGTGGTTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 12
US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/059,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Alignment Scores:
Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-118-984-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGCACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAATATAGTGGTTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCTCTCGAAATCAC 1389
QY 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGATAGCAACATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAGACCATT 1449
QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1510 CTTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1570 GAAGCTCGCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAATCTGTAGTACCAAGCTTACAGGACCTCAAAAGCTCAGACAAATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
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DB 1690 ACTACTGACATCCAAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProGlyThrProGluIleValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGGTCTTTCAGCTTACCCTGGAATATCTTGTGGTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTTACTTCAAAATATAAAGCATG 1833

RESULT 14
US-10-295-981-1
; Sequence 1, Application US/10295981
; Publication No. US2003012005SAI
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-295-981-1

Alignment Scores:
Pred. No.: 3,75e-136 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-295-981-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGCACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAATATAGTGGTTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCTCTCGAAATCAC 1389
QY 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGATAGCAACATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAGACCATT 1449
QY 105 ProCysSerSerAlaIleHisProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
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Db 1450 CCATGCTCTTTCAGCAATATAAATCCACTCTCAACTGCAGAAACTCAGAACGCTGTCAG 1509  
Qy 125 ProGlyLeuAlaGlnThrPileGlnSerLysArgGluAspLeuValAsnGlnMetThr 144  
Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAACAAATTGTGAACCAATGACA 1569  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuLeuMetLysGlu 164  
Db 1570 GAAGCGCTGCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACITTCATCATGAAAGAG 1629  
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
Db 1630 GACTATCAACTTGTGTAGTACCAAGCCTTACCAAGGACCTCAAAAGCTCAGACAAATTACTAGAC 1689  
Qy 185 ThrThrAspLeuGlnGluGluPheAlaLysValileValGlnLysLeuLysAspAsn 204  
Db 1690 ACTACTGACATCCAGGAGAAATTTGCCCAAGTTATAGTACAAAATTTGAAAGATAAC 1749  
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224  
Db 1750 AACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTTA 1809  
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232  
Db 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 15

US-09-918-995-20565  
; Sequence 20565, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20565  
; TYPE: DNA  
; LENGTH: 491  
; ORGANISM: Homo sapiens  
US-09-918-995-20565

Alignment Scores:  
Pred. No.: 2.02e-71 Length: 491  
Score: 650.00 Matches: 120  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.17% Mismatches: 0  
Query Match: 53.90% Indels: 0  
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-918-995-20565 (1-491)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
Db 128 AAGTTACAGAGTGTTTCAAGTGCCTTCCCTAATGTCACAGAGAAATGGAATTAATCT 187  
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44  
Db 188 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 247  
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
Db 248 GAAATAATAGTGGTTCTCTCTGAAACTTCAAGGTCCTGCGAGCTCTCAAGACAAATGATTTT 307  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84  
Db 308 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTGTGAAATCAC 367

Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 368 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCACT 427  
Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 428 CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGTCAG 487  
Qy 125 Pro 125  
Db 488 CCT 490

Search completed: April 1, 2004, 12:50:49  
Job time : 2517 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2004, 09:53:45 ; Search time 2693 Seconds  
(without alignments)  
2572.605 Million cell updates/sec

Title: US-09-771-161A-93  
Perfect score: 1206  
Sequence: 1 MYSLQSQVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cpn2.1/USPTO.spool/US9771161/runat.29032004.124819.19503/app.query.fasta\_1.391  
-DB=EST-QFMT=fastap-SUFFIX=p2n.rst-MINMATCH=0.1-LOOFCLO-LOOPEXT=0  
-UNITS=bits-START=1-END=1-MATRIX=biosum62-TRANS=human40.cdi-LIST=45  
-DOCALIGN=200-THR SCORE=pct-THR MAX=100-THR MIN=0-ALIGN=15-MODE=LOCAL  
-OUTFMT=ptc-NORM=ext-HEAPSIZE=500-MINLEN=0-MAXLEN=200000000  
-USER=US9771161@CGN.1.1.1906@runat.29032004.124819.19503-NCPU=3  
-NO MMAP-LARGEQUERY-NEG SCORES=0-WAIT-DSPBLOCK=100-LONGLOG  
-DEV TIMEOUT=120-WARN TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6  
-FGAPEXT=7-XGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database :  
EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_hic:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_hic:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: em\_gss\_hum:  
18: em\_gss\_inv:  
19: em\_gss\_pln:  
20: em\_gss\_vrt:  
21: em\_gss\_fun:  
22: em\_gss\_mam:  
23: em\_gss\_mus:  
24: em\_gss\_pro:  
25: em\_gss\_rod:  
26: em\_gss\_phg:  
27: em\_gss\_vrl:  
28: gb\_gesl:

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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C 2	1141	94.6	744	14	14	14	CD365404 UI-H-F72-
C 3	1132	93.9	938	13	13	13	BG670832 AGENCOURT
C 4	1105	91.6	852	12	12	12	BG57422 602711061
C 5	1099	91.1	870	10	10	10	B8877822 601486392
C 6	1088	90.2	683	14	14	14	CB852764 UI-CF-FNO
C 7	1085	90.0	812	12	12	12	B1257472 602967861
C 8	1080	89.6	1201	13	13	13	BX337147 BX337147
C 9	1077	89.3	715	14	14	14	CB851847 UI-CF-FNO
C 10	1067	88.5	883	12	12	12	BG393551 602411943
C 11	1029	85.3	660	12	12	12	BM840808 K-EST0117
C 12	1026	85.1	828	10	10	10	B8875947 601486423
C 13	1015	84.2	672	14	14	14	CA314123 UI-CF-FNO
C 14	1005	83.3	654	10	10	10	B8536247 601062632
C 15	1002.5	83.1	811	12	12	12	BG170405 60222736
C 16	988	81.9	1623	29	29	29	AY415527 Homo sapi
C 17	987	81.8	734	12	12	12	BQ008463 UI-H-ED1-
C 18	980	81.3	721	13	13	13	BQ774940 UI-H-FHO-
C 19	975	80.8	1623	29	29	29	AY415528 Pan trogl
C 20	973	80.7	656	12	12	12	BM973770 UI-CF-EC1
C 21	940	77.9	592	9	9	9	AI745575 wc34f12.x
C 22	917	76.0	647	10	10	10	AW960501 EST372572
C 23	904	75.0	667	13	13	13	BQ773811 UI-H-E21-
C 24	894	74.1	636	10	10	10	BE551615 7a42906.x
C 25	888	73.6	610	13	13	13	BUE23654 UI-H-FGI-
C 26	877	72.7	568	9	9	9	AA161113 z558405.s
C 27	858	71.1	709	14	14	14	CA413941 UI-H-E20-
C 28	839.5	69.6	1468	11	11	11	BC025611 Mus muscu
C 29	839.5	69.6	1947	11	11	11	BC050845 Mus muscu
C 30	838	69.5	606	9	9	9	AW085560 wy67c04.x
C 31	827.5	68.6	2826	11	11	11	BC058088 Mus muscu
C 32	794	65.8	1019	9	9	9	AV081633 AV081633
C 33	789	65.4	564	12	12	12	BM796243 K-EST0078
C 34	776	64.3	479	12	12	12	BM855477 K-EST0138
C 35	739.5	61.3	1201	13	13	13	BX401255 BX401255
C 36	725	60.1	505	13	13	13	BX280487 BX280487
C 37	713	59.1	483	9	9	9	AI343247 tb94a04.x
C 38	710.5	58.9	1599	29	29	29	AY415529 Mus muscu
C 39	703	58.3	476	9	9	9	AA913804 ol35d11.s
C 40	697	57.8	834	12	12	12	BM014010 603639652
C 41	692	57.4	423	9	9	9	AA574167 nl78b01.s
C 42	692	57.4	624	14	14	14	CD368863 UI-H-F71-
C 43	691.5	57.3	738	14	14	14	CD356485 AGENCOURT
C 44	688	57.0	476	14	14	14	CF528565 UI-1-BCL-
C 45	688	57.0	582	14	14	14	CB545226 AMGNNUC:N

ALIGNMENTS

RESULT 1  
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LOCUS BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
DEFINITION Homo sapiens cDNA clone CS0DL009YC19 3-PRIME, mRNA sequence.  
ACCESSION BX343071  
VERSION BX343071.1 GI:30334165  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)



US-09-771-161A-93 (1-232) x CD365404 (1-744)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db	718 AAGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAGAGAAATGGAATA-TCT 660
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
Db	659 CTGAACATACCTGTAAATCATGCTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 600
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
Db	599 GAAATAGTGGTCTCTCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACCAATGATTTT 540
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	539 TNATCTAGAAAGCTCAAGACTGTATTATTAAGCTGCATCAGCTGTCTGGAATAC 480
QY	85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db	479 AGTTGGATAGCACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 420
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	419 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAAGACGTCTGCAG 360
QY	125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	359 CTGTGTATAGCCAGCAGCTGGATCCAGACCAAAAGGGAAGACATTTGTGAACCAATGACA 300
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	299 GAAGCTGCTCTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATGATGAAGAG 240
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	239 GACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC 180
QY	185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db	179 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 120
QY	205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db	119 AAACAAATGGTCTTCCAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 60
QY	225 AsnLeuLeuGlnAsnLysSerMet 232
Db	59 AATTTACTTCAAAATAAAAGCATG 36
RESULT 3	
LOCUS	BQ670832
DEFINITION	AGENCYCOURT_8191703 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257019
VERSION	5', mRNA sequence.
KEYWORDS	BQ670832
SOURCE	BQ670832.1 GI:21781666
ORGANISM	EST.
REFERENCE	Homo sapiens (human)
AUTHORS	Homo sapiens
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT	1 (bases 1 to 938)
	NIH-MGC http://mgs.nci.nih.gov/.
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgabs-r@mail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Rubin Laboratory
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
	DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLCW2410 row: k column: 04	
High quality sequence stop: 659.	
FEATURES	
source	
1..938	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE:6257019"	
/tissue_type="epidermoid carcinoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/clone_lib="NIH_MGC_102"	
/note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN	
Alignment Scores:	
Pred. No.: 3.64e-112 Length: 938	
Score: 1132.00 Matches: 222	
Percent Similarity: 97.81% Conservative: 1	
Best Local Similarity: 97.37% Mismatches: 3	
Query Match: 93.86% Indels: 2	
DB: 13 Gaps: 0	
US-09-771-161A-93 (1-232) x BQ670832 (1-938)	
QY	5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db	136 AAGTTACAGAGTGTTCAGAGTCCATTACCTATGTGACAGAAATGGAATATCT 195
QY	25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 44
Db	196 CTGAACATACCTGTAAATCATGTTCCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 255
QY	45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
Db	256 GAAATAGTGGTCTCTCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACCAATGATTTT 315
QY	65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db	316 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTGTCTGGAATCAC 375
QY	85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db	376 AGTTGGATAGCACCATTTCTGGATCTCAAGGGTGCATTTCTGTGATCACAAGACCAT 435
QY	105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db	436 CCATGCTCTTCAAGCAATAATAATCACTCTCACTGAGGAACTCAGAACGCTCTGCAG 495
QY	125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db	496 CTGTGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGTGAACCAATGACA 555
QY	145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db	556 GAAGCTGCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATGATGAAGAG 615
QY	165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db	616 GACTATGAATCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 675
QY	185 ThrThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204
Db	676 ACTACTGACATCCAAAGGGAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATAA 735

QY 204 nLysGlnMetGlyLeuGlnProTyrProGluIleLeuVal-ValSerArgSerProSerL 224  
 DB 736 CAACCAATGGCTTTCAGCTTACCGGAAATACTTGTGGTTCTAGATCCCATCCT 795

QY 224 euAsnLeuGlnAsnLys 230  
 DB 796 TTAATTTACTTCCAAATAAA 815

RESULT 4  
 BG757422 852 bp mRNA linear EST 15-MAY-2001  
 LOCUS 602711061F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4851542 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG757422 GI:14068075  
 VERSION BG757422.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 852)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps@email.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHCMI694 row: i column: 15  
 High quality sequence stop: 814.  
 Location/Qualifiers  
 1..852  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4851542"  
 /tissue\_type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC 48"  
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.68e-109 Length: 852  
 Score: 1105.00 Matches: 221  
 Percent Similarity: 97.40% Conservative: 4  
 Best Local Similarity: 95.67% Mismatches: 2  
 Query Match: 91.63% Indels: 4  
 DB: 12 Gaps: 2

US-09-771-161A-93 (1-232) x BG757422 (1-852)

QY 5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
 DB 118 AAGTTACAGAGTGTTCAGAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATCT 177

QY 25 LeuAsnIleProValAsnHisGlyProGlnGluIleSerCysGlySerGlnLeuHis 44  
 DB 178 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 237

QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64  
 DB 238 GAAATAGTAGTGTCTCTCTGAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATTTT 297

QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 DB 298 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCGAAATCAC 357

QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 DB 358 AGTTGGATAGACCACTTCTGGATCTCAAGAGGCTGCATTTCTGTATCAAGACCACT 417

QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 DB 418 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGAAACTCAGAACGCTCTGCAG 477

QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 DB 478 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGACA 537

QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 DB 538 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 597

QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 DB 598 GACTATGAATCTGTAGTACCAAGCTTACAGGACCTCAAAAGCTCAGACAATTTACTAGAA 657

QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204  
 DB 658 CACTACTGACATCCAAAGGAGAGATTTGCGCAAGTTATAGTACAAAATTTGAAGATAA 717

QY 204 nLysGlnMetGlyLeuGlnProTyrProGluIleLeuVal-ValSerArgSerProSer- 223  
 DB 718 CAACCAATGGCTTTCAGCTTACCGGAAATACTTGTGGTTCTAGATCCCATC 777

QY 224 --LeuAsnLeuLeu---GlnAsnLysSer 231  
 DB 778 TTTTAATTTACTTTCAAAATAATAAAGC 806

RESULT 5  
 BE877822 870 bp mRNA linear EST 20-OCT-2000  
 LOCUS 601486392F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3888815 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE877822.1 GI:10326598  
 VERSION BE877822  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 870)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps@email.nih.gov  
 Tissue Procurement: DCTD/DTF/Gazdar  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM9669 row: g column: 24  
 High quality sequence stop: 739.  
 Location/Qualifiers  
 1..870  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

FEATURES  
 source

/clone="IMAGE:3888815"  
 /tissue\_type="large cell carcinoma, undifferentiated"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 69"  
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not I;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.1 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1-25e-108 Length: 870  
 Score: 1099.00 Matches: 224  
 Percent Similarity: 97.84% Conservatives: 2  
 Best Local Similarity: 96.97% Mismatches: 1  
 Query Match: 91.13% Indels: 5  
 DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x BB877822 (1-870)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24  
 ::  
 Db 44 AAGTTACAGAGTCTTCAAGTGCCATTACCTATGTGACAAAGAAAATGGAATTATCT 103  
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44  
 ::  
 Db 104 CTGAACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 163  
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64  
 ::  
 Db 164 GAATATAGTGGTCTCTGAACTTCAAGTCTCTGCCAGCTCTCTCAAGACAAATGATTT 223  
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
 ::  
 Db 224 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCCTCTCGAAATCAC 283  
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
 ::  
 Db 284 AGTTGGATAGACCACTTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCACT 343  
 QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
 ::  
 Db 344 CCATGCTCTTACGATATATATCACTCTCACTGAGGAACTCAGAACTCTGCGAG 403  
 QY 125 ProGlyIleAlaGlnIleTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
 ::  
 Db 404 CTGTGTATAGCCAGCAGTGGATCCAGACCAAAAGGGAAGACATTGTGAACCAATGACA 463  
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
 ::  
 Db 464 GAAGCTGCTTTAACCAGTCGTAGATGCCCTTCTGTCCAG-GACTTGATCATGAAGAG 522  
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184  
 ::  
 Db 523 GACTATGAACCTTTAGTACCAAGCTTACAGGACCTCAAAAGCTCAGAACTTACTAGAC 582  
 QY 185 ThrThrAspIleGln-GlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAs 204  
 ::  
 Db 583 ACTACTGACATCAAGGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 642  
 QY 204 nLysGlnMetGlyLeu--GlnProTyrProGluIleLeuValValSerArgSerProSer 223  
 ::  
 Db 643 CAAACAAATGGGTCTTTTCAGGCTTACCAGGAATACCTTTGTGGTTTCTAGATCACCATCT 702  
 QY 224 LeuAsn-LeuLeuGlnAsnLysSer 231  
 ::  
 Db 703 TTAATTTTACTTCAGAATAAAAGC 727

## RESULT 6

CB852764/c 683 bp mRNA linear EST 22-APR-2003  
 LOCUS  
 DEFINITION UI-CF-FN0-aex-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone  
 UI-CF-FN0-aex-p-08-0-UI 3', mRNA sequence.

ACCESSION CB852764  
 VERSION CB852764.1 GI:30047800  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 683)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Genes Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes

FEATURES  
 source

1..683  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-FN0-aex-p-08-0-UI"  
 /tissue\_type="Human Lung Epithelial cells"  
 /lab\_host="DH10B (Life Technologies) (Ti phage resistant)"  
 /clone\_lib="UI-CF-FN0"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-CF-FN0 is a subtracted cDNA library derived from two  
 normalized Human lung epithelial cell libraries (EN1 and  
 DU1) The library was subtracted according to according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. For additional information, contact:  
 bento-soares@uiowa.edu  
 TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1-31e-107 Length: 683  
 Score: 1088.00 Matches: 213  
 Percent Similarity: 98.61% Conservatives: 0  
 Best Local Similarity: 98.61% Mismatches: 3  
 Query Match: 90.22% Indels: 1  
 DB: 14 Gaps: 0  
 US-09-771-161A-93 (1-232) x CB852764 (1-683)

QY 17 AspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlu 36  
 ::  
 Db 681 GACAAAGATGAATAATGGAATA-TCTCTGAACATACCTGTAAATCATGGTCCACAAAGGAA 623  
 QY 37 SerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeu 56  
 ::  
 Db 622 TCATGTGGATCTCTCAGCTCCATGAATAATAGTGTCTCTCTGAAACTTCAAGGTCCTTG 563  
 QY 57 ProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLys 76  
 ::  
 Db 562 CCAGCTCTCTCAAGACAAATGATTTTTTATCTAGAAAAGCTCAGACTGTTATTTATGAAG 503  
 QY 77 LeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAla 96



FOUO

[illegible]

Best Local Similarity: 98.62% Mismatches: 2  
 Query Match: 89.30% Indels: 2  
 DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CB951847 (1-715)

QY 16 CysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlu 35  
 DB 714 TGTGACAGGAAGAAATGGAATA-TCTCTGACATACCTGTAATCATGTGTCACAGAG 656  
 QY 36 GluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSer 55  
 DB 655 GAATCATGTGGATCTCTCAGCTCCATGAAATAGTGT-TCTCTGAAATCTCAAGGTCC 597  
 QY 56 LeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMet 75  
 DB 596 CTGCCAGCTCTCAAGCAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTATG 537  
 QY 76 LysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArg 95  
 DB 536 AAGCTGCATCAGTCTGCGAATACAGTTGGATAGCACCATTTCTGGATCTCAAAGG 477  
 QY 96 AlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleLeuAsnProLeuSer 115  
 DB 476 GCTGCATTTCTGTATCACAGACCACTCCATGCTCTTCAGCAATAATAAATCCACTTCA 417  
 QY 116 ThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys 135  
 DB 416 ACTGCAGGAACCTCAGAACGTCGTGACGCTGGTATAGCCAGAGTGGATCCAGAGCAA 357  
 QY 136 ArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeu 155  
 DB 356 AGGAAGACATTTGTAACCAAAATCACAGAACGCTGCCTTAACAGTCCGTAGATGCCCTT 297  
 QY 156 LeuSerArgAspIleMetLysGluAspTyrGluLeuValSerThrLysProThrArg 175  
 DB 296 CTGTCCAGGACTTGTATCATGAAGAGGACTATGAATCTGTATGACCAAGCTTACAGG 237  
 QY 176 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluPheAlaLys 195  
 DB 236 ACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCCAGGAGAAATTTGCCAA 177  
 QY 196 ValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIle 215  
 DB 176 GTTATAGTACAAAATTTGAAGATATAACAAACAAATGGTCTTCAGCCCTTACCCGGAATA 117  
 QY 216 LeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232  
 DB 116 CTTGTGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATG 66

## RESULT 10

LOCUS BG393551 883 bp mRNA linear EST 12-MAR-2001  
 DEFINITION 602411943F1 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:4540787 5',  
 mRNA sequence.

ACCESSION BG393551

VERSION BG393551.1 GI:13286999

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 883)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM10471 row: e column: 12  
 High quality sequence stop: 767.

## FEATURES

source

1..883  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4540787"  
 /tissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 92"  
 /notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: Not I;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores: 3.86e-105 Length: 883  
 Pred. No.: 1067.00 Matches: 204  
 Score: 1067.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 88.47% Gaps: 0  
 DB: 12  
 US-09-771-161A-93 (1-232) x BG393551 (1-883)

QY 29 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 48  
 DB 2 GTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGGT 61  
 QY 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68  
 DB 62 TCTCTCGAAATCTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTTTTATCTAGAAA 121  
 QY 69 AlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAspSer 88  
 DB 122 GCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTTGGAAATCACAGTTGGATAGC 181  
 QY 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108  
 DB 182 ACCATTTCTGGATCTCAAAAGGGCTGCATCTCTGTGATCACAAAGACCCTCCATGCTCTTCA 241  
 QY 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128  
 DB 242 GCAATATATATCCATCTCACTCGAGGAACTCAGAACTCTGAGCTCTGAGCTGTGTATAGCC 301  
 QY 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
 DB 302 CAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAAGCTGCTCTT 361  
 QY 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
 DB 362 AACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAGGACTATGAACCT 421  
 QY 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 188  
 DB 422 GTTAGTACCAGCTCAAGGACCTCAAAAGTCAGACATATTACTAGACACTACTGACATC 481  
 QY 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 208  
 DB 482 CAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGGT 541  
 QY 209 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGln 228  
 DB 542 CTTACGCCCTTACCCGGAATACCTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 601  
 QY 229 AsnLysSerMet 232  
 DB 602 AATAAAGGATG 613



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RESULT 11
BM840808
LOCUS K-EST0117952 S12SNU216 Homo sapiens cDNA clone S12SNU216-38-G08 5',
DEFINITION mRNA sequence.
ACCESSION BM840808
VERSION BM840808.1 GI:19197217
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 660)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 38 row: G column: 08
High quality sequence stop: 660.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S12SNU216-38-G08"
/sex="F"
/tissue_type="lymph node"
/cell_type="Epithelial"
/lab_host="SNU-216"
/clone_lib="S12SNU216"
/notes="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dr-tailed vector. The dr-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
ORIGIN
Alignment Scores:
Pred. No.: 3,24e-101 Length: 660
Score: 1029.00 Matches: 197
Percent Similarity: 99.50% Conservative: 1
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 85.32% Indels: 0
DB: 12 Gaps: 0
US-09-771-161A-93 (1-232) x BM840808 (1-660)
QY 5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 64 AGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGCAAGAAATGGAATATCT 123
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 44

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---

```

Db 124 CTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 183
QY 45 GlnAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 184 GAAATAGTGGTTCCTCTCTGAAATCTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTTT 243
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 244 TTATCTAGAAAAGCTCAAGACTGTTATTTATTAAGAGCTGCATCCTCTCTCGAATCAC 303
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 304 AGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 363
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 364 CCATGCTCTTCAGCAATAATAATCACTCTCACTGCAGGAACCTCAGAGCTCTGCAG 423
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 424 CCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 483
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164
Db 484 GAAGCCTGCCTTAAACCAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAG 543
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 544 GACTATGAATCTGTGTAGTACCAAGCTACAGGACTCAAAAGTCAGACAATTAAGTAC 603
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAsp 203
Db 604 ACTACTGACATCCAAAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTGAAAGAT 660
RESULT 12
BM875947
LOCUS 601486423F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888965 5',
DEFINITION mRNA sequence.
ACCESSION BE875947
VERSION BE875947.1 GI:10324723
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 828)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9669 row: n column: 06
High quality sequence stop: 795.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.

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Average insert size 1.1 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:  
Pred. No.: 9,98e-101 Length: 828  
Score: 1028.00 Matches: 203  
Percent Similarity: 99.02% Conservative: 0  
Best Local Similarity: 99.02% Mismatches: 1  
Query Match: 85.07% Indels: 2  
DB: 10 Gaps: 0

US-09-771-161A-93 (1-232) x BE875947 (1-828)

Qy 29 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 48  
Db 5 GTRAAATCATGGTCCACAAAGGAATCATGTGGATCTCTCAGCTCCATGAATAAGTAGGT 64  
Qy 49 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 68  
Db 65 TCTCCTGAAATCTCAAGGTCCCTGCCAGCTCCTCAAGACCAATGATTTTATCTAGAAA 124  
Qy 69 AlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSer 88  
Db 125 GCTCAAGACTGTTATTTTGAAGCTGCATCAGTCTCTGGAATACAGTTGGATAGC 184  
Qy 89 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 108  
Db 185 ACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAGACCACTCCATGCTCTTCA 244  
Qy 109 AlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 128  
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Qy 129 GlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 148  
Db 305 CAGCAGTGGATCCAGACAAAGGAAGACATGTGAACCAATGACAGAGGCTGCCTT 364  
Qy 149 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 168  
Db 365 AACCACTCGTAGATGCCCTTCTGTCCAG-GACTTGATCATGAAGAGGACTATGAATT 423  
Qy 169 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrAspIle 188  
Db 424 GTTAGTACCAAGCCTACAGGACCTCAAAAGTCCAGACAATTACTAGACACTTGCATC 483  
Qy 189 GlnGlyGluGluPheAlaLysValIleValGlnLysLysAspAsnLysGlnMetGly 208  
Db 484 CAGGAGAGAAGATTGCAAGTTATAGTACAAAATTGAAGATACAAACAAATGGGT 543  
Qy 209 LeuGlnProTyrProGluIle-LeuValValSerArgSerProSerLeuAsnLeuGlu 228  
Db 544 CTTCAAGCTTACCGGAATATCTGGTGGTTCTTAGATCACCATCTTTAAATTACTTCA 603  
Qy 228 nAsnLysSerMet 232  
Db 604 AAATAAAGCATG 616

RESULT 13

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LOCUS 672 bp mRNA linear EST 04-NOV-2002  
DEFINITION UT-CF-FNO-aez-o-11-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
CA314123  
ACCESSION CA314123.1 GI:24532221  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 672)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES

source

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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR 1; Site 2: Not 1;  
UI-CF-FNO is a subtracted cDNA library derived from two  
normalized Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368  
TAG LIB=UI-CF-FNO  
TAG\_SEQ=GGCTGTAGGC"

ORIGIN

Alignment Scores:  
Pred. No.: 1,11e-99 Length: 672  
Score: 1015.00 Matches: 203  
Percent Similarity: 97.60% Conservative: 0  
Best Local Similarity: 97.60% Mismatches: 3  
Query Match: 84.16% Indels: 3  
DB: 14 Gaps: 0

US-09-771-161A-93 (1-232) x CA314123 (1-672)

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Db 670 ATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCATGAAA 611  
Qy 46 nSerGlySerProGluThrSerArgSerLeuProAlaPro-GlnAspAsnAspPheLeu 66  
Db 610 TAGTGGTCTCTCGTAAACTTCAAGGTCTCCAGCTCCCTCCAGCTCTCNAAGACAATGATTTT 551  
Qy 66 erArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerT 86  
Db 550 CTAGAAGACT-CAAGACTGTTATTTTATTAAGAGCTGCATCAGTCTCTCGAAAATCACAGTT 492  
Qy 86 rAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProC 106  
Db 491 GGGATAGCACCATTCTGGATCTCAAGAGGCTGCATTTCTGTATCAAGACCACTCCAT 432  
Qy 106 ysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG 126  
Db 431 GCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCAGCGCTG 372  
Qy 126 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 146

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Qy 146 laCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuileMetLysGluAspT 166
Db 311 CCTGCTTAACAGTCGCTAGATGCCCTCTCTCCAGGACTTGATCATGAAGAGGACT 252
Qy 166 yfGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrT 186
Db 251 ATGAACCTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAAATTTACTAGACACTA 192
Qy 186 hrAspIleGlnGlyGluPheAlaLysValileValGlnLysLeuLysAspAsnLysG 206
Db 191 CTGACATCAAGGAGGAAGATTTGCAAGTTATAGTACAAAATTTGAAGATAACAAC 132
Qy 206 InMetGlyLeuGlnProTyProGluileLeuValSerArgSerProSerLeuAsnL 226
Db 131 AAATGGGCTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTTAAAT 72
Qy 226 euLeuGlnAsnLysSerMet 232
Db 71 TACTTCAAAATAAAGCATG 52

RESULT 14
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LOCUS BE536247
DEFINITION BE536247.1 Homo sapiens cDNA clone IMAGE:3449311 5',
ACCESSION BE536247.1 GI:9764892
VERSION EST.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 654)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8425 row: 0 column: 08
High quality sequence stop: 650.
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 1.3e-98 Length: 654
Score: 1005.00 Matches: 206
Percent Similarity: 95.85% Conservative: 2
Best Local Similarity: 94.93% Mismatches: 5
Query Match: 83.33% Indels: 5
DB: 10 Gaps: 0

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US-09-771-161a-93 (1-232) x BE536247 (1-654)
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Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSer-GlnLeuHi 44
Db 69 CTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCANGCTCCA 128
Qy 44 sGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPh 64
Db 129 TGAATAATAGTGTCTCTCTGAACTTCAAGTCCCTCCAGCTCTCTCAAGCAATGATTT 188
Qy 64 eLeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisHisCysProGlyAsnHi 84
Db 189 TTTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGCTCTGGAATCA 248
Qy 84 sSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrTh 104
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Qy 104 rProCysSerSerAlaIleleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGl 124
Db 309 TCCATGCTCTTCAGCAATATAATCCACTCTCAACTGCAGGAACACTCAGAAGCTGTGCA 368
Qy 124 nProGlyleAlaGlnInTrpIleGlnSerLysArgGluAspIleValAsnGlnMetTh 144
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Qy 144 rGluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuileMetLysGl 164
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Qy 164 uAspTyrrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAs 184
Db 488 GGACTATGAACTTGTGTAGTACCAAGCTTCAAGAGCTTCAAAAGTCAGACATTTGCTAGA 547
Qy 184 pThrThrAspIleGlnGly-GluGluPheAlaLysValileValGlnLys-LeuLysAsp 203
Db 548 CACTACTGACATCCAAAGGCAGAGAATTTGGCANAGTTATAGTACAAAAATTTGCAAGAT 607
Qy 204 Asn-LysGlnMetGlyLeuGlnProTyProGluileLeuVal 217
Db 608 AACCAACAAATATGGGTCTTACGCCCTTACCCGGGAATACTTTGTG 650

RESULT 15
BE536247
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DEFINITION BE536247.1 Homo sapiens cDNA clone IMAGE:4426016 5',
ACCESSION BE536247.1 GI:12677108
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 811)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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FEATURES  
source

Location/Qualifiers  
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Site 2: SalI; Cloned unidirectionally; oligo-dt primed.  
Average insert size 1.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.47e-98 Length: 811  
Score: 1002.50 Matches: 201  
Percent Similarity: 95.81% Conservative: 5  
Best Local Similarity: 93.49% Mismatches: 8  
Query Match: 83.13% Indels: 3  
DB: 12 Gaps: 0

US-09-771-161A-93 (1-232) x BG170405 (1-811)

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Db 225 CTGAACATACCTGTAATATGCTGCACAAAGAGAAATCATGTGATCCTCTCAGTCCAT 284  
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Db 285 GAAATATAGTGGTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTT 344  
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84  
Db 345 TTATCTAGAAAGCTCAAGACTGTATTTATGAGCTGCATCCTCTCTGGAAATCAC 404  
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104  
Db 405 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCACAAGACCACT 464  
Qy 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124  
Db 465 CCATGCTCTTCAGCAATAATAATCCACTCTCACTCAGGAAACTCAGAACCGTCTGCAG 524  
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144  
Db 525 CTTGGTATAGCCAGCAGTGGATCCAGCAGAAAGGAGAGACATTGTGAACCAATGACA 584  
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164  
Db 585 GAAGCCTGCCTTAACCACTCGTAGATCGCCCTTCTGTCCAGGACATTGATCATGAAAGAG 644  
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Db 705 CACTACTGACATCAAGAGAGA-TTTGCCAAAGTTATACGTACAAAAAATTGACGATTA 763  
Qy 204 nLysGlnMetGlyLeuGlnProTyrProGluIleLeuValVal 218  
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Search completed: April 1, 2004, 12:07:12  
Job time : 2717 secs



Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiedand, D., Woods, K., Xie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W. I., and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
12975309  
PUBMED  
REFERENCE  
2 (bases 1 to 2521)  
AUTHORS  
Clark, H. F.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Matches 1334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCCTCAGCTCCA 450  
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LOCUS  
DEFINITION Sequence 3 from patent US 6426221.  
ACCESSION AR221453  
VERSION AR221453.1 GI:23328503

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 QY 511 TTATATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCAGTCTCTGGAATCA 570  
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 QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTGTGCA 690  
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 VERSION AF027706.1 GI:3123886  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2501)  
 AUTHORS Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.  
 TITLE RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis  
 JOURNAL J. Biol. Chem. 273 (20), 12296-12300 (1998)  
 MEDLINE 98241596  
 PUBMED 9575181  
 REFERENCE 2 (bases 1 to 2501)  
 AUTHORS Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr., Ann Arbor, MI 48109, USA

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		AUTHORS	Nunez G., Inohara, N. and Koseki, T.	
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AC004003.1 GI:2722557
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ozersky,P., Holmes,A. and Broym,M.
The sequence of Homo sapiens BAC clone CTA-437L15
Unpublished
2 (bases 1 to 116650)
Waterston,R.
Direct Submission
Submitted (15-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 116650)
Waterston,R.
Direct Submission
Submitted (27-JUN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 116650)
Waterston,R.
Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
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Center project name: H_RG437L15
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmc.org) at the Virginia Mason Research Institute.

SOURCE INFORMATION:  
Clone CTA-437L15 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).  
VECTOR: pBeloBAC11  
Selection: chloramphenicol

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is CTA-237G1. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.

This clone contains STS HS275YF1 (NID:91051703).

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sequence.
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VERSION AF117829.2 GI:38153762
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 320187)
AUTHORS Platzer M., Varon R., Sperling K., Reis A. and Rosenthal A.
TITLE Chromosome 8 genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 320187)
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AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Platzer M. and Varon R.  
Direct Submission  
Submitted (30-DEC-1998) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
3 (bases 1 to 320187)  
Platzer M.  
Direct Submission  
Submitted (04-NOV-2003) Genome Analysis, Institute of Molecular  
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany  
On Nov 4, 2003 this sequence version replaced gi:4151947.  
----- Genome Center  
Center: Institute of Molecular Biotechnology  
Center code: IMB  
Web site: http://genome.imb-jena.de/  
Contact: gscj-submit@genome.imb-jena.de  
----- Project Information  
Center project name: NBSlocusA  
Center clone name: RGP-64M4 to SCB-316M22  
----- Summary Statistics  
Sequencing vector: M13mp18; 100% of reads  
Chemistry: Dye-primer ET, Dye-terminator Big Dye;  
Consensus quality: 319496 bases at least Q40  
Consensus quality: 320184 bases at least Q30  
Consensus quality: 320187 bases at least Q20  
Quality coverage: 7.63  
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This sequence was finished as follows unless otherwise noted: all  
regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest.  
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Neighboring sequence information:  
This entry is part of a larger genomic contig. The start of this  
sequence is directed towards the centromere. The end  
(318188..320187) of this sequence overlaps with the start of  
Acc number AF049895. It covers RGP-64M4, SCB-282k6, SCB-273G1  
entirely and is overlapped by SCB-296N11, SCB-316M22.  
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Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
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of this entry's ASN.1 file.  
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ACCESSION BD251808
VERSION BD251808.1 GI:33061578
KEYWORDS JP 2002526035-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2024)
Hillman,J.L., Lal,P., Tang,T.Y., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Patterson,C., Bandman,O., Young,J.A., Gorgone,G.A.,
Yue,H., Azimzai,Y., Reddy,R., Lu,D.A.M. and Shih,L.L.
Phosphorylation effectors
Patent: JP 2002526035-A 6 20-AUG-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002526035-A/6
PD 20-AUG-2002
PF 28-JUL-1999 JP 2000562510
PR 28-JUL-1998 US 60/155213,14-SEP-1998 US 60/155196 PR
14-OCT-1998 US 60/155239,03-NOV-1998 US 60/106889 PR
19-NOV-1998 US 60/109093,22-DEC-1998 US 60/113796 PR
12-JAN-1999 US 60/155233
PI JENNIFER L HILLMAN,PREETI LAL,TOM Y TANG,NEIL C CORLEY,KARL J
PI GUEGLER,
PI MARIAH R BAUGHN,CHANDRA PATTERSON,OLGA BANDMAN,JANICE AU
YOUNG,
PI GINA A GORGONE,HENRY YUE,YALDA AZIMZAI,ROOPA REDDY,DYUNG AINA
PI M LU,
PI LEO L SHIH
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AUTHORS	Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.	
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JOURNAL	Patent: JP 2002017375-A 3014 22-JAN-2002;	
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002017375-A/3014 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253172 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO PI ISHII, PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA, PI TETSUJI OTSUKI,HISASHI KOGA PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10, PC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS Location/Qualifiers source 1..2033 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	
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ACCESSION	AK075213	
VERSION	AK075213.1 GI:22761157	
KEYWORDS	Oligo capping; fis (full insert sequence).	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.	
AUTHORS	NEDO human cDNA sequencing project	
TITLE	Unpublished	
JOURNAL	2 (bases 1 to 2033)	
REFERENCE	Isogai,T. and Otsuki,T.	
AUTHORS	Direct Submission	
TITLE	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	
JOURNAL	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).	
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----- Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L29371  
Center clone name: 706\_H\_15  
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\* NOTE: This record contains 67 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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31928 TAGTACAAAATTGAAGATAACAAACAAATGGGTCTTCAGCCTTACCCGGAATATCTTG 31869		TITLE		Direct Submission	
969 TGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAGTCACTGTTT 1028		JOURNAL		Submitted (14-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
31868 TGGTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAAGCATGTAGTCACTGTTT 31809		REMARK		NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
1029 TTCAAGAAGAAATGTGTTTCATAAAGGATATTATATCTCTGTGCTTTGACATTTTTTT 1088		COMMENT		On Aug 19, 2003 this sequence version replaced gi:13528713. Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTP cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc.mgc@hgrl.nih.gov">nisc.mgc@hgrl.nih.gov</a> Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd..

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 00:03:50 ; Search time 661 Seconds  
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10726.539 Million cell updates/sec

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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 674726

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 9: Geneseqn2003cs:\*
  - 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	879.4	52.7	2024	3	AAZ46143	CDNA sequ
6	876.8	52.5	2033	4	AAK94554	Human ful
7	861	51.6	2098	2	AAX02558	Human B1
8	786.2	47.1	1959	9	ADC99131	Human KPP
9	731.8	43.8	1931	2	AZ09246	Human CAR
10	731.8	43.8	1931	4	AAF30001	Human CAR
11	731.8	43.8	1931	6	ABK89280	Human CDN
12	731.8	43.8	1931	6	AAZ40752	CDNA of h
13	731.8	43.8	1931	7	ABX75869	Human CDN
14	731.8	43.8	1931	9	ADB81363	Human cas
15	681.8	40.9	1620	7	ABX75870	Human Cas
16	669.8	40.1	1619	6	AAZ40753	DNA of hu
17	447.6	26.8	575	4	AAK93010	Human CDN
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	29	59	3.5	19576	6	AA661258	Human gen
	30	58.2	3.5	23683	6	ABL34623	Human met
	31	58.2	3.5	23683	6	ABL70482	Chemical
	32	57.4	3.4	6286	4	AA646591	Human su
	33	57.4	3.4	8711	4	AA646700	Tumour su
	34	57.4	3.4	46951	9	ADE13891	Human opt
	35	57.2	3.4	883	4	AAI15210	Human bre
	36	57.2	3.4	6816	4	AA646688	Tumour su
	37	56.8	3.4	12142	6	ABL33673	Human imm
	38	56.6	3.4	7814	4	AA646530	Tumour su
	39	56.6	3.4	17848	4	AA645323	Chemical
	40	56.6	3.4	17848	6	ABK39976	Human che
	41	56.6	3.4	17848	6	ABK28164	DNA trans
	42	56.2	3.4	5945	6	ABL32085	Human imm
	43	56.2	3.4	6880	6	ABK31322	Signal tr
	44	56.2	3.4	6880	6	ABL70293	Chemical
	45	56.2	3.4	6880	6	AA661223	Human gen

ALIGNMENTS

RESULT 1  
AAC77779  
ID AAC77779 standard; cDNA; 2709 BP.  
XX  
AC AAC77779;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated gene sequence SEQ ID NO:173.  
XX  
KW Human; cancer associated gene; cancer antigen; detection; cancer;  
diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;  
antidiabetic; antiaesthetic; antirheumatic; antithrombotic; antiviral;  
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;  
dermatological; neuroprotective; thrombolytic; coagulant; neotropic;  
vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
immune disorder; haematopoietic cell disorder; autoimmune disorder;  
allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
neurological disease; drug screening; ss.  
XX Homo sapiens.  
OS  
PN WO200055350-A1.  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005882.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA Rosen CA, Ruben SM;  
XX  
PI WPI; 2000-587533/55.  
XX P-PSDB; AAB43570.  
DR  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
useful for treating or diagnosing e.g. cancer.  
XX  
PS Claim 1; Page 751-752; 2352pp; English.  
XX  
CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
AACB3398 to AAB44239. The proteins can have activities based on the  
tissues and cells the genes are expressed in. Example of activities





PA	(AXXI-) AXXIMA PHARM AG.	
XX	Subhart D, Habenberger P, Stein-Gerlach M, Bevec D;	
XX	WPI; 2002-373930/41.	
XX	P-PSDB; AAU0369.	
XX	Identifying agents for treatment or prevention of cytomegalovirus	
PT	infection, comprises contacting test compound with cellular kinase and	
PT	detecting change in cellular kinase activity.	
XX	Disclosure; Page 20-23; 49pp; English.	
XX	The present invention relates to a new method for identifying compounds	
CC	for treating and/or preventing cytomegalovirus (CMV) infection and/or	
CC	related diseases. The method of the invention comprises contacting a test	
CC	compound with at least one of the cellular kinases RICK, RIP, Nck-	
CC	Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase	
CC	activity. The method of the invention can be used to treat and/or prevent	
CC	CMV infections and related diseases. Oligonucleotides that can detect the	
CC	specified kinases can also be used for diagnosis of infection. The	
CC	present nucleic acid sequence encodes the human cellular kinase RICK	
CC	protein of the invention, as described above	
XX	Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;	
SQ		
	Query Match 78.4%; Score 1308; DB 6; Length 2501;	
	Best Local Similarity 99.0%; Pred. No. 2e-254;	
	Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;	
QY	331 ACAGTTACAGAGTGTTCAGTGGCCATTCACTATGTGACAGAGAAATGGAATTATC 390	
Db	1160 AAAAGTTACAGAGTGTTCAGTGGCCATTCACTATGTGACAGAGAAATGGAATTATC 1219	
QY	391 TCTGACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGTCCA 450	
Db	1220 TCTGACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGTCCA 1279	
QY	451 TGAATAATAGTGTCTCTCGTAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510	
Db	1280 TGAATAATAGTGTCTCTCGTAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1339	
QY	511 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTGGAATCA 570	
Db	1340 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTGGAATCA 1399	
QY	571 CAGTTGGGATGACCATTTCTGGATCTCAAGGGCTGCAATTCGTGATCACAAGACCAC 630	
Db	1400 CAGTTGGGATGACCATTTCTGGTCTCAAGGGGCTGCAATTCGTGATCACAAGACCAC 1459	
QY	631 TCCATGCTCTTCAGCAATATAAATCCACTCTCACTGCAGGAAACTCAGAACGTCTGCA 690	
Db	1460 TCCATGCTCTTCAGCAATATAAATCCACTCTCACTGCAGGAAACTCAGAACGTCTGCA 1519	
QY	691 GCCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAACCAATGAC 750	
Db	1520 GCCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAAACCAATGAC 1579	
QY	751 AGAAGCTGCCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGA 810	
Db	1580 AGAAGCTGCCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGA 1639	
QY	811 GGACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGA 870	
Db	1640 GGACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGA 1699	
QY	871 CACTACTGATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAA 930	
Db	1700 CACTACTGATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAA 1759	
QY	931 CAAACAAATGGGTCTTCAGCCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATCTTT 990	
Db	1760 CAAACAAATGGGTCTTCAGCCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATCTTT 1819	

QY	991 AAATTTACTTCAAAATAAAAGCATGTAAAGTGAAGTCTGTTTTTCAAGAGAAATGTGTTTCAT 1050	
Db	1820 AAATTTACTTCAAAATAAAAGCATGTAAAGTGAAGTCTGTTTTTCAAGAGAAATGTGTTTCAT 1879	
QY	1051 AAAAGGATATTATATCTCTGTTGCTTTGACTTTTTTTATATATAAAATCCGTGAGTATTAA 1110	
Db	1880 AAAAGGATATTATATCTCTGTTGCTTTGACTTTTTTTATATATAAAATCCGTGAGTATTAA 1939	
QY	1111 AGCTTTATTTGAAGTTCCTTTGGGTAATATTAGTCTCCCTCCATGACACTGCAGATATTTT 1170	
Db	1940 AGCTTTATTTGAAGTTCCTTTGGGTAATATTAGTCTCCCTCCATGACACTGCAGATATTT 1999	
QY	1171 TTTTAATTAATACAGTAAAAAGTT-----TGAATTTTGTCTACATAGTTCAATTTTT 1222	
Db	2000 TTTTAATTAATACAGTAAAAAGTTGAATTTGGTTGAATTTTGTACATAGTTCAATTTTT 2059	
QY	1223 ATGCTCTCTTTTGAACAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTATAACA 1282	
Db	2060 ATGCTCTCTTTTGAACAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTATAACA 2119	
QY	1283 GTGCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTTCATGG 1342	
Db	2120 GTGCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTACATTCATGTTCTTTCATGG 2179	
QY	1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 1402	
Db	2180 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCAC 2239	
QY	1403 CAGAGACAGTACAGNATCCCTGCCCTAAATCCAGGCTTAATTCGCCCTACAGAGGGTTA 1462	
Db	2240 CAGAGACAGTACAGNATCCCTGCCCTAAATCCAGGCTTAATTCGCCCTACAGAGGGTTA 2299	
QY	1463 TTAATTTAAAACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAAATTCCTTTA 1522	
Db	2300 TTAATTTAAAACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAAATTCCTTTA 2359	
QY	1523 AAAATGATATTTCAAAGGTAAAAACAATAATATAAAGAAAAATAAATATATTATATAC 1582	
Db	2360 AAAATGATATTTCAAAGGTAAAAACAATAATATAAAGAAAAATAAATATATTATATAC 2419	
QY	1583 CGGCTTCTGTCGCCATTTTAACTCAGCCCTCCCTACTGTCCACCAACCAAGCTTAA 1642	
Db	2420 CGGCTTCTGTCGCCATTTTAACTCAGCCCTCCCTACTGTCCACCAACCAAGCTTAA 2479	
QY	1643 ATAAAGTCAACAGCCTGATGTG 1664	
Db	2480 ATAAAGTCAACAGCCTGATGTG 2501	
RESULT 3		
AD45172		
ID	AD45172 standard; DNA; 2501 BP.	
XX		
AC	AD45172;	
XX		
DT	27-DEC-2002 (first entry)	
XX		
DE	Human receptor interacting protein (RIP)2 DNA.	
XX		
KW	Human; receptor interacting protein; RIP2; antisense; gene therapy; gene	
ds.		
XX	Homo sapiens.	
OS		
XX		
FT	Key	Location/Qualifiers
FT	CDS	225..1847
FT		/*tag= a
FT		/product= "Human RIP2 protein"
XX		
PN	US6426221-B1.	
XX		
PD	30-JUL-2002.	

XX 01-AUG-2001; 2001US-00920663.  
XX 01-AUG-2001; 2001US-00920663.  
XX (ISIS-) ISIS PHARM INC.  
XX Ward DT, Cowser LM;  
XX WPI; 2002-673017/72.  
XX P-PSDB; AAE27882.  
XX New antisense oligonucleotide that targets regions of a nucleic acid  
XX encoding human receptor interacting protein (RIP)2, for treating diseases  
XX associated with RIP2 expression.  
XX Claim 1; Col 49-54; 35pp; English.  
XX The invention relates to antisense compounds targetted to a nucleic acid  
XX encoding human receptor interacting protein (RIP)2 to inhibit its  
XX expression. Antisense compounds are used for treating diseases associated  
XX with RIP2 expression. They are also useful in antisense gene therapy. The  
XX present sequence is human RIP2 DNA  
XX  
SQ Sequence 2501 BP; 768 A; 535 C; 499 G; 699 T; 0 U; 0 Other;  
Query Match 78.4%; Score 1308; DB 6; Length 2501;  
Best Local Similarity 99.0%; Pred. No. 2e-254;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;  
QY 331 ACAGTTACAGAGTGTTCAGATGCCATTCACCTATGTGACAAAGAAATGAATATC 390  
DB 1160 AAAGTTACAGAGTGTTCAGATGCCATTCACCTATGTGACAAAGAAATGAATATC 1219  
QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGTCCA 450  
DB 1220 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCCTCTCAGTCCA 1279  
QY 451 TGAAGATAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTT 510  
DB 1280 TGAAGATAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTT 1339  
QY 511 TTATATCAGAAAGCTCAAGACGTGTTATTTATGAAGTGCATCATGCTCCTGGAATCA 570  
DB 1340 TTATATCAGAAAGCTCAAGACGTGTTATTTATGAAGTGCATCATGCTCCTGGAATCA 1399  
QY 571 CAGTTGGATGAGCACCATTCTCGATCTCAAGGGTGCATCTGTGATCACAAGACCAC 630  
DB 1400 CAGTTGGATGAGCACCATTCTCGATCTCAAGGGTGCATCTGTGATCACAAGACCAC 1459  
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCA 690  
DB 1460 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCA 1519  
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGAAACCAATGAC 750  
DB 1520 GCCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGAAACCAATGAC 1579  
QY 751 AGRAGCTGCTTAAACAGTCGCTAGATGCCCTCTGCTCAGGACTTGATCATGAAGA 810  
DB 1580 AGRAGCTGCTTAAACAGTCGCTAGATGCCCTCTGCTCAGGACTTGATCATGAAGA 1639  
QY 811 GGACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAACAATTTACTAGA 870  
DB 1640 GGACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAACAATTTACTAGA 1699  
QY 871 CACTACTGACATCCAGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAGATAA 930  
DB 1700 CACTACTGACATCCAGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAGATAA 1759  
QY 931 CAAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTT 990  
DB 1760 CAAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTT 1819

QY 991 AAATTTACTTTCAAAATAAAAGCATGTAAGTACTGTTTTCAGAGAATAATGTTTCAT 1050  
DB 1820 AAATTTACTTTCAAAATAAAAGCATGTAAGTACTGTTTTCAGAGAATAATGTTTCAT 1879  
QY 1051 AAAAGGATATTTATATCTCTGTTGCTTTCACCTTTTATATATAAAATCCGTCAGATTA 1110  
DB 1880 AAAAGGATATTTATATCTCTGTTGCTTTCACCTTTTATATATAAAATCCGTCAGATTA 1939  
QY 1111 AGCTTTATTGAAGGTTCTTTGGTAAATTAATAGTCTCCCTCCATGACACATGAGATTTT 1170  
DB 1940 AGCTTTATTGAAGGTTCTTTGGTAAATTAATAGTCTCCCTCCATGACACATGAGATTTT 1999  
QY 1171 TTTTAATTAATACAGATAAAAGTT-----TGAATTTTCTCATATAGTTCAATTTT 1222  
DB 2000 TTTTAATTAATACAGATAAAAGTTTGAATTTGTTGTAATTTGCTACATAGTTCAATTTT 2059  
QY 1223 ATGCTCTCTTTGTTAAACAGAAACCACTTTTAAAGGATAGTAATTTCTTGTATTATAA 1282  
DB 2060 ATGCTCTCTTTGTTAAACAGAAACCACTTTTAAAGGATAGTAATTTCTTGTATTATA 2119  
QY 1283 GTGCCTTAAAGGTATGATGATTTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 1342  
DB 2120 GTGCCTTAAAGGTATGATGATTTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 2179  
QY 1343 ATTATTTGTTACTGTTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCAC 1402  
DB 2180 ATTATTTGTTACTGTTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCAC 2239  
QY 1403 CAGAGACATGACAGATCCCTGCCCTTAAATCCAGGCTTAATTTGCCCTTACAAAGGTTA 1462  
DB 2240 CAGAGACATGACAGATCCCTGCCCTTAAATCCAGGCTTAATTTGCCCTTACAAAGGTTA 2299  
QY 1463 TTAATTTAAACCTCCATTTATAGGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 1522  
DB 2300 TTAATTTAAACCTCCATTTATAGGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 2359  
QY 1523 AAAATGATATTTCAAAGGTAAACCAATATATAAAGAAAAAATAATAATATTAATAC 1582  
DB 2360 AAAATGATATTTCAAAGGTAAACCAATATATAAAGAAAAAATAATAATATTAATAC 2419  
QY 1583 CGGCTTCTCTGCCCATTTTAACTCAGCTCCTTCCCTACTGTCCACCAACCAAGCTAA 1642  
DB 2420 CGGCTTCTCTGCCCATTTTAACTCAGCTCCTTCCCTACTGTCCACCAACCAAGCTAA 2479  
QY 1643 ATAAAGTCAACAGCCTGATGTG 1664  
DB 2480 ATAAAGTCAACAGCCTGATGTG 2501  
RESULT 4  
AAZ48762  
ID AAZ48762 standard; cDNA; 2502 BP.  
XX AAZ48762;  
AC AAZ48762;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
XX Human RICK coding sequence.  
XX  
XX RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO9955134-A2.  
XX  
XX 04-NOV-1999.  
XX  
XX 27-APR-1999; 99WO-US009183.

XX 27-APR-1998; 98US-00069023.  
XX (UNMI ) UNIV MICHIGAN.  
XX Nunez G, Inohara N, Koseki T;  
XX WPI; 2000-072163/06.  
XX P-PSDB; AAY59404.  
XX  
XX Compositions for identifying apoptosis signaling pathway inhibitors  
XX useful for treating diseases.  
XX  
XX Claim 8; Fig 7b; 93pp; English.  
XX  
XX This sequence encodes the human RICK (RIP-like interacting CLARP kinase)  
XX protein of the invention. The RICK protein acts as a positive regulator  
XX of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10  
XX during CD95 signalling. The invention provides methods for identifying  
XX apoptosis signalling pathway inhibitors and activators, and methods and  
XX compositions for screening compounds which will modulate the interactions  
XX of the various compositions identified: ARC, RICK, and the CIDE family of  
XX activators (CIDE-A, CIDE-B and DRBP-1). RICK is useful in screening  
XX assays for agents, useful in the diagnosis, prognosis or treatment of  
XX disease associated with excess cell growth and dysregulation of  
XX apoptosis. Complexes containing RICK and CLARP can be used in drug  
XX screening assays to identify inhibitor molecules blocking CD95-mediated  
XX apoptosis. Overexpression of ARC in an in vitro cell system can be used  
XX to identify inhibitors of the enzymatic activity of caspase-8.  
XX Identification of ARC-like inhibitory compounds may be useful for gene  
XX therapy treatment of disease with increased cell death in muscle tissue  
XX and cardiac disorders. Therapeutic compositions of CIDEs can be used to  
XX treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,  
XX ischaemic injury, and toxin-induced liver disease. Anti-RICK antibodies  
XX can be used as reagents for the preparation or affinity chromatography  
XX media, and for diagnostically measuring RICK levels. A specific inhibitor  
XX of an essential step in the biochemistry of apoptosis is needed. RICK  
XX interaction with intracellular factors such as CLARP and FADD appears to  
XX be essential for apoptosis, inhibitors of RICK binding to intracellular  
XX apoptosis factors are potential drug candidates  
XX  
XX Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 U; 0 Other;

Query Match 78.4%; Score 1308; DB 3; Length 2502;  
Best Local Similarity 99.0%; Pred. No. 2e-254;  
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 331 ACAGTTACAGAGCTTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
DB 1161 AAAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 1220  
QY 391 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB 1221 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1280  
QY 451 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACAATGATT 510  
DB 1281 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACAATGATT 1340  
QY 511 TTTATCTAGAAGAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTCTGGAAATCA 570  
DB 1341 TTTATCTAGAAGAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTCTGGAAATCA 1400  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCAAGAGCCAC 630  
DB 1401 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCAAGAGCCAC 1460  
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAAAGCTCTGCA 690  
DB 1461 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAAAGCTCTGCA 1520  
QY 691 GCCTGGTATAGCCACAGCTGGATTCAGAGCAAAAGGAGACATTTGTGAACCAAAATGAC 750

RESULT 5  
AAZ46143  
ID AAZ46143 standard; cdna; 2024 BP.  
XX  
AC AAZ46143;  
XX

DB 1521 GCCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGAC 1580  
QY 751 AGAAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGTATCATCAAGA 810  
DB 1581 AGAAGCCTGCCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGGACTTGTATCATCAAGA 1640  
QY 811 GGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAATAG 870  
DB 1641 GGACTATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAATAG 1700  
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGCTATAGTACAAAATTTGAAAGATAA 930  
DB 1701 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGCTATAGTACAAAATTTGAAAGATAA 1760  
QY 931 CAAACAAATGGGTCTTCAGCCTTACCCGAAATACCTGTGGTTCTAGATCACCAATCTTT 990  
DB 1761 CAAACAAATGGGTCTTCAGCCTTACCCGAAATACCTGTGGTTCTAGATCACCAATCTTT 1820  
QY 991 AAATTTACTTCAAAATAAAGCATGTAGTGACTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
DB 1821 AAATTTACTTCAAAATAAAGCATGTAGTGACTGTTTTTCAAGAGAAATGTGTTTCAT 1880  
QY 1051 AAAGGATATTTATATCTCTGTGCTTGTGACTTTTTTATATAAAATCCGTGAGTATTAA 1110  
DB 1881 AAAGGATATTTATATCTCTGTGCTTGTGACTTTTTTATATAAAATCCGTGAGTATTAA 1940  
QY 1111 AGCTTTATTGAAGGTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1170  
DB 1941 AGCTTTATTGAAGGTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 2000  
QY 1171 TTTTAATTAACAAGTAAAAAGTT-----TGAATTTGCTACATAGTTCAATTTTTT 1222  
DB 2001 TTTTAATTAACAAGTAAAAAGTTGAAATTTGGTTGAAATTTGCTACATAGTTCAATTTTT 2060  
QY 1223 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTTAAACA 1282  
DB 2061 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAAATTTCTTGTGTTTAAACA 2120  
QY 1283 GTGCCTTAAGGTATGATGTTTCTGTGATGGAGCCATTTTCAATTCATGTTCTTCATGG 1342  
DB 2121 GTGCCTTAAGGTATGATGTTTCTGTGATGGAGCCATTTTCAATTCATGTTCTTCATGG 2180  
QY 1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCAC 1402  
DB 2181 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTTACCCAC 2240  
QY 1403 CAGAGACAGTACAGAAATCCCTGCCCTTAAATCCCAAGGCTTAATTCCTTACAAAGGGTTA 1462  
DB 2241 CAGAGACAGTACAGAAATCCCTGCCCTTAAATCCCAAGGCTTAATTCCTTACAAAGGGTTA 2300  
QY 1463 TTAATTTAAACTCCATTTATTAGGATTACATTTTAAAGTTTTTATTATGAATTCCTCTTTA 1522  
DB 2301 TTAATTTAAACTCCATTTATTAGGATTACATTTTAAAGTTTTTATTATGAATTCCTCTTTA 2360  
QY 1523 AAAATGATATTTCAAAGGTAAACAAATATATAAGAAAAAATAATATATTAATAC 1582  
DB 2361 AAAATGATATTTCAAAGGTAAACAAATATATAAGAAAAAATAATATATTAATAC 2420  
QY 1583 CGGCTTCTGTCCCATTTTAAACCTTCAGCCTTCCCTACTGTCCACCAACCAAGCTAA 1642  
DB 2421 CGGCTTCTGTCCCATTTTAAACCTTCAGCCTTCCCTACTGTCCACCAACCAAGCTAA 2480  
QY 1643 ATAAAGTCAACAGCCTGATGTG 1664  
DB 2481 ATAAAGTCAACAGCCTGATGTG 2502



PI Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR P-PSDB; AAW93621.  
 XX  
 XX 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 PT  
 XX Claim 8; SEQ ID NO 3453; 1380pp + Sequence Listing; English.  
 XX  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a full length human cDNA of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in CD-ROM format directly  
 CC from EPO  
 XX  
 XX Sequence 2033 BP; 612 A; 447 C; 438 G; 536 T; 0 U; 0 Other;  
 SQ  
 Query Match 52.5%; Score 876.8; DB 4; Length 2033;  
 Best Local Similarity 99.8%; Pred. No. 2.1e-167;  
 Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATC 390  
 DB 1154 AAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATC 1213  
 QY 391 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCA 450  
 DB 1214 TCTGAACATACCTGTAATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCA 1273  
 QY 451 TGAATAATAGTGTTCCTGAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACAAATGATT 510  
 DB 1274 TGAATAATAGTGTTCCTGAACTTCAAGGTCCCTGCCAGCTCTCTCAAGACAAATGATT 1333  
 QY 511 TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGTGCATCACTGCTCGGAATCA 570  
 DB 1334 TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGTGCATCACTGCTCGGAATCA 1393  
 QY 571 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATCTGTGATCAGACACAC 630  
 DB 1394 CAGTTGGATAGACACATTTCTGGATCTCAAGGGCTGCATCTGTGATCAGACACAC 1453  
 QY 631 TCCATGCTCTTTCAGCAATAAATCACTCTCAAGTCCCTGCCAGCTCTCTCAAGACCTGCA 690  
 DB 1454 TCCATGCTCTTTCAGCAATAAATCACTCTCAAGTCCCTGCCAGCTCTCTCAAGACCTGCA 1513  
 QY 691 GCCTGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAAGCAATTTGTAACCAATGAC 750  
 DB 1514 GCCTGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAAGCAATTTGTAACCAATGAC 1573  
 QY 751 AGAAGCTGCTTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 810  
 DB 1574 AGAAGCTGCTTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1633  
 QY 811 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAGGACCTCAAAAGTTCAGACAT 870  
 DB 1634 GGACTATGAATTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTTCAGACAT 1693  
 QY 871 CACTACTGACATCAAGGGAAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 930  
 DB 1694 CACTACTGACATCAAGGGAAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 1753  
 QY 931 CAAACAAATGGTCTTTCAGCTTACCCGGAAATATCTGTGGTTCTTAGATCACCATCTTT 990  
 DB 1754 CAAACAAATGGTCTTTCAGCTTACCCGGAAATATCTGTGGTTCTTAGATCACCATCTTT 1813

QY 991 AAATTTACTTCAAAATAAAAGCATCTAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCAAT 1050  
 DB 1814 AAATTTACTTCAAAATAAAAGCATCTAAGTGAAGTCTTTTCAAGAGAAATGTGTTTCAAT 1873  
 QY 1051 AAAGGATATTTATATCTCTGTTGCTTTGACCTTTTATATATAAAATCCGTGAGTATTA 1110  
 DB 1874 AAAGGATATTTATATCTCTGTTGCTTTGACCTTTTATATATAAAATCCGTGAGTATTA 1933  
 QY 1111 AGCTTTATTTGAAGTCTTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1170  
 DB 1934 AGCTTTATTTGAAGTCTTTTGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1993  
 QY 1171 TTTTAATTAATACAAAGTAAAAAGTTTGAATTTTGTCTACAT 1210  
 DB 1994 TTTTAATTAATACAAAGTAAAAAGTTTGAATTTTGTCTACAT 2033  
 RESULT 7  
 AAX02558  
 ID AAX02558 standard; cDNA; 2098 BP.  
 XX  
 AC AAX02558;  
 XX  
 DT 07-MAY-1999 (first entry)  
 XX  
 DE Human B1 cDNA.  
 XX  
 KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
 KW cell survival pathway; intracellular signalling; AIDS; cancer; human; sp.  
 OS Homo sapiens.  
 XX  
 PN W09855507-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 01-JUN-1998; 98WO-IL000255.  
 XX  
 PR 05-JUN-1997; 97IL-00121011.  
 PR 30-JUN-1997; 97IL-00121199.  
 PR 11-SEP-1997; 97IL-00121746.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Wallach D, Boldin M, Malinin N;  
 XX  
 DR WPI; 1999-070258/06.  
 DR P-PSDB; AAW92795.  
 XX  
 PT New B1 protein regulates cell death and cell survival pathways -  
 PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
 PT ; for treating AIDS, cancer.  
 XX  
 PS Claim 4; Fig 3B; 90pp; English.  
 XX  
 CC This invention describes the isolation of a novel human B1 protein which  
 CC can interact with intracellular mediators or modulators of inflammation,  
 CC cell death and/or cell survival pathways; directly or indirectly. Cells  
 CC can be modulated or mediated in inflammation, cell death or cell survival  
 CC pathways or another intracellular signalling activity using B1.  
 CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
 CC oligonucleotides and ribozymes can also be used to regulate the above  
 CC pathways  
 XX  
 SQ Sequence 2098 BP; 649 A; 452 C; 449 G; 539 T; 0 U; 9 Other;  
 Query Match 51.6%; Score 861; DB 2; Length 2098;  
 Best Local Similarity 98.5%; Pred. No. 3.2e-164;  
 Matches 858; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATATC 390

Db 1195 AAAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGCAAGAGAAAATGGAATATC 1254  
 QY 391 TCTGAACATACCTGTAATCATGTCTCACAAGAGGAATCATGTGATCCCTCTCAGCTCCA 450  
 Db 1255 TCTGAACATACCTGTAATCATGTCTCACAAGAGGAATCATGTGATCCCTCTCAGCTCCA 1314  
 QY 451 TGAATAATAGTGGTCTCTCTGAAACTTCAAGTCTCCCTCCAGCTCTCTCAAGACAAATGATTT 510  
 Db 1315 TGAATAATAGTGGTCTCTCTGAAACTTCAAGTCTCCCTCCAGCTCTCTCAAGACAAATGATTT 1374  
 QY 511 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATGTCTGGAATCA 570  
 Db 1375 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATGTCTGGAATCA 1434  
 QY 571 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTATCACAAGACCAC 630  
 Db 1435 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTATCACAAGACCAC 1494  
 QY 631 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
 Db 1495 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1554  
 QY 691 GCCTGATATGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
 Db 1555 GCCTGATATGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1614  
 QY 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTCTCAGGGACTTGTATCATGAAGA 810  
 Db 1615 AGAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTCTCAGGGACTTGTATCATGAAGA 1674  
 QY 811 GGACTATGAATCTTGTATGATACCAAGCCCTACAAGGACCTCAAAAGTTCAGACAAATTTACTAGA 870  
 Db 1675 GGACTATGAATCTTGTATGATACCAAGCCCTACAAGGACCTCAAAAGTTCAGACAAATTTACTAGA 1734  
 QY 871 CACTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930  
 Db 1735 CACTACTGACATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1794  
 QY 931 CAAACAAATGGTCTTACAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTT 990  
 Db 1795 CAAACAAATGGTCTTACAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTT 1854  
 QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
 Db 1855 AAATTTACTTCAAAATAAAGCATGTAAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAT 1914  
 QY 1051 AAAGGATATTTATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGCTGAGTATAA 1110  
 Db 1915 AAAGGATATTTATCTCTGTTGCTTTGACTTTTTTATATAAAATCCGCTGAGTATAA 1974  
 QY 1111 AGCTTTATGAAGTCTTTGGGTAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1170  
 Db 1975 AGCTTTATGAAGTCTTTGGGTAATATTAGTCTCCCTCCATGACACTGCAGTATTTT 1234  
 QY 1171 TTTTAAATTAACAAAGTAAAGTTGAATTT 1201  
 Db 2035 TTTTAAATTAACAAAGTAAAGTTGAATTT 2065

RESULT 8  
 ID ADC99131  
 standard; cdna; 1959 BP.

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

XX AC ADC99131;

KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipruritic;  
 KW uropathic; ophthalmologic; antirheumatic; haemostatic; antibacterial;  
 KW viricide; protozoicide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;  
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 KW helminthic infection; transgenic; gene therapy; human; ss; gene.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO2003033680-A2.  
 XX 24-APR-2003.  
 XX 17-OCT-2002; 2002WO-US033723.  
 XX 19-OCT-2001; 2001US-0345474P.  
 PR 02-NOV-2001; 2001US-0343910P.  
 PR 13-NOV-2001; 2001US-0333098P.  
 PR 16-NOV-2001; 2001US-0332424P.  
 PR 30-NOV-2001; 2001US-0334288P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;  
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebajradian Y;  
 XX WPI; 2003-403214/38.  
 DR P-PSDB; ADC99079.  
 XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX Claim 5; SEQ ID NO 84; 424pp; English.  
 PS The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP cDNA of the  
 CC invention.  
 XX SQ Sequence 1959 BP; 597 A; 430 C; 420 G; 512 T; 0 U; 0 Other;

Query Match 47.1%; Score 786.2; DB 9; Length 1959;  
 Best Local Similarity 99.6%; Pred. No. 4e-149;  
 Matches 788; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 421 AGAGGATCATGTGGATCTCTCAGCTCCATGAAATAGTGGTCTCTGAAACTTCAAG 480  
 Db 1156 AAAGGATCATGTGGATCTCTCAGCTCCATGAAATAGTGGTCTCTGAAACTTCAAG 1215  
 QY 481 GTCCCTGCCAGCTCCCTCAAGACAAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTT 540  
 Db 1216 GTCCCTGCCAGCTCCCTCAAGACAAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTT 1275  
 QY 541 TATGAGCTGCATCATCTGCTTCCGAAATACAGTGGATAGACCAATTTCTGATCTCA 600





QY 571 CAGTTGGATAGCACCATTCTCTGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 630  
DB 1389 CAGTTGGATAGCACCATTCTCTGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 1448  
QY 631 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGACGAGAACTCAGAACGTCTGCA 690  
DB 1449 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGACGAGAACTCAGAACGTCTGCA 1508  
QY 691 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGAC 750  
DB 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTCGTAGATGCTCTCTCTGTCAGGACCTTGATCATGAAGA 810  
DB 1569 AGAAGCTGCTTAAACAGTCGTAGATGCTCTCTCTGTCAGGACCTTGATCATGAAGA 1628  
QY 811 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 870  
DB 1629 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 1688  
QY 871 CACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAA 930  
DB 1689 CACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAA 1748  
QY 931 CAAACAAATGGGCTTTCAGGCTTACCCGGAATATCTTGTGTTCTAGATCACCATCTTT 990  
DB 1749 CAAACAAATGGGCTTTCAGGCTTACCCGGAATATCTTGTGTTCTAGATCACCATCTTT 1808  
QY 991 AAATTTACTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTTCAT 1050  
DB 1809 AAATTTACTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTTCAT 1868  
QY 1051 AAAAGGATATTATA 1065  
DB 1869 AAAAGGATATTATA 1883

RESULT 10  
AAF30001  
ID AAF30001 standard; cDNA; 1931 BP.  
XX AC AAF30001;  
XX AC  
DT 23-APR-2001 (first entry)  
XX DE Human CARD-3 cDNA.  
XX KW CARD-3; caspase recruitment domain; human; cancer; infection;  
KW autoimmune disease; neurological disease; haematological disease;  
KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
KW antiinflammatory; apoptosis; diagnosis; gene therapy; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 214..1826  
FT /\*tag= a  
FT /note= "the open reading frame is also specifically  
FT claimed in Claim 1(a)"  
XX PN WO200100826-A2.  
XX XX  
XX PD 04-JAN-2001.  
XX PF 28-JUN-2000; 2000WO-US017691.  
XX PR 28-JUN-1999; 99US-00340620.  
XX XX (MILL-) MILLENNIUM PHARM INC.  
XX PI Bertin J;  
XX XX

DR WPI; 2001-061973/07.  
XX P-PSDB; AAB20079.  
PT Isolated intracellular proteins predicted to be involved in regulating  
PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
PT viral infections, autoimmune diseases, neurological diseases and  
PT hematological disorders.  
XX  
PS Claim 1(a); Fig 1; 208pp; English..  
XX  
CC The present sequence is that of cDNA encoding human caspase recruitment  
CC domain 3 (CARD-3, see AAB20079). The cDNA was isolated following a  
CC database search using known CARD sequences. Plasmid pXel17A containing  
CC CARD-3 cDNA is deposited as ATCC 203037. CARD-3 is an intracellular  
CC protein predicted to be involved in regulating caspase activation. It is  
CC useful as a modulating agent in regulating cellular processes include  
CC cell growth and cell death. Methods of diagnosing and treating patients  
CC suffering from a disorder associated with an abnormal level or rate of  
CC apoptotic cell death, abnormal activity of the Fas/APO-1 receptor  
CC complex, abnormal activity of the tumour necrosis factor receptor complex  
CC or abnormal activity of a caspase involve administering a compound that  
CC modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6  
CC e.g. a small molecule, antisense nucleic acid, ribozyme or polypeptide.  
CC Such disorders include cancer, viral infection, autoimmune disorders,  
CC neurological diseases, haematological disorders, inflammatory disorders,  
CC and immune disorders. CARD nucleic acids can be used to express CARD  
CC proteins in a host cell e.g. for gene therapy applications, to detect a  
CC genetic lesion and to modulate CARD activity  
XX  
SQ Sequence 1931 BP; 613 A; 428 C; 416 G; 474 T; 0 U; 0 Other;  
Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 3.8e-138;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390  
DB 1149 AAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208  
QY 391 TCTGACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
DB 1209 TCTGACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 1268  
QY 451 TGAATAAGTGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCTCAAGACAATGATT 510  
DB 1269 TGAATAAGTGTCTCTCTGAAATCTCAAGGTCCCTGCCAGCTCTCAAGACAATGATT 1328  
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTGGAAATCA 570  
DB 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTGGAAATCA 1388  
QY 571 CAGTTGGATAGCACCATTCTCTGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 630  
DB 1389 CAGTTGGATAGCACCATTCTCTGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCAC 1448  
QY 631 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGACGAGAACTCAGAACGTCTGCA 690  
DB 1449 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGACGAGAACTCAGAACGTCTGCA 1508  
QY 691 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGAC 750  
DB 1509 GCCTGGTATAGCCACAGTGGATCCAGAGCAAAAGGGAGACATTTGTAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTCGTAGATGCTCTCTCTGTCAGGACCTTGATCATGAAGA 810  
DB 1569 AGAAGCTGCTTAAACAGTCGTAGATGCTCTCTCTGTCAGGACCTTGATCATGAAGA 1628  
QY 811 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 870  
DB 1629 GGAATATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 1688  
QY 871 CACTACTGACATCAAGGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAA 930



Db 1689 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTCGAAGATAA 1748  
 Qy 931 CAAACAAATGGTCTTACGCTTACCGGAATACCTGTGGTTCTTAGATACCAATCTTT 990  
 Db 1749 CAAACAAATGGTCTTACGCTTACCGGAATACCTGTGGTTCTTAGATACCAATCTTT 1808  
 Qy 991 AAATTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCGAAGAGAAATGTGTTTCAAT 1050  
 Db 1809 AAATTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCGAAGAGAAATGTGTTTCAAT 1868  
 Qy 1051 AAAAGGATATTATA 1065  
 Db 1869 AAAAGGATATTATA 1883

## RESULT 11

ABK89280

ID ABK89280 standard; cDNA; 1931 BP.

XX ABK89280;

XX 21-OCT-2002 (first entry)

XX Human cDNA encoding caspase recruitment domain protein CARD-3.

XX Human; ss; gene; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
 KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; aschma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FH CDS 214..1836

FT /\*tag= a

FT /product= "CARD-3"

XX WO200253765-A1.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-US049798.

XX 29-DEC-2000; 2000US-0258724P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J, Philpott D, Sansonetti P, Girardin S;

XX WPI; 2002-583627/62.

XX P-PSDB; ABG31075.

XX Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.  
 XX Example 2; Fig 1; 139pp; English.

XX The invention relates to identifying (M1) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a

CC cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (M1) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as asthma, allergy, psoriasis, contact dermatitis, atopic conditions, allergic, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and disorders of tissues. The present sequence is the human cDNA encoding CARD-3

XX Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

XX Query Match 43.8%; Score 731.8; DB 6; Length 1931;

XX Best Local Similarity 99.7%; Pred. No. 3.8e-138;

XX Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 390

Db 1149 AAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 1208

Qy 391 TCTGAACATACCTGTAATATCATGTGTCACAGAGAGAAATCATGTGATCTCTCAGTCCTCA 450

Db 1209 TCTGAACATACCTGTAATATCATGTGTCACAGAGAGAAATCATGTGATCTCTCAGTCCTCA 1268

Qy 451 TGAATAATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 510

Db 1269 TGAATAATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 1328

Qy 511 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGCTCGGAAATCA 570

Db 1329 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGCTCGGAAATCA 1388

Qy 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAACAAGACCAC 630

Db 1389 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAACAAGACCAC 1448

Qy 631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAATCTCAGAACGCTGCA 690

Db 1449 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAATCTCAGAACGCTGCA 1508

Qy 691 GCCTGGTATAGCCACAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 750

Db 1509 GCCTGGTATAGCCACAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 1568

Qy 751 AGAGCCCTGCTTAACACAGTCGTAGATGCCCTCTGTCCAGGGACTTGATCATGAAAGA 810

Db 1569 AGAGCCCTGCTTAACACAGTCGTAGATGCCCTCTGTCCAGGGACTTGATCATGAAAGA 1628

Qy 811 GGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTTACTAGA 870

Db 1629 GGACTATGAATCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTTACTAGA 1688

Qy 871 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTCGAAGATAA 930

Db 1689 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTATATAGTACAAAATTCGAAGATAA 1748

Qy 931 CAAACAAATGGTCTTACGCTTACCGGAATACCTGTGGTTCTTAGATACCAATCTTT 990

Db 1749 CAAACAAATGGTCTTACGCTTACCGGAATACCTGTGGTTCTTAGATACCAATCTTT 1808

Qy 991 AAATTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCGAAGAGAAATGTGTTTCAAT 1050

Db 1809 AAATTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCGAAGAGAAATGTGTTTCAAT 1868

Qy 1051 AAAGGATATTATA 1065

Db	1869	AAAAAGGATATTATA	1883	QY	391	TCCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA	450
				Db	1209	TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA	1268
RESULT 12				QY	451	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCTGCGAGCTCTCAAGACAATGATTT	510
AAL40752				Db	1269	TGAAAATAGTGGTCTCTCTGAAACCTTCAAGGTCCTGCGAGCTCTCAAGACAATGATTT	1328
AC	AAL40752;			QY	511	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTGCTCTGGAAATCA	570
DT	27-SEP-2002	(first entry)		Db	1329	TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCACTGCTCTGGAAATCA	1388
XX	cdna of human CARD-3	SEQ ID No 1.		QY	571	CAGTTGGGATACACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAACAAGCAC	630
XX	Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimers;			Db	1389	CAGTTGGGATACACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAACAAGCAC	1448
KW	cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological;			QY	631	TCCATGCTCTTCAGCAATAAATAATCACTCTCAACTGCGAGGAACTCGAAGCTGTGCA	690
KW	neotropic; antianemic; Caspase Recruitment Domain; CARD; CARD-4L; p53;			Db	1449	TCCATGCTCTTCAGCAATAAATAATCACTCTCAACTGCGAGGAACTCGAAGCTGTGCA	1508
KW	cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder;			QY	691	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGAC	750
KW	hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer;			Db	1509	GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGAC	1568
KW	systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease;			QY	751	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA	810
KW	anaemia; neutropenia; myelodysplastic syndrome; human; gene; ss.			Db	1569	AGAAGCCTGCCTTAACCACTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA	1628
OS	Homo sapiens.			QY	811	GGACTATGAACTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTTACTAGA	870
XX	US6369196-B1.			Db	1629	GGACTATGAACTTGTAGTACCAAGCCTCAAAAGTCAGACAAATTTACTAGA	1688
XX	09-APR-2002.			QY	871	CACTACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTCGAAAGATAA	930
XX	05-FEB-1999; 99US-00245281.			Db	1689	CACTACTGACATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTCGAAAGATAA	1748
XX	06-FEB-1998; 98US-00019942.			QY	931	CAACAAATGGGTCTTACCGGAAATATCTGTGGTTCTAGATCAACCATCTTT	990
XX	17-JUN-1998; 98US-00099041.			Db	1749	CAACAAATGGGTCTTACCGGAAATATCTGTGGTTCTAGATCAACCATCTTT	1808
XX	08-DEC-1998; 98US-00207359.			QY	991	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTTCAT	1050
XX	(MILL-) MILLENNIUM PHARM INC.			Db	1809	AAATTTACTTCAAAATAAAGCATGTAGTACTGTTTTCAGAGGAATATGTTTTCAT	1868
XX	Bertin J;			QY	1051	AAAAGGATATTATA	1065
XX	WPI; 2002-391988/42.			Db	1869	AAAAGGATATTATA	1883
XX	N-PSDB; AAO22107, AAO22108, AAO22109, AAO22110.						
XX	Isolated Caspase Recruitment Domain (CARD) polypeptides (CARD-4L and CARD						
XX	-4S) useful for diagnosing and treating e.g. Parkinson's and Alzheimer's						
XX	disease, cancers and viral infections.						
XX	Example 2; Fig 1; 116pp; English.						
XX	The invention relates to novel isolated Caspase Recruitment Domain (CARD)						
XX	polypeptides, CARD-4L and CARD-4S. The CARD proteins of the invention may						
XX	be used to treat disorders associated with decreased CARD expression by						
XX	supplementing the patient's own production of CARD. Disorders associated						
XX	with the expression and activity of CARD include cancers (particularly						
XX	follicular lymphomas, carcinomas associated with mutations in p53, and						
XX	hormone-dependent tumours such as breast cancer, prostate cancer, and						
XX	ovarian cancer), autoimmune disorders (such as systemic lupus						
XX	erythematosus, immune-mediated glomerulonephritis), viral infections						
XX	(such as those caused by herpes viruses, poxviruses, and adenoviruses),						
XX	neurological diseases (such as Alzheimer's disease, Parkinson's disease,						
XX	amyotrophic lateral sclerosis (ALS) reinitis pigmentosa, spinal						
XX	muscular atrophy, and various forms of cerebellar degeneration), anaemia						
XX	associated with chronic disease, aplastic anaemia, chronic neutropenia,						
XX	and the myelodysplastic syndromes. This polynucleotide sequence						
XX	represents the cDNA of a human CARD relating to the invention						
XX	Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;						
SQ	Query Match 43.8%; Score 731.8; DB 6; Length 1931;						
	Best Local Similarity 99.7%; Pred. No. 3.8e-138;						
	Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;						
QY	331	ACAGTTACAGAGTGTTCACGTGCGATTCACCTATGTGACAGAGAAATGGAATATC	390				
Db	1149	AAAGTTACAGAGTGTTCACGTGCGATTCACCTATGTGACAGAGAAATGGAATATC	1208				

XX PD 22-OCT-2002.  
XX PF 08-DEC-1998; 98US-00207359.  
XX PR 06-FEB-1998; 98US-00019942.  
XX PR 17-JUN-1998; 98US-00099041.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Bertin J;  
XX PI WPI; 2003-147109/14.  
XX DR P-PSDB; ABUS6269.  
XX XX  
XX PT Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z  
XX PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,  
XX PT detection assays, predictive medicine, and in therapeutic applications.  
XX PS Example 2; Fig 1; 99pp; English.  
XX CC The invention relates to an isolated polypeptide, comprising at least 25  
XX CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,  
XX CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)  
XX CC polypeptide. Also included is an isolated fusion protein, comprising the  
XX CC CARD polypeptide covalently linked by a peptide bond to a heterologous  
XX CC polypeptide. The CARD polypeptide is useful in screening assays,  
XX CC detection assays (e.g. chromosomal mapping, tissue typing and forensic  
XX CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,  
XX CC monitoring clinical trials and pharmacogenomics), and in therapeutic and  
XX CC prophylactic treatments (in diseases associated with apoptotic cell death  
XX CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and  
XX CC immune related glomerulonephritis), viral infections, AIDS (acquired  
XX CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's  
XX CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
XX CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),  
XX CC haematological diseases (e.g. anaemia, neutropaenia and myelodysplastic  
XX CC syndromes), myocardial infarction and stroke). The CARD polypeptide is  
XX CC useful as bait protein in a two-hybrid assay or three hybrid assay to  
XX CC identify other proteins, which bind to or interact with other CARD  
XX CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
XX CC human CARD-4 is located on chromosome 7. The present sequence is a human  
XX CC CARD cDNA  
XX SQ Sequence 1931 BP; 613 A; 430 C; 416 G; 472 T; 0 U; 0 Other;

Query Match 43.8%; Score 731.8; DB 7; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 3.8e-138;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 390  
DB 1149 AAAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 1208  
QY 391 TGTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 450  
DB 1209 TGTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGTCCA 1268  
QY 451 TGAATAATAGTGGTTCCTCGAACTTCAAGTCCCTGAGGTCCTCTCAGAGCAATGATT 510  
DB 1269 TGAATAATAGTGGTTCCTCGAACTTCAAGTCCCTGAGGTCCTCTCAGAGCAATGATT 1328  
QY 511 TTATCTAGAAAGCTCAAGACATGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 570  
DB 1329 TTATCTAGAAAGCTCAAGACATGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 1388  
QY 571 CAGTTGGGATAGACCATTTCTGGATCTCAAGGGGCTGCAATCTGTGATCAAGACAC 630  
DB 1389 CAGTTGGGATAGACCATTTCTGGATCTCAAGGGGCTGCAATCTGTGATCAAGACAC 1448  
QY 631 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGAGGAACTCAGACGCTGCA 690  
DB 1449 TCCATGCTCTTCAGCAATAATAAATCACTCTCACTGAGGAACTCAGACGCTGCA 1508

QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
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QY 751 AGAGCCCTGCTTACCAAGTGGTATAGTCCAGGACCTTGTCCAGGGACTTGTATCATGAA 810  
DB 1569 AGAGCCCTGCTTACCAAGTGGTATAGTCCAGGACCTTGTCCAGGGACTTGTATCATGAA 1628  
QY 811 GGACTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGA 870  
DB 1629 GGACTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCAAGCAATTTACTAGA 1688  
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DB 1689 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATATAGTACAAAATTTGAAAGATAA 1748  
QY 931 CAAACAATGGTCTTCCAGCCTTACCCGGGAATCTGTGGTCTTGTAGATCACCATCTTT 990  
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DB 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTTTCAT 1868  
QY 1051 AAAGGATATTATTA 1065  
DB 1869 AAAGGATATTATTA 1883

RESULT 14  
ADB81363  
ID ADB81363 standard; cDNA; 1931 BP.  
XX ADB81363;  
XX 04-DEC-2003 (first entry)  
DE Human caspase recruitment domain 3 (CARD-3) cDNA.  
XX human; ss; gene; CARD-3; CARD-4; caspase recruitment domain; apoptosis;  
KW p75; tumour necrosis factor; TNF; neutrophin receptor; cancer;  
KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;  
KW viral infection; neurological; retinitis pigmentosa; haematologic;  
KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH CDS 214..1836  
FT /\*tag= a  
FT /product= "CARD-3 protein"  
XX  
PN US2002061833-A1.  
XX 23-MAY-2002.  
XX 26-DEC-2000; 2000US-00748537.  
XX 06-FEB-1998; 98US-00019942.  
XX 17-JUN-1998; 98US-00099041.  
XX (BERT/) BERTIN J.  
XX (CHAO/) CHAO M V.  
XX Bertin J, Chao MV;  
XX WPI; 2003-657125/62.  
XX P-PSDB; ADB81362.  
XX  
XX Detecting compounds which alter binding of the caspase recruitment domain  
XX (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful  
XX to provide compounds for treating CARD-3 mediated disorders.



CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for  
 CC human CARD-4 is located on chromosome 7. The present sequence is a human  
 CC CARD cDNA  
 XX  
 SQ Sequence 1620 BP; 517 A; 360 C; 320 G; 423 T; 0 U; 0 Other;

Query Match 40.9%; Score 681.8; DB 7; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-128;  
 Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390  
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 QY 936 AAAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAGAGAGAAATGGAATTATC 995  
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 QY 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
 DB |||||||  
 QY 996 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055  
 DB |||||||  
 QY 451 TGAATAATAGTGTCTCTGAACTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510  
 DB |||||||  
 QY 1056 TGAATAATAGTGTCTCTGAACTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115  
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 QY 511 TTATATCTAGAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 570  
 DB |||||||  
 QY 1116 TTTAICTAGAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 1175  
 DB |||||||  
 QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGTGATCAAGAACCAC 630  
 DB |||||||  
 QY 1176 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGTGATCAAGAACCAC 1235  
 DB |||||||  
 QY 631 TCCATGCTCTTTCAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAAGCTGTGCA 690  
 DB |||||||  
 QY 1236 TCCATGCTCTTTCAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAAGCTGTGCA 1295  
 DB |||||||  
 QY 691 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
 DB |||||||  
 QY 1296 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1355  
 DB |||||||  
 QY 751 AGAAGCTCGCTTAAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGA 810  
 DB |||||||  
 QY 1356 AGAAGCTCGCTTAAACCACTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGA 1415  
 DB |||||||  
 QY 811 GGACTATGAACCTTTAGTACGAGCTACAGGACCTCAAAAGTCAGACAATTTACTAGA 870  
 DB |||||||  
 QY 1416 GGACTATGAACCTTTAGTACGAGCTACAGGACCTCAAAAGTCAGACAATTTACTAGA 1475  
 DB |||||||  
 QY 871 CACTACTGACATCCAGAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930  
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 Job time : 670 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:38:40 ; Search time 156 Seconds  
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	78.4	2501	4	US-09-920-663-3
2	1308	78.4	2502	4	US-09-069-023-2
3	731.8	43.8	1931	3	US-09-019-942-2
4	731.8	43.8	1931	4	US-09-099-041A-1
5	731.8	43.8	1931	4	US-09-245-281-1
6	731.8	43.8	1931	4	US-09-470-271-2
7	731.8	43.8	1931	4	US-09-207-359B-1
8	731.8	43.8	1931	4	US-09-340-620A-1
9	731.8	43.8	1931	4	US-09-865-364-1
10	731.8	43.8	1931	4	US-09-748-537-2
11	695.4	41.7	1060	4	US-09-023-655-684
12	681.8	40.9	1620	4	US-09-099-041A-3
13	681.8	40.9	1620	4	US-09-245-281-3
14	681.8	40.9	1620	4	US-09-207-359B-3
15	681.8	40.9	1620	4	US-09-340-620A-3
16	681.8	40.9	1620	4	US-09-865-364-3
17	54.2	3.2	19124	2	US-08-487-826B-13
18	52.8	3.2	20674	4	US-09-641-638-651
19	50.4	3.0	832	4	US-09-621-976-2813
20	48	2.9	6152	3	US-08-973-462-1
21	48	2.9	6156	4	US-10-204-708-60
22	47.8	2.9	6583	4	US-10-204-708-25
23	47.6	2.9	396	4	US-09-640-173-53
24	47.6	2.9	396	4	US-09-713-550-53
25	47.6	2.9	834	3	US-08-998-416-305
26	47.6	2.9	10144	4	US-10-204-708-93
27	47.4	2.8	5610	4	US-10-204-708-54

c	28	47.4	2.8	5852	1	US-07-867-106-2	Sequence 2, Appli
	29	47.4	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
	30	47	2.8	640681	4	US-09-790-988-1	Sequence 1, Appli
	31	46.2	2.8	474	4	US-09-621-976-18033	Sequence 18033, A
	32	46	2.8	5562	4	US-10-204-708-63	Sequence 63, Appl
	33	45.8	2.7	701	3	US-08-998-416-701	Sequence 701, Appl
c	34	45.8	2.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
	35	45.8	2.7	6669	4	US-10-204-708-6	Sequence 6, Appli
	36	45.8	2.7	8920	2	US-08-446-855A-1	Sequence 1, Appli
	37	45.8	2.7	8920	3	US-09-150-741-1	Sequence 1, Appli
	38	45.6	2.7	9347	4	US-10-204-708-35	Sequence 35, Appl
	39	45.6	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
c	40	45.2	2.7	711	3	US-08-998-416-786	Sequence 786, App
	41	44.8	2.7	6317	4	US-10-204-708-11	Sequence 11, Appl
	42	44.2	2.6	636	3	US-08-998-416-1137	Sequence 1137, Ap
c	43	44.2	2.6	3095	6	5231168-1	Patent No. 5231168
	44	44.2	2.6	5455	4	US-10-204-708-33	Sequence 33, Appl
	45	44.2	2.6	6182	4	US-10-204-708-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1

US-09-920-663-3  
; Sequence 3, Application US/09920663  
; Patent No. 6426221  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Lex M. Cowert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION  
; FILE REFERENCE: RTS-0233  
; CURRENT APPLICATION NUMBER: US/09/920,663  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 3  
; LENGTH: 2501  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (225)...(1847)  
US-09-920-663-3

Query Match	78.4%	Score 1308;	DB 4;	Length 2501;
Best Local Similarity	99.0%	Pred. No. 2.3e-293;		
Matches 1329;	Conservative	0;	Mismatches 5;	Indels 8; Gaps 1;
Qy	331	ACAGTTACAGAGTGTTC	CAAGTGGCCATTCACCTATGTGACAGAGAAATGGAATTTATC	390
Db	1160	AAAGTTACAGAGTGTTC	CAAGTGGCCATTCACCTATGTGACAGAGAAATGGAATTTATC	1219
Qy	391	TCTGAACATACCTGTAAATCATGTC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCA	450
Db	1220	TCTGAACATACCTGTAAATCATGTC	CAAGAGGAATCATGTGGATCCTCTCAGCTCCA	1279
Qy	451	TGAAATAGTGGTTCCTCTGAAACTT	CAAGTCCCTGCCAGCTCCTCAAGCAATGATTT	510
Db	1280	TGAAATAGTGGTTCCTCTGAAACTT	CAAGTCCCTGCCAGCTCCTCAAGCAATGATTT	1339
Qy	511	TTTATCTAGAAAGCTCAAGACTGT	TATTTATGAAGCTGATCACTGCTCTGGAAATCA	570
Db	1340	TTTATCTAGAAAGCTCAAGACTGT	TATTTATGAAGCTGATCACTGCTCTGGAAATCA	1399
Qy	571	CAGTTGGGATAGCACCATTTCTGGAT	CTCAAGGSGCTCATTCTGTGATCAAGACCAAC	630
Db	1400	CAGTTGGGATAGCACCATTTCTGGAT	CTCAAGGSGCTCATTCTGTGATCAAGACCAAC	1459
Qy	631	TCCATGCTCTTTCAGCAATAATAAAT	TCCACTCTCAACTGCAGGAAACTCAGAACGCTGCA	690
Db	1460	TCCATGCTCTTTCAGCAATAATAAAT	TCCACTCTCAACTGCAGGAAACTCAGAACGCTGCA	1519
Qy	691	GCCTGGTATAGCCCGACAGCTGGAT	CCAGAGGAAAGGGAAGACATTTGTGAAACCAATGAC	750





Db 1941 ACCTTTATGAAGGTTCTTTGGTAAATATAGTCTCCCTCCTGACACTGCGATTTT 2000  
Qy 1171 TTTTAATTAATACAAAGTAAAGTT-----TGAATTTTGCTACATAGTTTCAATTTT 1222  
Db 2001 TTTTAATTAATACAAAGTAAAGTTGAAATTTGGTTGAAATTTGCTACATAGTTTCAATTTT 2060  
Qy 1223 ATGTCCTTTTGTAAACAGAAACCACTTTAAAGGATAGTAATTTCTTGTGTTATAACA 1282  
Db 2061 ATGTCCTTTTGTAAACAGAAACCACTTTAAAGGATAGTAATTTCTTGTGTTATAACA 2120  
Qy 1283 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCACTTCAATTTCTTCATGG 1342  
Db 2121 GTGCTTAAAGGTATGATGATTTCTGATGGAAGCCATTTTCACTTCAATTTCTTCATGG 2180  
Qy 1343 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATATACCCCTTTACCCAC 1402  
Db 2181 ATTATTTGTTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATATACCCCTTTACCCAC 2240  
Qy 1403 CAGACAGAGTACAGAAATCCCTGCTTAAATCCAGGCTTAATTCGCCCTACAAAGGTTA 1462  
Db 2241 CAGACAGAGTACAGAAATCCCTGCTTAAATCCAGGCTTAATTCGCCCTACAAAGGTTA 2300  
Qy 1463 TTAATTTAAACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAATTCCTTTA 1522  
Db 2301 TTAATTTAAACTCCATTTATAGGATTAATTTTAAAGTTTATTTATGAATTCCTTTA 2360  
Qy 1523 AAAATGATATTTCAAAGGTAAACCAATACAAATATAAGAAAGAAATATAATATTAATAC 1582  
Db 2361 AAAATGATATTTCAAAGGTAAACCAATACAAATATAAGAAAGAAATATAATATTAATAC 2420  
Qy 1583 CGCTTCTGTCCTCCATTTTAACTCAGCTTCCCTACTGTGTCACCAACCAAGCTAA 1642  
Db 2421 CGCTTCTGTCCTCCATTTTAACTCAGCTTCCCTACTGTGTCACCAACCAAGCTAA 2480  
Qy 1643 ATAAAGTCAACAGCCTGATGTG 1664  
Db 2481 ATAAAGTCAACAGCCTGATGTG 2502

RESULT 3

US-09-019-942-2  
; Sequence 2, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,942  
; FILING DATE: 06-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/068001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1931 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-09-019-942-2

Query Match 43.8%; Score 731.8; DB 3; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 331 ACAGTTACAGAGTGTTCACAGTGCACATTCACCTATGTGACAGAAAGAAATGGAATATC 390  
Db 1149 AAAGTTACAGAGTGTTCACAGTGCACATTCACCTATGTGACAGAAAGAAATGGAATATC 1208  
Qy 391 TCTGAAATACATCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCA 450  
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Db 1269 TGAATAATAGTGTCTCTGCTGAAACTTCAAGGTCCCTGCGAGCTCCTCAAGCAATGATTT 1328  
Qy 511 TTTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGGAATCA 570  
Db 1329 TTTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGGAATCA 1388  
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Db 1449 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTCGCAGAAATCATGTGAAACCAATGAC 1508  
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Qy 811 GGACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGA 870  
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Qy 871 CACTACTGACATCCAAAGGAGGAAGATTTGCCAAAGTTATAGTACAAAATTTCAAGAGATA 930  
Db 1689 CACTACTGACATCCAAAGGAGGAAGATTTGCCAAAGTTATAGTACAAAATTTCAAGAGATA 1748  
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Qy 991 AAATTTACTTCAAAATAAAAGCATGTAGTGAATGCTGTTTTTCAAGAGAAATGTGTTTCA 1050  
Db 1809 AAATTTACTTCAAAATAAAAGCATGTAGTGAATGCTGTTTTTCAAGAGAAATGTGTTTCA 1868  
Qy 1051 AAAAGGATATTATA 1065  
Db 1869 AAAAGGATATTATA 1883

RESULT 4

US-09-099-041A-1  
; Sequence 1, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:

; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-099-041A-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTATC 390  
DB 1149 AAAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTATC 1208  
QY 391 TCTGAACATACCTGTAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB 1209 TCTGAACATACCTGTAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATT 510  
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DB 1329 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAATCA 1388  
QY 571 CAGTTGGGATAGACACCATTTCTGTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630  
DB 1389 CAGTTGGGATAGACACCATTTCTGTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1448  
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QY 871 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930  
DB 1689 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1748  
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DB 1749 CAAACAAATGGCTTTCAGGCTTACCCGGAAATTAATTTGTGGTTCTAGATCACCACATCTTT 1808  
QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAT 1050  
DB 1809 AAATTTACTTCAAAATAAAGCATGTAAAGTCACTGTTTTTCAAGAGAAATGTGTTTCAT 1868  
QY 1051 AAAGGATATTATTA 1065  
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Db 1869 AAAAGGATATTATTA 1883  
RESULT 5  
US-09-245-281-1  
; Sequence 1, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (214)...(1833)  
US-09-245-281-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTATC 390  
DB 1149 AAAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAGAAATGGAATTATC 1208  
QY 391 TCTGAACATACCTGTAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
DB 1209 TCTGAACATACCTGTAATCATGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATT 510  
DB 1269 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATT 1328  
QY 511 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAATCA 570  
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DB 1389 CAGTTGGGATAGACACCATTTCTGTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1448  
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DB 1629 GGAATATGAATTTAGTACCAAGCCTCAAGGACCTCAAAAGTTCAGACAAATTAATCTAGA 1688  
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Db 1689 CACTACTGACATCCAAAGGAGAAATTTCCCAAGTTATATAGTACAAAAATTTGAAAGATAA 1748  
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 Db 1809 AAATTACTTCAAAATMAAGCATGTAACTGCTGTTTTTCAAGAGAAATGTGTTTCAAT 1868  
 QY 1051 AAAAGGATATTATA 1065  
 Db 1869 AAAGGATATTATA 1883

RESULT 6  
 US-09-470-271-2  
 ; Sequence 2, Application US/09470271  
 ; Patent No. 6410689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/470,271  
 ; FILING DATE:  
 ; PRIOR APPLICATION NUMBER:  
 ; APPLICATION NUMBER: 09/019,942  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.  
 ; REGISTRATION NUMBER: 35,283  
 ; REFERENCE/DOCKET NUMBER: 07334/068001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1931 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cdna  
 US-09-470-271-2

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
 Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
 Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTTACAGAGTGTTCAGTGCCATTCCACCTATGTGCAAGAGAAATGGAATTATC 390  
 Db 1149 AAGTTTACAGAGTGTTCAGTGCCATTCCACCTATGTGCAAGAGAAATGGAATTATC 1208  
 QY 391 TCTGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
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 QY 1051 AAAAGGATATTATA 1065  
 Db 1869 AAAGGATATTATA 1883

RESULT 7  
 US-09-207-359B-1  
 ; Sequence 1, Application US/09207359B  
 ; Patent No. 6469140  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/207,359B  
 ; CURRENT FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)...(1833)  
 US-09-207-359B-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
 Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
 Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 331 ACAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAAGATAGTGGTCTCTCAAGTGCATTCACCTATGTGACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 510
Db 1269 TGAAGATAGTGGTCTCTCAAGTGCATTCACCTATGTGACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 1328
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QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

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RESULT 8  
US-09-340-620A-1  
; Sequence 1, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-340-620A-1

Query Match      43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 4.le-160;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTCTTCAAGTGCATTCACCTATGTGACAAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 1268
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Db 1269 TGAAGATAGTGGTCTCTCAAGTGCATTCACCTATGTGACAAAGAGAAATCATGTGGATCTCTCAGCTCCA 1328
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QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

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RESULT 9  
US-09-364-1  
; Sequence 1, Application US/09865364  
; Patent No. 6613521  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

;; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
;; FILE REFERENCE: 07334-112001  
;; CURRENT APPLICATION NUMBER: US/09/865,364  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 09/207,359  
;; PRIOR FILING DATE: 1998-12-08  
;; PRIOR APPLICATION NUMBER: US 09/099,041  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; NUMBER OF SEQ ID NOS: 47  
;; SEQ ID NO 1  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (214)...(1833)  
US-09-865-364-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
Db |||||||  
QY 391 TCTGACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
Db |||||||  
QY 1209 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TCAAAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510  
Db |||||||  
QY 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328  
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 570  
Db |||||||  
QY 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 1388  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAC 630  
Db |||||||  
QY 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAT 1448  
QY 631 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCA 690  
Db |||||||  
QY 1449 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCA 1508  
QY 691 GCTGGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
Db |||||||  
QY 1509 GCCTGGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTGCATAGTCCCTTCTGTCCAGGACTTGCATCATGAAGA 810  
Db |||||||  
QY 1569 AGAAGCTGCTTAAACAGTGCATAGTCCCTTCTGTCCAGGACTTGCATCATGAAGA 1628  
QY 811 GGACTATGAATTTGTTAGTACCAAGGCTTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 870  
Db |||||||  
QY 1629 GGACTATGAATTTGTTAGTACCAAGGCTTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1688  
QY 871 CACTACTGACATCCAGGGAAGAATTTGCAAAAGTTATAGTACAAAAATTTGAAGATAA 930  
Db |||||||  
QY 1689 CACTACTGACATCCAGGGAAGAATTTGCAAAAGTTATAGTACAAAAATTTGAAGATAA 1748  
QY 931 CAAACAAATGGGTCTTACCGGAAATCTATGTGGTTCTTAGATCACCATCTTT 990  
Db |||||||  
QY 1749 CAAACAAATGGGTCTTACCGGAAATCTATGTGGTTCTTAGATCACCATCTTT 1808  
QY 991 AATTTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAAGAAATGTGTTTCAT 1050  
Db |||||||  
QY 1809 AATTTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAAGAAATGTGTTTCAT 1868  
Db |||||||

QY 1051 AAAAGGATATTATA 1065  
Db |||||||  
Db 1869 AAAAGGATATTATA 1883  
RESULT 10  
US-09-748-537-2  
;; Sequence 2, Application US/09748537  
;; Patent No. 6680167  
;; GENERAL INFORMATION:  
;; APPLICANT: Bertin, John  
;; APPLICANT: Chao, Moses V.  
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
;; FILE REFERENCE: 07334-316001  
;; CURRENT APPLICATION NUMBER: US/09/748,537  
;; CURRENT FILING DATE: 2000-12-26  
;; PRIOR APPLICATION NUMBER: US 09/099,041  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: US 09/019,942  
;; PRIOR FILING DATE: 1998-02-06  
;; NUMBER OF SEQ ID NOS: 14  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 1931  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-748-537-2  
  
Query Match 43.8%; Score 731.8; DB 4; Length 1931;  
Best Local Similarity 99.7%; Pred. No. 4.1e-160;  
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390  
Db |||||||  
QY 391 TCTGACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
Db |||||||  
QY 1209 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
QY 451 TCAAAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510  
Db |||||||  
QY 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328  
QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 570  
Db |||||||  
QY 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCATCTGCTCGGAAATCA 1388  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAC 630  
Db |||||||  
QY 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGAGCCAT 1448  
QY 631 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCA 690  
Db |||||||  
QY 1449 TCCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGTCGCA 1508  
QY 691 GCTGGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750  
Db |||||||  
QY 1509 GCCTGGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
QY 751 AGAAGCTGCTTAAACAGTGCATAGTCCCTTCTGTCCAGGACTTGCATCATGAAGA 810  
Db |||||||  
QY 1569 AGAAGCTGCTTAAACAGTGCATAGTCCCTTCTGTCCAGGACTTGCATCATGAAGA 1628  
QY 811 GGACTATGAATTTGTTAGTACCAAGGCTTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 870  
Db |||||||  
QY 1629 GGACTATGAATTTGTTAGTACCAAGGCTTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1688  
QY 871 CACTACTGACATCCAGGGAAGAATTTGCAAAAGTTATAGTACAAAAATTTGAAGATAA 930  
Db |||||||  
QY 1689 CACTACTGACATCCAGGGAAGAATTTGCAAAAGTTATAGTACAAAAATTTGAAGATAA 1748  
QY 931 CAAACAAATGGGTCTTACCGGAAATCTATGTGGTTCTTAGATCACCATCTTT 990  
Db |||||||

Db 1749 CAACAAATGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTT 1808  
 Qy 991 AAATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGCAAAATGTTTCAT 1050  
 Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAGCAAAATGTTTCAT 1868  
 Qy 1051 AAAAGGATATTATA 1065  
 Db 1869 AAAAGGATATTATA 1883

RESULT 11  
 US-09-023-655-684  
 ; Sequence 684, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 684:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1060 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: MPHGNOT03  
 ; CLONE: 445186  
 ; US-09-023-655-684

Query Match 41.7%; Score 695.4; DB 4; Length 1060;  
 Best Local Similarity 99.7%; Pred. No. 8.8e-152;  
 Matches 707; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 Qy 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTCAGAGCAAAATGGAATATC 390  
 Db 352 AAAGTTACAGAGTGTTCAGTGCCTTACCTATGTCAGAGCAAAATGGAATATC 411  
 Qy 391 TCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
 Db 412 TCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCA 471

Qy 451 TGAATAA- GTGTTCTCTGAAATTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATT 509  
 Db 472 TGAATAAAGTGTGTTCTCTGAAATTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATT 531  
 Qy 510 TTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTTGAAATC 569  
 Db 532 TTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGTCTTGAAATC 591  
 Qy 570 ACAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGCATTTCTGTGATCAAGACCA 629  
 Db 592 ACAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGCATTTCTGTGATCAAGACCA 651  
 Qy 630 CTCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGAACTCAGAACGTCGTC 689  
 Db 652 CTCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGAACTCAGAACGTCGTC 711  
 Qy 690 AGCTGTGTATAGCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGA 749  
 Db 712 AGCTGTGTATAGCCGAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGA 771  
 Qy 750 CAGAAGCTGCTTAAACCACTGCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
 Db 772 CAGAAGCTGCTTAAACCACTGCTAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831  
 Qy 810 AGGACTATGAACCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGAAATTTAGTAG 869  
 Db 832 AGGACTATGAACCTTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCAAGAAATTTAGTAG 891  
 Qy 870 ACATCTACTGACATCCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATA 929  
 Db 892 ACATCTACTGACATCCCAAGGAGAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATA 951  
 Qy 930 ACAACAAATGGTCTTACGCTTACCGGAAATATCTGTTGTTTCTAGATCAACCATCTT 989  
 Db 952 ACAACAAATGGTCTTACGCTTACCGGAAATATCTGTTGTTTCTAGATCAACCATCTT 1011  
 Qy 990 TAAATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAAAGA 1038  
 Db 1012 TAAATTTACTTCAAAATAAAGCATGTAAGTACCTGTTTTCAGAAAGA 1060

RESULT 12  
 US-09-099-041A-3  
 ; Sequence 3, Application US/09099041A  
 ; Patent No. 6340576  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/09/099,041A  
 ; CURRENT FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-099-041A-3

Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
 Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 331 ACAGTTACAGAGTGTTCAGTGCCTTACCTATGTCAGAGCAAAATGGAATATC 390  
 Db 936 AAAGTTACAGAGTGTTCAGTGCCTTACCTATGTCAGAGCAAAATGGAATATC 995  
 Qy 391 TCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCA 450  
 Db 996 TCTGAACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCTCTCAGCTCCA 1055

QY 451 TGAATAATAGTGGTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTT 510  
 DB 1056 TGAATAATAGTGGTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTT 1115  
 QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 570  
 DB 1116 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 1175  
 QY 571 CAGTTGGGATAGCACCATTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGAACAC 630  
 DB 1176 CAGTTGGGATAGCACCATTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGAACAC 1235  
 QY 631 TCCATGCTCTTCAAGCAATAAATCCACTTCAAGCTGCGAGAAACTCAGAACCTGCA 690  
 DB 1236 TCCATGCTCTTCAAGCAATAAATCCACTTCAAGCTGCGAGAAACTCAGAACCTGCA 1295  
 QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 750  
 DB 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 1355  
 QY 751 AGAAGCTGCTTTAACCCAGTCCCTGCTAGATGCCCTTCTGTCAGGGACTTGCATGAAAGA 810  
 DB 1356 AGAAGCTGCTTTAACCCAGTCCCTGCTAGATGCCCTTCTGTCAGGGACTTGCATGAAAGA 1415  
 QY 811 GGACTATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGCAATTAAGTACA 870  
 DB 1416 GGACTATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGCAATTAAGTACA 1475  
 QY 871 CACTACTGACATCCCAAGGAGAGATTTGCCAAAGTATAGTACAAAATTTGAAAGATAA 930  
 DB 1476 CACTACTGACATCCCAAGGAGAGATTTGCCAAAGTATAGTACAAAATTTGAAAGATAA 1535  
 QY 931 CAAACAAATGGTCTTTCAGCCTTACCGGAATATCTTGTGTTTCTAGATCACCATCTTT 990  
 DB 1536 CAAACAAATGGTCTTTCAGCCTTACCGGAATATCTTGTGTTTCTAGATCACCATCTTT 1595

RESULT 13  
 US-09-245-281-3  
 ; Sequence 3, Application US/09245281  
 ; Patent No. 6369196  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/09/245,281  
 ; EARLIER FILING DATE: 1999-02-05  
 ; EARLIER APPLICATION NUMBER: US 09/207,359  
 ; EARLIER FILING DATE: 1998-12-08  
 ; EARLIER APPLICATION NUMBER: US 09/099,041  
 ; EARLIER FILING DATE: 1998-06-17  
 ; EARLIER APPLICATION NUMBER: US 09/019,942  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-245-281-3  
 Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
 Matches 663; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGGTTCAGTCCCTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTTATC 390

DB 936 AAAGTTACAGAGTGGTTCAGTCCCTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTTATC 995  
 QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
 DB 996 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055  
 QY 451 TGAATAATAGTGGTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTT 510  
 DB 1056 TGAATAATAGTGGTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTT 1115  
 QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 570  
 DB 1116 TTTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 1175  
 QY 571 CAGTTGGGATAGCACCATTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGAACAC 630  
 DB 1176 CAGTTGGGATAGCACCATTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGAACAC 1235  
 QY 631 TCCATGCTCTTCAAGCAATAAATCCACTTCAAGCTGCGAGAAACTCAGAACCTGCA 690  
 DB 1236 TCCATGCTCTTCAAGCAATAAATCCACTTCAAGCTGCGAGAAACTCAGAACCTGCA 1295  
 QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 750  
 DB 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGGAACCAATGAC 1355  
 QY 751 AGAAGCTGCTTTAACCCAGTCCCTGCTAGATGCCCTTCTGTCAGGGACTTGCATGAAAGA 810  
 DB 1356 AGAAGCTGCTTTAACCCAGTCCCTGCTAGATGCCCTTCTGTCAGGGACTTGCATGAAAGA 1415  
 QY 811 GGACTATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGCAATTAAGTACA 870  
 DB 1416 GGACTATGAATCTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGCAATTAAGTACA 1475  
 QY 871 CACTACTGACATCCCAAGGAGAGATTTGCCAAAGTATAGTACAAAATTTGAAAGATAA 930  
 DB 1476 CACTACTGACATCCCAAGGAGAGATTTGCCAAAGTATAGTACAAAATTTGAAAGATAA 1535  
 QY 931 CAAACAAATGGTCTTTCAGCCTTACCGGAATATCTTGTGTTTCTAGATCACCATCTTT 990  
 DB 1536 CAAACAAATGGTCTTTCAGCCTTACCGGAATATCTTGTGTTTCTAGATCACCATCTTT 1595

RESULT 14  
 US-09-207-359B-3  
 ; Sequence 3, Application US/09207359B  
 ; Patent No. 6469140  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; FILE REFERENCE: 07334-112001  
 ; CURRENT APPLICATION NUMBER: US/09/207,359B  
 ; CURRENT FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1620  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-207-359B-3  
 Query Match 40.9%; Score 681.8; DB 4; Length 1620;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-148;  
 Matches 663; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390
Db |
QY 936 AAGTTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 995
Db |
QY 391 TCTGAACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db |
QY 996 TCTGAACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
Db |
QY 1056 TGAATAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCTGGAATCA 570
Db |
QY 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCTGGAATCA 1175
QY 571 CAGTTGGGATAGCACCANTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630
Db |
QY 1176 CAGTTGGGATAGCACCANTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1235
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCA 690
Db |
QY 1236 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCA 1295
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db |
QY 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1355
QY 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA 810
Db |
QY 1356 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA 1415
QY 811 GGACTATGAATTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGCAATTTACTAGA 870
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QY 1416 GGACTATGAATTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1475
QY 871 CACTACTGACATCCAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATA 930
Db |
QY 1476 CACTACTGACATCCAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATA 1535
QY 931 CAAACAAATGGGCTTTCAGCCTTACCGGAAATACCTGTGGTTCCTAGATCACCATCTTT 990
Db |
QY 1536 CAAACAAATGGGCTTTCAGCCTTACCGGAAATACCTGTGGTTCCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAGCATG 1015
Db |
QY 1596 AAATTTACTTCAAAATAAAGCATG 1620
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## RESULT 15

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US-09-340-620A-3
; Sequence 3, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
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; ORGANISM: Homo sapiens

US-09-340-620A-3

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Query Match 40.9%; Score 681.8; DB 4; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.4e-148;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 390
Db |
QY 936 AAGTTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAGAGAGAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db |
QY 996 TCTGAACATACCTGTAAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
Db |
QY 1056 TGAATAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCTGGAATCA 570
Db |
QY 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCTGGAATCA 1175
QY 571 CAGTTGGGATAGCACCANTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630
Db |
QY 1176 CAGTTGGGATAGCACCANTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1235
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCA 690
Db |
QY 1236 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACCTCTGCA 1295
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db |
QY 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1355
QY 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA 810
Db |
QY 1356 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGA 1415
QY 811 GGACTATGAATTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGCAATTTACTAGA 870
Db |
QY 1416 GGACTATGAATTTGTAGTACCAAGCTTACAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1475
QY 871 CACTACTGACATCCAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATA 930
Db |
QY 1476 CACTACTGACATCCAGAGGAAGAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATA 1535
QY 931 CAAACAAATGGGCTTTCAGCCTTACCGGAAATACCTGTGGTTCCTAGATCACCATCTTT 990
Db |
QY 1536 CAAACAAATGGGCTTTCAGCCTTACCGGAAATACCTGTGGTTCCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAGCATG 1015
Db |
QY 1596 AAATTTACTTCAAAATAAAGCATG 1620
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Search completed: April 1, 2004, 06:19:40

Job time : 176 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:55:40 ; Search time 648 Seconds  
(without alignments)  
9589.048 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 1669

Sequence: 1 acctagtattaccagata.....caacagcgtgtgtgtaaaa 1669

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PTUS\_PUBCOMB.seq.\*
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- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
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- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
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- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1668	99.9	1669	US-09-771-161A-2	Sequence 2, Appli
2	1332.4	78.8	2709	US-09-925-301-173	Sequence 173, Appl
3	1308	78.4	2501	US-09-981-397A-13	Sequence 13, Appl
4	731.8	43.8	1931	US-09-748-537-2	Sequence 2, Appli
5	731.8	43.8	1931	US-09-728-721-1	Sequence 1, Appli
6	731.8	43.8	1931	US-10-133-780-2	Sequence 2, Appli
7	731.8	43.8	1931	US-10-105-931-1	Sequence 1, Appli
8	731.8	43.8	1931	US-10-118-984-1	Sequence 1, Appli
9	731.8	43.8	1931	US-10-295-981-1	Sequence 1, Appli
10	681.8	40.9	1620	US-09-728-721-3	Sequence 3, Appli
11	681.8	40.9	1620	US-10-105-931-3	Sequence 3, Appli
12	681.8	40.9	1620	US-10-118-984-3	Sequence 3, Appli
13	681.8	40.9	1620	US-10-295-981-3	Sequence 3, Appli
14	363.4	21.8	491	US-09-918-995-20565	Sequence 20565, A
15	271	16.2	299	US-09-919-580-544	Sequence 544, App

16	14.4	242	14	US-10-066-543-3282	Sequence 3282, Ap
17	4.3	158001	16	US-10-211-179-11	GENERAL INFORMATI
18	60	3.6	10	US-09-908-975-13799	Sequence 13799, A
19	60	3.6	10	US-09-908-975-31279	Sequence 31279, A
20	60	3.6	10	US-09-908-975-31541	Sequence 31541, A
21	59	3.5	19576	US-10-221-613-219	Sequence 219, Appl
22	59	3.5	3673778	US-10-312-841-1	Sequence 1, Appli
23	58.2	3.5	499	US-09-783-590-4473	Sequence 4473, Ap
24	58.2	3.5	23683	US-10-240-485-176	Sequence 176, Appl
25	57.6	3.5	960	US-10-198-846-6381	Sequence 6381, Ap
26	57.4	3.4	6286	US-10-221-714A-313	Sequence 313, Appl
27	57.4	3.4	8711	US-10-221-714A-424	Sequence 424, Appl
28	57.4	3.4	46951	US-10-091-281-2	Sequence 2, Appli
29	57.4	3.4	3673778	US-10-312-841-2	Sequence 2, Appli
30	57.2	3.4	6816	US-10-221-714A-411	Sequence 411, Appl
31	56.8	3.4	12142	US-10-311-455-1646	Sequence 1646, Ap
32	56.6	3.4	3510	US-10-027-632-253392	Sequence 253392,
33	56.6	3.4	3510	US-10-027-632-253393	Sequence 253393,
34	56.6	3.4	7814	US-10-221-714A-252	Sequence 252, Appl
35	56.6	3.4	17848	US-10-239-676-28	Sequence 28, Appl
36	56.6	3.4	17848	US-10-240-453-38	Sequence 38, Appl
37	56.6	3.4	17848	US-10-257-166-58	Sequence 58, Appl
38	56.2	3.4	5945	US-10-311-455-58	Sequence 58, Appl
39	56.2	3.4	6880	US-10-221-613-183	Sequence 183, Appl
40	56.2	3.4	7001	US-10-172-086-60	Sequence 60, Appl
41	56	3.4	6109	US-10-221-613-33	Sequence 33, Appl
42	56	3.4	6109	US-10-311-455-299	Sequence 299, Appl
43	55.8	3.3	7455	US-10-311-455-1732	Sequence 1732, Ap
44	55.6	3.3	14919	US-10-221-714A-227	Sequence 227, Appl
45	55	3.3	7597	US-10-311-455-386	Sequence 386, Appl

ALIGNMENTS

RESULT 1

US-09-771-161A-2  
; Sequence 2, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724, 676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1669  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: (1)..(1669)  
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'  
US-09-771-161A-2

Query Match	99.9%	Score 1668	DB 9	Length 1669
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1669	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
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Db	1	ACCTAGTTTATACCAGATATTTTCATATTTATAGCTCAATCTCTAGAACCACTCTGCA	60	
Qy	61	TGTAGTAATTGTAGATTTTCGAGATCGAAGCTTGTGACACTGTGAGAGTAACCAAT	120	



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QY 451 TGAATAATAGTGTTCCTGTAATCATGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 510
DB 1322 TGAATAATAGTGTTCCTGTAATCATGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 1381
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DB 1382 TTTATCTAGAAAGCTCAAGAGCTGTATTTATGAGCTGATCATCTCTCTGGAATCA 1441
QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGATTCCTGATCAAGAGCCAC 630
DB 1442 CAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGATTCCTGATCAAGAGCCAC 1501
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAATCTCAGAACGCTGCTCA 690
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QY 871 CACTACTGACATCCAGAGGAAGAAATTTGCCAAAGTTATAGTACAAAAATGAAAGATAA 930
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DB 1862 AAATTTACTTCAAAATAAAAGCATGTAGTACTGTCTTTTCAAGAGAAATGTGTTTCT 1921
QY 1051 AAAGGATATTTATATCTCTGTTGCTTTGACTTTTATATAAAATCCGTGAGTATTA 1110
DB 1922 AAAGGATATTTATATCTCTGTTGCTTTGACTTTTATATAAAATCCGTGAGTATTA 1981
QY 1111 AGCTTTATGAGGTTCTTTGGGTAATATAGTCTCCCTCCATCAGACCTGAGTATTT 1170
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DB 2102 TTTGTTAAACAGAAACCACTTTTAAAGGATAGTAAATTTTGTGTTTATAACAGTGCCTTA 2161
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DB 2222 TTACTTGTCTAAGATCAATTTTGAATTTTATGAGTATATACCTTTTACCACAGAGACA 2281
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DB 2522 AACAGCCTGATGTGTA 2537

RESULT 3
US-09-981-397A-13
; Sequence 13, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981.397A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-397A-13

Query Match 78.4%; Score 1308; DB 10; Length 2501;
Best Local Similarity 99.0%; Pred. No. 2.6e-267;
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGATATATC 390
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QY 391 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 450
DB 1220 TCTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 1279
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QY 511 TTTATCTAGAAAGCTCAAGAGCTGTATTTATGAGCTGATCATCTCTCTGGAATCA 570
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QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGATTCCTGATCAAGAGCCAC 630
DB 1400 CAGTTGGGATAGCACCATTTCTGGATCTCAAGAGGCTGATTCCTGATCAAGAGCCAC 1459
QY 631 TCCATGCTCTTCAGCAATAAATCCACTCTCAACTGCAGGAATCTCAGAACGCTGCTCA 690
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 QY CACTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930  
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 QY AAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTTTATATAAAATCCCGTGAATATA 1110  
 Db AAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTTTATATAAAATCCCGTGAATATA 1939  
 QY AGCTTTATGAAGTCTTGTGGTAAATATAGTCTCCCTCCATGACACATGCAATATTT 1170  
 Db AGCTTTATGAAGTCTTGTGGTAAATATAGTCTCCCTCCATGACACATGCAATATTT 1999  
 QY TTTTAAATTAACAAGTAAAGTGTAAATTTGGTTGAATTTGTCTACATAGTTCAATTTTT 1222  
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 QY AAAATGATATTTCAAAGTAAACATACATAATAAAGAAATAAATAATATATATATAC 1582  
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 QY ATAAAGTCAACAGCTGATGTG 1664  
 Db ATAAAGTCAACAGCTGATGTG 2501

RESULT 4

US-09-748-537-2  
 ; Sequence 2, Application US/09748537  
 ; Patent No. US2002006183A1

GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Chao, Moses V.  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE  
 ; FILE REFERENCE: 07334-316001  
 ; CURRENT APPLICATION NUMBER: US/09/748,537  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-748-537-2

Query Match 43.8%; Score 731.8; DB 9; Length 1931;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-145;  
 Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGA CAAGAGAAAATGGAATATC 390  
 Db 1149 AAAGTTACAGAGTGTTCAGAGTCCCATTCACCTATGTGA CAAGAGAAAATGGAATATC 1208  
 QY 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450  
 Db 1209 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268  
 QY 451 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510  
 Db 1269 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1328  
 QY 511 TTTATCTAGAAAGCTCAAGACATGTTTATTTATGAAGTGCATCACTGTCTGGAATCA 570  
 Db 1329 TTTATCTAGAAAGCTCAAGACATGTTTATTTATGAAGTGCATCACTGTCTGGAATCA 1388  
 QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAGAGACCAC 630  
 Db 1389 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAGAGACCAC 1448  
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 Db 1449 TCCATCTCTTCAAGCAATAATAATCCACTCACTCACTGAGGAACTCAGAACTCTGCA 1508  
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 Db 1509 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAAGGGAAGACATTTGTGAACCAATGAC 1568  
 QY 751 AGAAGCTGCTTAACTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 810  
 Db 1569 AGAAGCTGCTTAACTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1628  
 QY 811 GGAATATGAATCTTGTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 870  
 Db 1629 GGAATATGAATCTTGTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAAAGTCAAGCAATTTACTAGA 1688  
 QY 871 CACTACTGATCCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930  
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 Db 1749 CAAACAAATGGGTCTTACCGCTTACCGGAAATACCTTGTGGTTTCTAGATCACCATCTTT 1808  
 QY 991 AATTTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAAATGTGTTTCAT 1050  
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 QY 1051 AAAAGGATATTTATA 1065  
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Db 1869 AAAAGCATATTATA 1883

RESULT 5

US-09-728-721-1

Sequence 1, Application US/09728721

Patent No. US20020061845A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07334-124001

CURRENT APPLICATION NUMBER: US/09/728,721

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/340,620

PRIOR FILING DATE: 1999-06-28

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1931

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (214)...(1833)

US-09-728-721-1

Query Match 43.8%; Score 731.8; DB 9; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390

Db 1149 AAAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450

Db 1209 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268

QY 451 TGAATAATAGTGTTCCTGAACTTTCAAGTCCCTGCCAGTCCCTCAAGACAAATGATTT 510

Db 1269 TGAATAATAGTGTTCCTGAACTTTCAAGTCCCTGCCAGTCCCTCAAGACAAATGATTT 1328

QY 511 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 570

Db 1329 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 1388

QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCGTGATCAAGAACAC 630

Db 1389 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCGTGATCAAGAACAC 1448

QY 631 TCCATCTCTTTCAGCAATAAATCACTCTCACTCACTCACTCACTCACTCACTCACTCACT 690

Db 1449 TCCATCTCTTTCAGCAATAAATCACTCTCACTCACTCACTCACTCACTCACTCACTCACT 1508

QY 691 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGCATTGTGAACCAATGAC 750

Db 1509 GCTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGCATTGTGAACCAATGAC 1568

QY 751 AGAAGCCTGCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAGA 810

Db 1569 AGAAGCCTGCTTAACCAAGTCCGTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAGA 1628

QY 811 GGAATATGAATGTTAGTACCAAGCTTCAAGGAGCTCAAGGAGCTCAAGGAGCTCAAGGAG 870

Db 1629 GGAATATGAATGTTAGTACCAAGCTTCAAGGAGCTCAAGGAGCTCAAGGAGCTCAAGGAG 1688

QY 871 CACTACTGATCTCAAGAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAA 930

Db 1689 CACTACTGATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCGAAGATAA 1748

QY 931 CAACAAAATGGGTCTTTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 990

Db 1749 CAACAAAATGGGTCTTTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 1808

QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1050

Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAAATGTTTCAT 1868

QY 1051 AAAAGCATATTATA 1065

Db 1869 AAAAGCATATTATA 1883

RESULT 6

US-10-133-780-2

Sequence 2, Application US/10133780

Publication No. US20020123115A1

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/133,780

FILING DATE: 26-Apr-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1931 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-133-780-2

Query Match 43.8%; Score 731.8; DB 13; Length 1931;

Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390

Db 1149 AAAAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450

Db 1209 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268

QY 451 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 510  
 DB 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 1328  
 QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATCA 570  
 DB 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATCA 1388  
 QY 571 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 630  
 DB 1389 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 1448  
 QY 631 TCCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
 DB 1449 TCCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1508  
 QY 691 GCCTGGATAGCCAGCAGTGGATCCAGAGAAAGGAAAGACATTTGTGAACCAATGAC 750  
 DB 1509 GCCTGGATAGCCAGCAGTGGATCCAGAGAAAGGAAAGACATTTGTGAACCAATGAC 1568  
 QY 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGTATCATGAAGA 810  
 DB 1569 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGTATCATGAAGA 1628  
 QY 811 GGACTATGAATTTGTATGATACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGA 870  
 DB 1629 GGACTATGAATTTGTATGATACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGA 1688  
 QY 871 CACTACTGACATCAAGGAGAAGATTTGCAAGTTATAGTACAAAATTTGAAGATAA 930  
 DB 1689 CACTACTGACATCAAGGAGAAGATTTGCAAGTTATAGTACAAAATTTGAAGATAA 1748  
 QY 931 CAAACAATGGTCTTACAGCTTACCCGGAATACCTTGTGCTTCTAGATCACCCTTT 990  
 DB 1749 CAAACAATGGTCTTACAGCTTACCCGGAATACCTTGTGCTTCTAGATCACCCTTT 1808  
 QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAATAATGTTTCAT 1050  
 DB 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAATAATGTTTCAT 1868  
 QY 1051 AAAAGGATATTTATA 1065  
 DB 1869 AAAAGGATATTTATA 1883

RESULT 7

US-105-931-1  
 ; Sequence 1, Application US/10105931  
 ; Publication No. US20020150987A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
 ; FILE REFERENCE: 07334-076001  
 ; CURRENT APPLICATION NUMBER: US/10/105,931  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1931  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (214)...(1833)  
 US-105-931-1

Query Match 43.8%; Score 731.8; DB 13; Length 1931;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-145;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 331 ACAGTTACAGAGTGTTCCTCAAGTCCCTCAAGTCCCTCCAGCTCTCTCAAGACAATGATTT 390  
 DB 1149 AAAGTTACAGAGTGTTCCTCAAGTCCCTCAAGTCCCTCCAGCTCTCTCAAGACAATGATTT 1208  
 QY 391 TCTGAACATACCTGTAATCATGTCCTCAAGAGGAATCATGTCAGTCTCA 450  
 DB 1209 TCTGAACATACCTGTAATCATGTCCTCAAGAGGAATCATGTCAGTCTCA 1268  
 QY 451 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 510  
 DB 1269 TGAATAATAGTGGTCTCTCTGAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTT 1328  
 QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATCA 570  
 DB 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATCA 1388  
 QY 571 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 630  
 DB 1389 CAGTTGGATAGCACCATTCTTGATCTCAAGGGCTGCAATCTTGATCACAAGACCAC 1448  
 QY 631 TCCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGCA 690  
 DB 1449 TCCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACTCTGCA 1508  
 QY 691 GCCTGGATAGCCAGCAGTGGATCCAGAGAAAGGAAAGACATTTGTGAACCAATGAC 750  
 DB 1509 GCCTGGATAGCCAGCAGTGGATCCAGAGAAAGGAAAGACATTTGTGAACCAATGAC 1568  
 QY 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGTATCATGAAGA 810  
 DB 1569 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGTATCATGAAGA 1628  
 QY 811 GGAATATGAATTTGTATGATACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGA 870  
 DB 1629 GGAATATGAATTTGTATGATACCAAGCTTCAAGGACCTCAAAAGTCAAGACAATTTACTAGA 1688  
 QY 871 CACTACTGACATCAAGGAGAAGATTTGCAAGTTATAGTACAAAATTTGAAGATAA 930  
 DB 1689 CACTACTGACATCAAGGAGAAGATTTGCAAGTTATAGTACAAAATTTGAAGATAA 1748  
 QY 931 CAAACAATGGTCTTACAGCTTACCCGGAATACCTTGTGCTTCTAGATCACCCTTT 990  
 DB 1749 CAAACAATGGTCTTACAGCTTACCCGGAATACCTTGTGCTTCTAGATCACCCTTT 1808  
 QY 991 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAATAATGTTTCAT 1050  
 DB 1809 AAATTTACTTCAAAATAAAAGCATGTAAGTACTGTTTTTCAAGAGAATAATGTTTCAT 1868  
 QY 1051 AAAAGGATATTTATA 1065  
 DB 1869 AAAAGGATATTTATA 1883

RESULT 8

US-110-118-984-1  
 ; Sequence 1, Application US/10118984  
 ; Publication No. US20020197693A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: 07334/118001  
 ; CURRENT APPLICATION NUMBER: US/10/118,984  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942



Db 1749 CAAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTT 1808

Qy 991 AATTTTACTTCARATTAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTTCAT 1050

Db 1809 AATTTTACTTCARATTAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTTCAT 1868

Qy 1051 AAAAGGATATTATA 1065

Db 1869 AAAAGGATATTATA 1883

RESULT 10

US-09-728-721-3

; Sequence 3, Application US/09728721

; Patent No. US20020061845A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/728,721

; CURRENT FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: 09/340,620

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/207,359

; PRIOR FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1620

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-728-721-3

Query Match 40.9%; Score 681.8; DB 9; Length 1620;

Best Local Similarity 99.7%; Pred. No. 1.7e-134;

Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 331 ACAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 390

Db 936 AAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 995

Qy 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCCTCAGCTCCA 450

Db 996 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCCTCAGCTCCA 1055

Qy 451 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510

Db 1056 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115

Qy 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCATCTGCTGGAATCA 570

Db 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCATCTGCTGGAATCA 1175

Qy 571 CAGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630

Db 1176 CAGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1235

Qy 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAAGGAACTCAGAACTCTGCA 690

Db 1236 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAAGGAACTCAGAACTCTGCA 1295

Qy 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 750

Db 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 1355

Qy 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGA 810

Db 1356 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGA 1415

Qy 811 GGACTATGAACCTTTAGTACCAAGCTTACCAAGCTTCAAAAGTCTAGACAAATTTACTAGA 870

Db 1416 GGACTATGAACCTTTAGTACCAAGCTTACCAAGCTTCAAAAGTCTAGACAAATTTACTAGA 1475

Qy 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAAGTTATAGTACAAAAATTTGAAAGATAA 930

Db 1476 CACTACTGACATCCAAAGGAGAAATTTGCCAAAAGTTATAGTACAAAAATTTGAAAGATAA 1535

Qy 931 CAAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 990

Db 1536 CAAACAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTT 1595

Qy 991 AATTTTACTTCAAAATAAAAAGCATG 1015

Db 1596 AATTTTACTTCAAAATAAAAAGCATG 1620

RESULT 11

US-10-105-931-3

; Sequence 3, Application US/10105931

; Publication No. US20020150987A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-076001

; CURRENT APPLICATION NUMBER: US/10/105,931

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1620

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-931-3

Query Match 40.9%; Score 681.8; DB 13; Length 1620;

Best Local Similarity 99.7%; Pred. No. 1.7e-134;

Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 331 ACAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 390

Db 936 AAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 995

Qy 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCCTCAGCTCCA 450

Db 996 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCCCTCAGCTCCA 1055

Qy 451 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510

Db 1056 TGAATAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115

Qy 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCATCTGCTGGAATCA 570

Db 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGTGCATCATCTGCTGGAATCA 1175

Qy 571 CAGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 630

Db 1176 CAGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC 1235

Qy 631 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAAGGAACTCAGAACTCTGCA 690

Db 1236 TCCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAAGGAACTCAGAACTCTGCA 1295

Qy 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 750

Db 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 1355

Qy 751 AGAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAGA 810



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Db 1356 AGAAGCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGA 1415
QY 811 GGACTATGAATCTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAAATTAAGTACA 870
Db 1416 GGACTATGAATCTGTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAAATTAAGTACA 1475
QY 871 CACTACTGACATCCAAAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930
Db 1476 CACTACTGACATCCAAAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1535
QY 931 CAAACAAATGGTCTTCAGCCTTACCGGAATACCTGTGGTTCTAGATCACCATCTTT 990
Db 1536 CAAACAAATGGTCTTCAGCCTTACCGGAATACCTGTGGTTCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAAGCATG 1015
Db 1596 AAATTTACTTCAAAATAAAAGCATG 1620

RESULT 12
US-10-118-984-3
; Sequence 3, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-118-984-3

Query Match 40.9%; Score 681.8; DB 13; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390
Db 936 AAAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 996 TCTGAACATACCTGTAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGTTCCTGAAACTTTCAAGTGCCCTGCCAGCTCTCTCAAGACAATGATTT 510
Db 1056 TGAATAATAGTGTTCCTGAAACTTTCAAGTGCCCTGCCAGCTCTCTCAAGACAATGATTT 1115
QY 511 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 570
Db 1116 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 1175
QY 571 CAGTTGGGATAGCACCATTCTCGATCTCAAAGGGCTGCATTCGTGATCAAGAACAC 630
Db 1176 CAGTTGGGATAGCACCATTCTCGATCTCAAAGGGCTGCATTCGTGATCAAGAACAC 1235
QY 631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAATCTCAGACGTCTGCA 690
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Db 1236 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAAATCTCAGAACGTCTGCA 1295
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 750
Db 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGAC 1355
QY 751 AGAAGCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGA 810
Db 1356 AGAAGCCTGCCTTAAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGA 1415
QY 811 GGACTATGAATCTGTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAGACAAATTAAGTACA 870
Db 1416 GGACTATGAATCTGTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAGACAAATTAAGTACA 1475
QY 871 CACTACTGACATCCAAAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930
Db 1476 CACTACTGACATCCAAAGGAGAAAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1535
QY 931 CAAACAAATGGTCTTCAGCCTTACCGGAATACCTGTGGTTCTAGATCACCATCTTT 990
Db 1536 CAAACAAATGGTCTTCAGCCTTACCGGAATACCTGTGGTTCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAAGCATG 1015
Db 1596 AAATTTACTTCAAAATAAAAGCATG 1620

RESULT 13
US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3

Query Match 40.9%; Score 681.8; DB 14; Length 1620;
Best Local Similarity 99.7%; Pred. No. 1.7e-134;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 390
Db 936 AAAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAGAGAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 996 TCTGAACATACCTGTAATCATGGTCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGTTCCTGAAACTTTCAAGTGCCCTGCCAGCTCTCTCAAGACAATGATTT 510
Db 1056 TGAATAATAGTGTTCCTGAAACTTTCAAGTGCCCTGCCAGCTCTCTCAAGACAATGATTT 1115
QY 511 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAATCA 570
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Db 1116 TTTATCTAGAAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 1175  
QY 571 CAGTTGGATAGACACCAATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGAGCCAC 630  
Db 1176 CAGTTGGATAGACCAATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGACCAT 1235  
QY 631 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAAAGTCTGCA 690  
Db 1236 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAAAGTCTGCA 1295  
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAGGAGAGACATTTGTGAACCAATGAC 750  
Db 1296 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAGGAGAGACATTTGTGAACCAATGAC 1355  
QY 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGAGCTTGTATCATGAAGA 810  
Db 1356 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGAGCTTGTATCATGAAGA 1415  
QY 811 GGACTATGAATCTTTAGTAGTACCAAGCCTCAAGGACCTCAAAAGTTCAGACAATTTACTAGA 870  
Db 1416 GGACTATGAATCTTTAGTAGTACCAAGCCTCAAGGACCTCAAAAGTTCAGACAATTTACTAGA 1475  
QY 871 CACTACTGACATCAAGAGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATA 930  
Db 1476 CACTACTGACATCAAGAGAGAGAAATTTGCCAAGTTATAGTACAAAAATTTGAAGATA 1535  
QY 931 CAAACAAATGGCTTTCAGGCTTACCCGGAATTAATCTTGTGTTCTAGATCACCATCTTT 990  
Db 1536 CAAACAAATGGCTTTCAGGCTTACCCGGAATTAATCTTGTGTTCTAGATCACCATCTTT 1595  
QY 991 AAATTTACTTCAAAATTAAGCATG 1015  
Db 1596 AAATTTACTTCAAAATTAAGCATG 1620

## RESULT 14

US-09-918-995-20565  
; Sequence 20565, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20565  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-20565

Query Match 21.8%; Score 363.4; DB 10; Length 491;  
Best Local Similarity 99.7%; Pred. No. 3.4e-67;  
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 331 ACAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAAGAGAAATTTGAATATC 390  
Db 127 AAAGTTACAGAGTGTTCAGATGCGCATTCACCTATGTGACAAGAGAAATTTGAATATC 186  
QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGATCCCTCAGCTCCA 450  
Db 187 TCTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGATCCCTCAGCTCCA 246  
QY 451 TGAATAATAGTGGTTCCTCTGAAATTTCAAGGTCCTCCAGCTCCTCAAGACATGATTT 510  
Db 247 TGAATAATAGTGGTTCCTCTGAAATTTCAAGGTCCTCCAGCTCCTCAAGACATGATTT 306  
QY 511 TTTATCTAGAAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 570

Db 307 TTTATCTAGAAAAAGCTCAAGAGCTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCA 366  
QY 571 CAGTTGGATAGACACCAATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGAGCCAC 630  
Db 367 CAGTTGGATAGACACCAATTTCTGGATCTCAAGGGCTGCAATCTGTGATCACAGAGCCAC 426  
QY 631 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAAAGTCTGCA 690  
Db 427 TCCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAAAGTCTGCA 486  
QY 691 GCCTG 695  
Db 487 GCCTG 491

## RESULT 15

US-09-919-580-544/c  
; Sequence 544, Application US/09919580  
; Patent No. US20020110832A1  
; GENERAL INFORMATION:  
; APPLICANT: Pyle, Ruth  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121-552  
; CURRENT APPLICATION NUMBER: US/09/919,580  
; CURRENT FILING DATE: 2001-07-30  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 544  
; LENGTH: 299  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 243  
; OTHER INFORMATION: n = A,T,C or G  
US-09-919-580-544

Query Match 16.2%; Score 271; DB 9; Length 299;  
Best Local Similarity 97.9%; Pred. No. 1.1e-47;  
Matches 274; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1390 ACCCTTTACCCACAGAGACAGTACAGAAATCCCTGCCCTAAATCCAGGCTTAATTGCC 1449  
Db 293 ACCCTTTACCCACAGAGACAGTACAGAAATCCCTGCCCTAAATCCAGGCTTAATTGCC 234  
QY 1450 CTACAAAGGGTTATTAATTTAAACTCCATTTAGGATTTACATTTTAAAGTTTATTTA 1509  
Db 233 CTACAAAGGGTTATTAATTTAAACTCCATTTAGGATTTACATTTTAAAGTTTATTTA 174  
QY 1510 TGAATTCCTTTAAAAATGATATTTCAAAGGTHAAAACAATATATAAGAAAAAATA 1569  
Db 173 TGAATTCCTTTAAAAATGATATTTCAAAGGTHAAAACAATATATAAGAAAAAATA 114  
QY 1570 AATATATTAATACCGGCTTCTGTCCTCCCATTTTTTAACCTCAGCTTCCCTACTGTACCA 1629  
Db 113 AATATATTAATACCGGCTTCTGTCCTCCCATTTTTTAACCTCAGCTTCCCTACTGTACCA 54  
QY 1630 ACAACCAAGCTTAATAAAGTCAACAGCTGATGTGTAATA 1669  
Db 53 ACAACCAAGCTTAATAAAGTCAACAGCTGATGTGTAATA 14

Search completed: April 1, 2004, 06:30:51  
Job time : 673 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 02:23:55 ; Search time 4639 Seconds  
(without alignments)  
10743.690 Million cell updates/sec

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Perfect score: 1669  
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Scoring table: IDENTITY NUC  
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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hcc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pin:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_nam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rtd:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gsl:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	1033.4	61.9	1201	13	BX401255
c 2	783	46.9	834	12	BM014010
c 3	732.8	43.9	738	9	AI824070
c 4	721	43.2	738	10	AW978568

5	702.6	42.1	883	12	BG393551
c 6	695.8	41.7	1201	13	BX343071
c 7	692.8	41.5	744	14	CD365404
c 8	692	41.5	709	14	CA413941
c 9	691.4	41.4	1201	13	BX337147
c 10	689	41.3	734	12	BQ008463
c 11	676.4	40.5	715	14	CB851847
c 12	673	40.3	721	13	BQ774940
c 13	660	39.5	812	12	B1257472
c 14	657.2	39.4	828	10	BE875947
c 15	656.6	39.3	683	14	CB852764
c 16	653.4	39.0	938	13	BQ670832
c 17	642.4	38.5	870	10	BE877822
c 18	637	38.2	667	13	BQ773811
c 19	636	38.1	1081	12	BM557041
c 20	629.8	37.7	852	12	BG757422
c 21	624.2	37.4	672	14	CA314123
c 22	624	37.4	656	12	BM973770
c 23	621.8	37.3	636	10	BE551615
c 24	619.8	37.1	641	10	AW150819
c 25	607.4	36.4	624	14	CD368863
c 26	600.8	36.0	628	12	BQ000991
c 27	594.8	35.6	660	12	BM840808
c 28	593	35.5	606	9	AW085560
c 29	592.4	35.5	1623	29	AY415527
c 30	592	35.5	592	9	AY415575
c 31	589.2	35.3	1623	29	AY415528
c 32	588.8	35.3	647	10	AW960501
c 33	581.2	34.8	811	12	BG170405
c 34	579.4	34.7	615	9	AI801150
c 35	578.4	34.7	654	10	BE536247
c 36	568	34.0	610	13	BUE23654
c 37	564	33.8	600	10	BF793767
c 38	563.6	33.8	2826	11	BC058088
c 39	560.4	33.6	616	9	AI307810
c 40	542	32.5	559	12	BQ010938
c 41	532.6	31.9	568	9	AA161113
c 42	529.4	31.7	546	12	BQ013098
c 43	509.6	30.5	518	10	AW593657
c 44	505	30.3	505	13	BX280487
c 45	499	29.9	1468	11	BC025611

ALIGNMENTS

RESULT 1  
BX401255/c  
LOCUS BX401255 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA clone CSODK011Y17 3-PRIME, mRNA sequence.  
ACCESSION BX401255  
VERSION BX401255.1 GI:30610587  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 4797.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODK011AE09NP1&cluster=4797.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradise Avenue Genoscope sequence ID : CS0DK011AE09NP1.

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      Location/Qualifiers
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        /db_xref="taxon:9606"
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        /cell_type="HELA"
        /cell_line="HELA"
        /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
        /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      61.9%; Score 1033.4; DB 13; Length 1201;
Best Local Similarity 97.0%; Pred. No. 6.3e-164;
Matches 1060; Conservative 6; Mismatches 25; Indels 2; Gaps 2;

QY 551 CATCACTGCTCTGGAATCAAGTGGATAGCACCATTCTCGATCTCAAGGGCTGCA 610
DB 1093 CATCACTKTCCTGG-AATCAAGTGGATAGCACCATTCT-GATCTCAAGGGCTGCA 1036

QY 611 TTCTGTGATCAAGACCACTCCATGCTCTTCAAGCAATATAAATCCACTCTCAACTGCA 670
DB 1035 TTCTGTGATCAAGACCACTCCATGCTCTTCAAGCAATATAAATCCACTCTCAACTGCA 976

QY 671 GGAACCTCAGAACGCTGCGAGCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAA 730
DB 975 GAAACCTCAGAACGCTGCGAGCTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAA 916

QY 731 GACATGTGAAACCAATGACAGAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCC 790
DB 915 GACATGTGAAACCAATGACAGAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCC 856

QY 791 AGGACCTTGATCATGAAGAGGACTATGAATCTTGTAGTACCAAGCCCTACAAGGACCTCA 850
DB 855 AGGACCTTGATCATGAAGAGGACTATGAATCTTGTAGTACCAAGCCCTACAAGGACCTCA 796

QY 851 AAGTCAGACAAATCTAGACACTACTGACATCCAGGAGAAATTTGCCAAAGTTATA 910
DB 795 AAGTCAGACAAATCTAGACACTACTGACATCCAGGAGAAATTTGCCAAAGTTATA 736

QY 911 GTACAAAATTTGAAGAGATAACAACAAATGGCTCTTCCAGCTTACCCGGAAATCTGTG 970
DB 735 GTACAAAATTTGAAGAGATAACAACAAATGGCTCTTCCAGCTTACCCGGAAATCTGTG 676

QY 971 GTTCTAGATCACCACCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTT 1030
DB 675 GTTCTAGATCACCACCTTTAAATTTACTTCAAAATAAAAGCATGTAAGTGACTGTTTT 616

QY 1031 CAAGAAGAAATGTTTCATAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTAT 1090
DB 615 CAAGAAGAAATGTTTCATAAAGGATATTTATCTCTGTTGCTTTGACTTTTTTAT 556

QY 1091 ATAAATCCGTGAGTATTAAAGCTTTTAAAGGTTCTTTGGGTAATAATTTAGTCTCCCT 1150
DB 555 ATAAATCCGTGAGTATTAAAGCTTTTAAAGGTTCTTTGGGTAATAATTTAGTCTCCCT 496

QY 1151 CCATGACACTGCAGTATTTTTTTTAAATATAATACAAAGTAAAGTTGAATTTGCTACAT 1210
DB 495 CCATGACACTGCAGTATTTTTTTTAAATATAATACAAAGTAAAGTTGAATTTGCTACAT 436

QY 1211 AGTTCAATTTTATGCTCTTTGTTAAAGACCACTTTTAAAGCATAGTAAATATTC 1270
DB 435 AGTTCAATTTTATGCTCTTTGTTAAAGACCACTTTTAAAGCATAGTAAATATTC 376

QY 1271 TTGTTTATAACAGTGCCTTTAAGGTATGATGATTTCTTGATGGAGCCATTTTCACATTC 1330
DB 375 TTGTTTATAACAGTGCCTTTAAGGTATGATGATTTCTTGATGGAGCCATTTTCACATTC 316

QY 1331 TGTCTTCATGGATATTGTTTACTTGTCTTAAGATGCAATTTGATTTTATGAAGTATATA 1390
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DB 315 TGTCTTCATGGATATTGTTTACTTGTCTAAGATGCAAGTTTGAATTTATGAAGTATATA 256
QY 1391 CCCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTAAATCCAGGCTTAATTCGCC 1450
DB 255 CCCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTAAATCCAGGCTTAATTCGCC 196
QY 1451 TACAAAGGGTATTAAATTTAAACCTCCATTATTAGGATTACATTTTAAAGTTTATTTAT 1510
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QY 1511 GAATTCCTCTTTAAAAATGATATTTCAAAGGTAAACCAATATAAAGAAAAAATAA 1570
DB 135 GAATTCCTCTTTAAAAATGATATTTCAAAGGTAAACCAATATAAAGAAAAAATAA 76
QY 1571 ATATATTATACGGCTTCTCTGCCATTTTAACTTCAGCTTCCCTTCTGTCACCAA 1630
DB 75 ATATATTATACGGCTTCTCTGCCATTTTAACTTCAGCTTCCCTTCTGTCACCAA 16
QY 1631 CAACCAAGCTAAA 1643
DB 15 NAAAAAATAAAWAA 3

RESULT 2
LOCUS BM014010 834 bp mRNA linear EST 30-OCT-2001
DEFINITION 603639652F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5415612 5',
  mRNA sequence.
ACCESSION BM014010
VERSION BM014010.1 GI:16528364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
  Email: cgabbs@mail.nih.gov
  Tissue Procurement: DCTD/DTF
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLNL2060 row: h column: 13
  High quality sequence stop: 829.

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      /notes="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
        Average insert size 1.383 kb. Library enriched for
        full-length clones and constructed by Life Technologies.
        Note: this is a NIH_MGC Library."

ORIGIN
Query Match      46.9%; Score 783; DB 12; Length 834;
Best Local Similarity 98.0%; Pred. No. 7.5e-122;
Matches 814; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 583 CACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGACCACTCATGCTCTTC 642
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QY 1472 AACTCCATTATTAGGATTACATTTTAAAGTTTATTTATGAATTCCTTTTAAAAATGATA 1531
Db |||||||
QY 1532 TTTCAAAGGTAAACAATAACAATAAAGAAAAAATAATATATTAATACCGGCTTCCT 1591
Db |||||||
QY 1592 GTCCCAATTTTAACTTCAGCTTCCTACTGTGTCACCAACAACCAAGCTAAATAAGTCA 1651
Db |||||||
QY 1652 ACAGCCTGATGTGTAAAA 1669
Db |||||||
QY 18 ACAGCCTGATGTGTAAAA 1
Db |||||||

RESULT 4
AW978568/c
LOCUS EST390677 MAGE resequences, MAGP Homo sapiens cDNA, mRNA sequence.
ACCESSION AW978568
VERSION AW978568.1 GI:8169836
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 738)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 394
Seq primer: Forward.
FEATURES
source
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGP"
/note="Vector: pBluescript-SKm"

ORIGIN
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Best Local Similarity 98.5%; Pred. No. 2e-111;
Matches 727; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 848 TCAAAGTCAGACAAATTACTAGACACTACTGACATCAAGAGAGAAATTTGCCAAAGTT 907
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QY 738 TCAAAGTCAGACAAATTACTAGCCTCTTGACATCAAGAGAGAAATTTGCCAAAGTT 679
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QY 908 ATAGTACAAAATTTGAAGATAACAACAATGGGCTCTTCAGCCTTACCCGGAAATACTT 967
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QY 678 ATAGTACAAAATTTGAAGATAACAACAATGGGCTCTTCAGCCTTACCCGGAAATACTT 619
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QY 968 GTGGTTTCTAGATCACCATTCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTT 1027
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QY 618 GTGGTTTCTAGATCACCATTCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTT 559
Db |||||||
QY 1028 TTTCAGAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTCTTTGACTTTTTT 1087
Db |||||||
QY 558 TTTCAGAAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTCTTTGACTTTTTT 499
Db |||||||
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QY 1088 TATATAAAATCCGTGAGTATTAAGCTTTATTTGAAGGTTCTTTTGGGTAATATTAGTCTC 1147
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QY 498 TATATAAAATCCGTGAGTATTAAGCTTTATTTGAAGGTTCTTTTGGGTAATATTAGTCTC 439
Db |||||||
QY 1148 CTTCATGACACGTGAGTATTTTATTAATATACAGTAAAGAGTTTGAATTTTGCTA 1207
Db |||||||
QY 438 CTTCATGACACGTGAGTATTTTATTAATATACAGTAAAGAGTTTGAATTTTGCTA 379
Db |||||||
QY 1208 CATAGTTTCAATTTTATGTCCTCTTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTA 1267
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QY 378 CATAGTTTCAATTTTATGTCCTCTTTGTAAACAGAAACCACTTTTAAAGGATAGTAATTA 319
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QY 1268 TTCTTGTATATAACAGTGCCTTAAAGTATCATGTATTTCTGATGGAAGCCATTTTCCAT 1327
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QY 318 TTCTTGTATATAACAGTGCCTTAAAGTATCATGTATTTTGTAGTGAAGCCATTTTCCAT 259
Db |||||||
QY 1328 TCATGTTCTTCATGGATTTATTTGTTACTTGTCTTAAGATGCAATTTTATGTAAGTAT 1387
Db |||||||
QY 258 TCATGTTCTTCATGGATTTATTTGTTACTTGTCTTAAAGATGCAATTTTATGTAAGTAT 199
Db |||||||
QY 1388 ATACCTCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTTAAATCCAGGCTTAAATG 1447
Db |||||||
QY 198 ATACCTCTTTACCCACAGACAGACAGTACAGATCCCTGCCCTTAAATCCAGGCTTAAATG 139
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QY 1508 TATGAATTCCTTTTAAAGATGATTTTCAAGGTAAACCAATATATAAGAAAAA 1567
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QY 78 TATGAATTCCTTTTAAAGATGATTTTCAAGGTAAACCAATATATAAGAAAAA 19
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QY 1568 TAAATATATTAATACCCGG 1585
Db |||||||
QY 18 TAAATATATTAATACCCGG 1
Db |||||||

RESULT 5
BG393551
LOCUS 883 bp mRNA linear EST 12-MAR-2001
DEFINITION 602411943F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4540787 5',
mRNA sequence.
ACCESSION BG393551
VERSION BG393551.1 GI:13286999
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10471 row: e column: 12
High quality sequence stop: 767.
FEATURES
source
1..883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4540787"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
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/note="Organ: testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 42.1%; Score 702.6; DB 12; Length 883;  
Best Local Similarity 98.6%; Pred. No. 2.2e-108;  
Matches 761; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

QY 403 TGTAAATCATGCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGG 462  
DB 1 TGTAAATCATGCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGG 60  
QY 463 TTCTCTGAAACTTCAAGTCTCCAGCTCCTCAAGCAATGATTTTATCTAGAAA 522  
DB 61 TTCTCTGAAACTTCAAGTCTCCAGCTCCTCAAGCAATGATTTTATCTAGAAA 120  
QY 523 AGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCAAGTTGGATAG 582  
DB 121 AGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCGAAATCAAGTTGGATAG 180  
QY 583 CACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTTC 642  
DB 181 CACCATTTCTGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATGCTCTTC 240  
QY 643 AGCAATATAAATCAACTCTCAACTGCAGAACTCAGAACTCTGCAGCCTGGTATAGC 702  
DB 241 AGCAATATAAATCAACTCTCAACTGCAGAACTCAGAACTCTGCAGCCTGGTATAGC 300  
QY 703 CCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 762  
DB 301 CCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAAAATGACAGAGCCTGCCT 360  
QY 763 TAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAAC 822  
DB 361 TAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAAC 420  
QY 823 TGTAGTACCAAGCCTTACAGAGCACTCAAAAGTTCAGACAAATTTACTAGACACTGACAT 882  
DB 421 TGTAGTACCAAGCCTTACAGAGCACTCAAAAGTTCAGACAAATTTACTAGACACTGACAT 480  
QY 883 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGG 942  
DB 481 CCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAACAAACAAATGGG 540  
QY 943 TCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCA 1002  
DB 541 TCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCA 600  
QY 1003 AAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTTTCATATAAAGGATAT 1061  
DB 601 AAATAAAGCATGTAAGTCACTGTTTTCAGAGAAATGTTTTCATATAAAGGATAT 660  
QY 1062 TATATCTCTGTGCTTTGACTTTTTTATATAAATCCCGTGTAGTATTAAGCTTTATTGA 1121  
DB 661 TATATCTCTGTGCTTTGACTTTTTTATATAAATCCCGTGTAGTATTAAGCTTTATTGA 718  
QY 1122 AGTTCTTTGGTAAATATAGTCTCCCTCCATGACACTGCAAGTATTTTTT 1173  
DB 719 AGCT--CTTGGGTAACTATTAGTCT--CTCCATGACACTGCAAGTATTTTTT 767

RESULT 6  
BX343071/c  
LOCUS  
DEFINITION BX343071 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
ACCESSION BX343071  
VERSION BX343071.1 GI:30334165  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: secre@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 4797.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DL009AB1ONP1&cluster=4797.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DL009AB1ONP1.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS0DL009YCI9"  
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/cell\_line="RAMOS CELL LINE"  
/clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT  
25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.7%; Score 695.8; DB 13; Length 1201;  
Best Local Similarity 97.9%; Pred. No. 2.6e-107;  
Matches 693; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCACAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 390  
DB 710 AAAGTTACAGAGTGTTCACAGTGCCATTCACCTATGTGACAGAGAAATGGAATTATC 651  
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCA 450  
DB 650 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGAGCTCTCAGCTCA 591  
QY 451 TGAAATAGTGTTCCTCTGAAACTTCAAGTCTCCAGCTCCTCAAGCAATGATTT 510  
DB 590 TGAAATAGTGTTCCTCTGAAACTTCAAGTCTCCAGCTCCTCAAGCAATGATTT 531  
QY 511 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGGAAATCA 570  
DB 530 TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGGAAATCA 471  
QY 571 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGTATCAAGAACCA 630  
DB 470 CAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGTATCAAGAACCA 411  
QY 631 TCCATGCTCTTCAGCAATAAATAATCCATCTCAACTGTCAGGAAAATCTGAAACGCTGCA 690  
DB 410 TCCATGCTCTTCAGCAATAAATAATCCATCTCAACTGTCAGGAAAATCTGAAACGCTGCA 351  
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 750  
DB 350 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 291  
QY 751 AGAAGCCTGCCTTAACCAAGTGCCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA 810  
DB 290 AGAAGCCTGCCTTAACCAAGTGCCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA 231  
QY 811 GGACTATGAATGTTGTAGTACCAAGCCTCAAGAGACCTCAAAAGTTCAGACAATTTACTAGA 870  
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Db      230 GGACTATGAACCTGTAGTACCAAGGCTACCAAGGACBTCAAAAGTCAGACAATTAATCTAGTA 171
QY      871 CACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 930
Db      170 CACTACTGACATCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATTA 111
QY      931 CAACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTCTTAGATCACCATCTTT 990
Db      110 CADACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTCTTAGATCACCATCTTT 51
QY      991 AAATTTACTTCAAAATTAAGAGCATGTAAGTACTGTTTTCAGAAGA 1038
Db      50 AAATTTACTTCAAAATTAAGAGCATGTAAGTACTGTTTTCAGGNGM 3

RESULT 7
LOCUS   CD365404/c
DEFINITION UI-H-FT2-bjj-h-03-0-UI.s1 NCI CGAP FT2 Homo sapiens CDNA clone
ACCESSION UI-H-FT2-bjj-h-03-0-UI 3', mRNA sequence.
VERSION    CD365404
KEYWORDS   EST.
SOURCE     CD365404.1 GI:311149494
ORGANISM   Homo sapiens (human)
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 744)
JOURNAL     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
             source     1..744
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="UI-H-FT2-bjj-h-03-0-UI"
                        /tissue_type="Aveolar Macrophage"
                        /dev_stage="Adult"
                        /lab_host="DH10B (Life Technologies)"
                        /clone_lib="NCI CGAP FT2"
                        /notes="Organ: Lung; Vector: p77T3-Pac (Pharmacia) with a
                        modified polylinker; Site: 1: Ecor I; Site: 2: Not I;
                        NCI CGAP FT2 is a subtracted cDNA library constructed from
                        a pool of 81 RNA samples from Alveolar Macrophages
                        challenged with different treatments. The library was
                        subcloned according to Bonaldo, Lennon and Soares, Genome
                        Research, 6:791-806, 1996. The tissue was provided by Dr.
                        Gary W. Hunninghake of the University of Iowa.
                        TAG TISSUE=Human Lung Aveolar Macrophage
                        TAG LIB=UI-H-FT2
                        TAG_SEQ=GGCCATCGCG"

ORIGIN
Query Match 41.5%; Score 692.8; DB 14; Length 744;
Best Local Similarity 99.3%; Pred. No. 1.1e-106;
Matches 705; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      331 ACAGTTACAGAGTGTTCCTCAAGTGCATTACCTATGTGACAGAAGAAAATGGAATTATC 390
Db      719 AAAGTTACAGAGTGTTCCTCAAGTGCATTACCTATGTGACAGAAGAAAATGGAATTATC 661

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QY      391 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db      660 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCA 601
QY      451 TGAATATAGTGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
Db      600 TGAATATAGTGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 541
QY      511 TTATCTAGAAAAGCTCAAGACCTGTTATTTATGAAGCTGCACTCACTGCTCTGGAATCA 570
Db      540 TTATCTAGAAAAGCTCAAGACCTGTTATTTATGAAGCTGCACTCACTGCTCTGGAATCA 481
QY      571 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCAC 630
Db      480 CAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCAAGAACCAC 421
QY      631 TCCATGCTCTTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGACGCTGCA 690
Db      420 TCCATGCTCTTTCAGCAATATAAATCCACTCTCAACTGCAGGAACTCAGACGCTGCA 361
QY      691 GCCTGTATAGCCCGCAGTCAGTGGATCCAGAGCAAAAGGGAGACATTTGTGAACCAATGAC 750
Db      360 GCCTGTATAGCCCGCAGTCAGTGGATCCAGAGCAAAAGGGAGACATTTGTGAACCAATGAC 301
QY      751 AGAAGCCTCCCTTAACACGTCGCTAGATGCCCTTCTGTCCAGGACTTGAATCAAGAAAGA 810
Db      300 AGAAGCCTCCCTTAACACGTCGCTAGATGCCCTTCTGTCCAGGACTTGAATCAAGAAAGA 241
QY      811 GGACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTAATCTAGA 870
Db      240 GGACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTAATCTAGA 181
QY      871 CACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 930
Db      180 CACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAA 121
QY      931 CAAACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTCTTAGATCACCATCTTT 990
Db      120 CAAACAAATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTCTTAGATCACCATCTTT 61
QY      991 AAATTTACTTCAAAATTAAGAGCATGTAAGTACTGTTTTCAGAAGAA 1040
Db      60 AAATTTACTTCAAAATTAAGAGCATGTAAGTACTGTTTTCAGAAGAA 11

RESULT 8
LOCUS   CA413941/c
DEFINITION UI-H-EZ0-bau-f-07-0-UI.s1 NCI CGAP Chl Homo sapiens CDNA clone
ACCESSION UI-H-EZ0-bau-f-07-0-UI 3', mRNA sequence.
VERSION    CA413941
KEYWORDS   EST.
SOURCE     CA413941.1 GI:24776592
ORGANISM   Homo sapiens (human)
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 709)
JOURNAL     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
            Orthopaedics
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this cDNA
            sequence: 1-64, >At_rich#Low_complexity (matched complement)

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Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="UI-H-EZO-bau-f-07-0-UI"
                /tissue_type="Chondrosarcoma Grade II"
                /dev_stage="Adult"
                /lab_host="DH10B (Life Technologies)"
                /clone_lib="NCI CGAP Ch1"
                /note="Organ: Left Pelvis; Vector: pVT3-Pac (Pharmacia)
                with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
                NCI CGAP Ch1 is a cDNA library containing the following
                tissue(s): Chondrosarcoma Grade II. The library was
                constructed according to Bonaldo, Lennon and Soares,
                Genome Research, 6:791-806, 1996. First strand cDNA
                synthesis was primed with an oligo-dT primer containing a
                Not I site. Double stranded cDNA was ligated to an EcoR I
                adaptor, digested with Not I, and cloned directionally
                into pVT3-Pac vector. The oligonucleotide used to prime
                the synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (d)18 tail. The sequence tag for this library is
                TGATCAGCGT.
                TAG_TISSUE=grade-2-chondrosarcoma
                TAG_LIB=UI-H-EZO
                TAG_SEQ=ATCTAATG"
    ORIGIN
        Query Match 41.5%; Score 692; DB 14; Length 709;
        Best Local Similarity 100.0%; Pred. No. 1.5e-106;
        Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 520 AAAAGCTCAAGCTGTTATTTATGAAGCTGATCACTGCTCTGGAATCAAGTTGGGA 579
    DB 709 AAAAGCTCAAGCTGTTATTTATGAAGCTGATCACTGCTCTGGAATCAAGTTGGGA 650
    QY 580 TAGCACCATTCTGGATCTCAAGGCGTCATTCTGTGTATCAAGACCACTCCATGCTC 639
    DB 649 TAGCACCATTCTGGATCTCAAGGCGTCATTCTGTGTATCAAGACCACTCCATGCTC 590
    QY 640 TTCAAGCAATATAATCCACTCTCACTCGAGGAACTCAGAACGCTGTCAGCCCTGGTAT 699
    DB 589 TTCAAGCAATATAATCCACTCTCACTCGAGGAACTCAGAACGCTGTCAGCCCTGGTAT 530
    QY 700 AGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATACAGAGAGCCTG 759
    DB 529 AGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATACAGAGAGCCTG 470
    QY 760 CCTTAACCACTGCTAGATGCCCTCTGTCCAGGACTTGTATCATGAAGAGGACTATGA 819
    DB 469 CCTTAACCACTGCTAGATGCCCTCTGTCCAGGACTTGTATCATGAAGAGGACTATGA 410
    QY 820 ACTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATCTAGACACTACTGA 879
    DB 409 ACTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATCTAGACACTACTGA 350
    QY 880 CATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAACAAT 939
    DB 349 CATCCAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAACAACAAT 290
    QY 940 GGGTCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCCTCTTTAAATTTACT 999
    DB 289 GGGTCTTACGCTTACCCGGAATATCTGTGGTTTCTAGATCACCCTCTTTAAATTTACT 230
    QY 1000 TCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGTGTTTTCATATAAAGGATA 1059
    DB 229 TCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGTGTTTTCATATAAAGGATA 170
    QY 1060 TTTATATCTGTGTTGACTTTTTTTTATATAAATCCGTGAGTATTAAGCTTTTAT 1119
    DB 169 TTTATATCTGTGTTGACTTTTTTTTATATAAATCCGTGAGTATTAAGCTTTTAT 110
    QY 1120 GAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTAATA 1179
    DB 109 GAAGGTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAGTATTTTTTAATA 50
    QY 1180 ATACAGTAAAAAGTTTGAATTTTCTCTACATA 1211
    DB 49 ATACAGTAAAAAGTTTGAATTTTCTCTACATA 18
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    LOCUS
    DEFINITION
        BX337147 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
        clone CS0DI037YA07 3-PRIME, mRNA sequence.
    ACCESSION
        BX337147
    VERSION
        BX337147.1 GI:30339578
    KEYWORDS
        EST.
    ORGANISM
        Homo sapiens (human)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    REFERENCE
        1 (bases 1 to 1201)
    AUTHORS
        Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
    TITLE
        Full-length cDNA libraries and normalization
    JOURNAL
        Unpublished (2001)
    COMMENT
        Contact: Genoscope
        Genoscope - Centre National de Sequencage
        BP 191 91006 EVRY cedex - France
        Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
        Library was constructed by Life Technologies, a division of
        Invitrogen. This sequence belongs to sequence cluster 4797.f For
        more information about this cluster, see
        http://www.genoscope.cns.fr/
        cgi-bin/cluster.cgi?seq=CS0DI037AA04NP1&cluster=4797.f. Contact :
        Feng Liang Email : fliang@lifetech.com URL :
        http://fulllength.invitrogen.com/Invitrogen Corporation 1600
        Faraday Avenue Genoscope sequence ID : CS0DI037AA04NP1.
    FEATURES
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DI037YA07"
                /tissue_type="PLACENTA COT 25-NORMALIZED"
                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."
    ORIGIN
        Query Match 41.4%; Score 691.4; DB 13; Length 1201;
        Best Local Similarity 94.9%; Pred. No. 1.4e-106;
        Matches 685; Conservative 23; Mismatches 14; Indels 0; Gaps 0;
    QY 331 ACAGTTACAGAGTGTTCAGAGTGCCATTCACTATGTGACAGAGAAATGGAATTATC 390
    DB 722 AAAGTTACAGAGTGTTCAGAGTGCCATTCACTATGTGACAGAGAAATGGAATTATC 663
    QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
    DB 662 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCA 603
    QY 451 TGAATAATAGTGTCTCTCTGAAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATT 510
    DB 602 TGAATAATAGTGTCTCTCTGAAACTTCAAGTCCCTGCCAGTCTCTCAAGACAATGATT 543
    QY 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGTCATCACTGTCTGGAATCA 570
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FH0"
/notes="Organ: Bone; Vector: p77T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FH0 is a cDNA library containing the following
tissue(s): Human Grade 1 Chondrosarcoma Cell Line The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into p77T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGAATCCGGC. The cell line was provided by Dr
James Martin from University of Iowa
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
TAG LIB=UI-H-FHO
TAG_SEQ=AGAATCCGGC"

ORIGIN

Query Match 40.3%; Score 673; DB 13; Length 721;
Best Local Similarity 99.6%; Pred. No. 2.3e-103;
Matches 695; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 414 GTCCACAAGAGGATCATGTGGATCCTCTCAGTCCATGAATAATAGTGTTCCTCGAAA 473
DB 711 GTCCACAAGAGGATCATGT-GATCCTCTCAGTCCATGAATAATAGT-GTTCCTCGAAA 654
QY 474 CTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACT 533
DB 653 CTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTTATCTAGAAAAGCTCAAGACT 594
QY 534 GTTATTTTATGAAGTCATCATCTGTCTCTGGAATACAGTGGGATGAGCACCATTCTG 593
DB 593 GTTATTTTATGAAGTCATCATCTGTCTCTGGAATACAGTGGGATGAGCACCATTCTG 534
QY 594 GATCTCAAGGGCTGCAATCTGTGATCACAAGACCCTCATCTCTTCAGCAATATAA 653
DB 533 GATCTCAAGGGCTGCAATCTGTGATCACAAGACCCTCATCTCTTCAGCAATATAA 474
QY 654 ATCCACTCTCACTGCAGGAACTCAGAACGCTGTGAGCCTGGTATAGCCCGCAGTGGA 713
DB 473 ATCCACTCTCACTGCAGGAACTCAGAACGCTGTGAGCCTGGTATAGCCCGCAGTGGA 414
QY 714 TCCAGACAAAGGGAAGACATTTGTGAACCAATGACAGAGGCTGCTTTAACAGTCGC 773
DB 413 TCCAGACAAAGGGAAGACATTTGTGAACCAATGACAGAGGCTGCTTTAACAGTCGC 354
QY 774 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTGTAGTACCA 833
DB 353 TAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAGGACTATGAATTTGTAGTACCA 294
QY 834 AGCCTACAAGGACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCAAGGAGAAG 893
DB 293 AGCCTACAAGGACCTCAAAAGTCAGACAAATTTACTAGACACTACTGACATCAAGGAGAAG 234
QY 894 AATTTGCCAAGTTATAGTACAAAATTTGAAGATATAACAAATGGGCTTTTCAGCCTT 953
DB 233 AATTTGCCAAGTTATAGTACAAAATTTGAAGATATAACAAATGGGCTTTTCAGCCTT 174
QY 954 ACCGGGAATCTTGTGGTTCTAGATCACCATCTTTAAATTTTACTTCAAAATAAAGCA 1013
DB 173 ACCGGGAATCTTGTGGTTCTAGATCACCATCTTTAAATTTTACTTCAAAATAAAGCA 114
QY 1014 TGTAAAGTGACTGTTTTTCAAGAGAAATGTGTTTTCATAAAGGATATTTATATCTCTGTT 1073
DB 113 TGTAAAGTGACTGTTTTTCAAGAGAAATGTGTTTTCATAAAGGATATTTATATCTCTGTT 54
QY 1074 GCTTTGACTTTTTTATATAAATCCGTCGAGTATTAAA 1111
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53 GCTTTCACCTTTTATATATAAATCCGTCGATTTAAA 16

RESULT 13
BI257472
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI257472 812 bp mRNA linear EST 17-JUL-2001
602967861F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5107310 5',
mRNA sequence.
BI257472
BI257472.1 GI:14812879
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 812)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11259 row: j column: 15
High quality sequence stop: 806.
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/clone_lib="NIH MGC 12"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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Query Match 39.5%; Score 660; DB 12; Length 812;
Best Local Similarity 97.8%; Pred. No. 3.2e-101;
Matches 691; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 331 ACAGTTTACAGAGTGTTCAGTGCCATTCCACCTATCTGACAGAGAAATGGAATTATC 390
DB 107 AAAGTTACAGAGTGTTCAGTGCCATTCCACCTATCTGACAGAGAAATGGAATTATC 166
QY 391 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGATCTCTCAGTCCA 450
DB 167 TCTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGATCTCTCAGTCCA 226
QY 451 TGAATAATAGTGTTCCTCTGAAACTTCAGGTCCCTGCCAGTCTCTCAAGACAATGATTT 510
DB 227 TGAATAATAGTGTTCCTCTGAAACTTCAGGTCCCTGCCAGTCTCTCAAGACAATGATTT 286
QY 511 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCA 570
DB 287 TTTATCTAGAAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCATCACTGTCTGGAATCA 346
QY 571 CAGTTGGGATAGCAACATTTCTGGATCTCAAGGGCTGCAATTCGTGTATCACAAGACCAC 630
DB 347 CAGTTGGGATAGCAACATTTCTGGATCTCAAGGGCTGCAATTCGTGTATCACAAGACCAC 406
QY 631 TCCATGCTCTTCAGCAATAATAATCCACTCACTCACTGAGGAACTCAGAACGTCGTGCA 690
DB 407 TCCATGCTCTTCAGCAATAATAATCCACTCACTCACTGAGGAACTCAGAACGTCGTGCA 466
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691 GCTGTATAGCCACAGTGTGATCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 750  
467 GCTGTATAGCCACAGTGTGATCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 526  
751 AGAGCGCTGCTTACCAAGTGTGATCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 810  
527 AGAGCGCTGCTTACCAAGTGTGATCAGAGCAAAAGGGAAGACATTTGTGAACCAAAATGAC 585  
811 GGAATATGAATTTGTAGTACCAAGCTTACCAAGGACCTCAAAAGTGTGATCAGAGCAAAATGAC 870  
586 GGAATATGAATTTGTAGTACCAAGCTTACCAAGGACCTCAAAAGTGTGATCAGAGCAAAATGAC 645  
871 CACTACTGATCCTCAAGGAGAGAAATTTGCCAAAGTTATAGTACCAAAATTTGAAAGATTA 930  
646 CACTACTGATCCTCAAGGAGAGAAATTTGCCAAAGTTATAGTACCAAAATTTGAAAGATTA 704  
931 CAAACAAATGGGCTTACCGCTTACCGGAAATACCTTTGTGGTTCTAGATCACCACCTTT 990  
705 CAAACAAATGGGCTTACCGCTTACCGGAAATACCTTTGTGGTTCTAGATCACCACCTTT 764  
991 AAATTTACTTCAAAATTAAGGATGTAAGTGAAGTGTGTTTTCAGGAAGA 1038  
765 AAATTTACTTCAAAATTAAGGATGTAAGTGAAGTGTGTTTTCAGGAAGA 812

RESULT 14  
LOCUS BE875947 828 bp mRNA linear EST 20-OCT-2000  
DEFINITION 601486423F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:388965 5',  
mRNA sequence.  
ACCESSION BE875947  
VERSION BE875947.1 GI:10324723  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 828)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs@mai.nih.gov](mailto:cgabs@mai.nih.gov)  
Tissue Procurement: DCTD/DTF/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9669 row: n column: 06  
High quality sequence stop: 795.  
Location/Qualifiers  
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/clone\_lib="NIH MGC 69"  
/notes="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."

FEATURES  
source  
1. 828  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:388965"  
/tissue\_type="large cell carcinoma, undifferentiated"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 69"  
/notes="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."

ORIGIN  
Query Match 39.4%; Score 657.2; DB 10; Length 828;  
Best Local Similarity 96.8%; Pred. No. 9.5e-101;  
Matches 726; Conservative 0; Mismatches 13; Indels 11; Gaps 5;  
403 TGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGTCCATGAAATAGTGG 462

4 TGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGTCCATGAAATAGTGG 63  
463 TTCTCTGAAATCTCAAGGTCCCTGCGAGCTCCTCAAGACAAATGATTTTTTATCTAGAAA 522  
64 TTCTCTGAAATCTCAAGGTCCCTGCGAGCTCCTCAAGACAAATGATTTTTTATCTAGAAA 123  
523 AGCTCAAGACTGTTATTTTATGAAGCTGCATCTGTCTCGGAAATCAAGTTGGATAG 582  
124 AGCTCAAGACTGTTATTTTATGAAGCTGCATCTGTCTCGGAAATCAAGTTGGATAG 183  
583 CACCAATTTCTGATCTCAAGGGCTGCATCTGTCTCAGACACACCTCCATGCTCTTC 642  
184 CACCAATTTCTGATCTCAAGGGCTGCATCTGTCTCAGACACACCTCCATGCTCTTC 243  
643 AGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCTGGTATAGC 702  
244 AGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAGCTGGTATAGC 303  
703 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCTGCCT 762  
304 CCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACAGAGCTGCCT 363  
763 TAACCAAGTGGTGTAGATGCCCTTCTGTCCA-GGACTTGATCATGAAGAGGACTATGA 822  
364 TAACCAAGTGGTGTAGATGCCCTTCTGTCCA-GGACTTGATCATGAAGAGGACTATGA 422  
823 TGTAGTACCAAGCTTACAGGACCTCAAAAGTGCAGACAAATTTACTAGACACTTACTG 882  
423 TGTAGTACCAAGCTTACAGGACCTCAAAAGTGCAGACAAATTTACTAGACACTTACTG 482  
883 CCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATTAACAAACAAATGG 942  
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943 TCTTCAGCTTACCCGGAAATACCTT-GTGGTTCTAGATCACCATCTTTAAATTTACTTC 1001  
543 TCTTCAGCTTACCCGGAAATACCTTGGTGGTTCTAGATCACCATCTTTAAATTTACTTC 602  
1002 AAAATAAAGCATGTAAGTGAAGTCTTTTCAAGAGAAATGTTTTCATAAAGGATATT 1061  
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1062 TATATCTCTGTTGCTTTCAGCTTTTATATAAATTCGCTGAGTATTAAGCTTTATTGA 1121  
663 TATATCTCTGTTG--TTGACTTTTATATAA-----TCGGAGTATAAGCTTTATTGA 715  
1122 AGTTCTTTGGTAAATATTAGTCTCCCTC 1151  
716 AGGT--CTTGGGTTAATATAGTCTCCCTC 743

RESULT 15  
LOCUS CB852764/c 683 bp mRNA linear EST 22-APR-2003  
DEFINITION UI-CF-FNO-aex-p-08-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
UI-CF-FNO-aex-p-08-0-UI 3', mRNA sequence.  
ACCESSION CB852764  
VERSION CB852764.1 GI:30047800  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Ronald, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab

University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
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Location/Qualifiers  
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/clone="UI-CF-FNO-aex-p-08-0-UI"  
/tissue\_type="Human Lung Epithelial cells"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-FNO"  
/notes="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized human lung epithelial cell libraries (EN1 and DUI). The library was subtracted according to Ronaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu  
TAG\_SEQ=None found"

# ORIGIN

Query Match 39.3%; Score 656.6; DB 14; Length 683;  
Best Local Similarity 99.3%; Pred. No. 1.3e-100;  
Matches 670; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy	426	AATCATGTGGATCCTCTCAGTCCATGAAATAGTGGTCTCTGAAACTTCAAGGTCCC	485
Db	624	AATCATGTGGATCCTCTCAGTCCATGAAATAGTGGTCTCTGAAACTTCAAGGTCCC	565
Qy	486	TGCCAGTCTCTCAGACAAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTATGA	545
Db	564	TGCCAGTCTCTCAGACAAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTATGA	505
Qy	546	AGCTGCATCACTGCTCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAGGG	605
Db	504	AGCTGCATCACTGCTCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAGGG	445
Qy	606	CTGCATTTCTGTGATPACAAGACCACTCCATGCTCTTTCAGCAATAATAATCCACTCTCAA	665
Db	444	CTGCATTTCTGTGATPACAAGACCACTCCATGCTCTTTCAGCAATAATAATCCACTCTCAA	385
Qy	666	CTGCAGAAACTCAGACGCTGAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAA	725
Db	384	CTGCAGAAACTCAGACGCTGAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAAA	325
Qy	726	GGGAAGACATTTGTAACCAATAGACAGAGCTGCTTTAACAGTTCGCTAGATGCCCTTC	785
Db	324	GGGAAGACATTTGTAACCAATAGACAGAGCTGCTTTAACAGTTCGCTAGATGCCCTTC	265
Qy	786	TGTCAGGGACTTGATCATGAAAGAGGACTATGAACTTTGTAGTACCAAGCTTACAGGA	845
Db	264	TGTCAGGGACTTGATCATGAAAGAGGACTATGAACTTTGTAGTACCAAGCTTACAGGA	205
Qy	846	CCTCAAGAGTACAGCAATTTACTAGACACTCTGACATCCAGGAGAGATTTGCCAAG	905
Db	204	CCTCAAGAGTACAGCAATTTACTAGACACTCTGACATCCAGGAGAGATTTGCCAAG	145

Qy	906	TTATAGTACAAAAATTGAAAGATAACAAAAAATGGTCTTTCAGCCTTACCCGGAATAC	965
Db	144	TTATAGTACAAAAATTGAAAGATAACAAAAAATGGTCTTTCAGCCTTACCCGGAATAC	85
Qy	966	TTGTGTTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAGTGACTG	1025
Db	84	TTGTGTTTTCTAGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAGTGACTG	25
Qy	1026	TTTTTCAAGAGAAA	1040
Db	24	TTTTTCAAGAGAAA	10

Search completed: April 1, 2004, 06:17:29  
Job time : 4694 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:13:27 ; Search time 81.5 Seconds  
(without alignments)

11572.314 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

Sequence: 1 acctagttataccagata.....caacagcctgattgtataaa 1669

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB-A Geneseq 29Jan04 -QWAT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161@cgn 1 1 81 @runat 29032004.124824.13654 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6  
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A\_Geneseq 29Jan04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182	41.0	284	3 AAY59406	Aay59406 Human RIC
2	1182	41.0	478	3 AAY59405	Aay59405 Human RIC
3	1182	41.0	531	3 AAY59404	Aay59404 Human RIC
4	1182	41.0	540	2 AAW92795	Aay62795 Human BI
5	1182	41.0	540	3 AAY68774	Aay68774 Amino aci
6	1182	41.0	540	4 AAM93621	Aam93621 Human pol
7	1182	41.0	540	5 AAU80369	Aau80369 Human cel
8	1182	41.0	540	5 AAE27882	Aae27882 Human rec
9	1182	41.0	544	3 AB43570	Ab43570 Human can
10	1176	40.8	540	2 AAY31140	Aay31140 Human CAR

11	1176	40.8	540	4 AAB20079	Aab20079 Human CAR
12	1176	40.8	540	5 AAB31075	Abg31075 Human cas
13	1176	40.8	540	5 AAO22107	Aao22107 Protein o
14	1176	40.8	540	6 ABU56269	Abu56269 Human cas
15	1176	40.8	540	7 ADB81362	Adb81362 Human cas
16	1027	35.7	510	7 ADC99079	Adc99079 Human KPP
17	867	30.1	167	3 AAY59407	Aay59407 Human RIC
18	632	21.9	131	5 AAO22109	Aao22109 Protein o
19	632	21.9	131	6 ABUS6271	Abu56271 Human CAR
20	548	19.0	110	6 ABUS6272	Abu56272 Human CAR
21	544	18.9	109	5 AAO22110	Aao22110 protein o
22	461	16.0	92	5 ABJ04754	Abj04754 RICK prot
23	125	4.3	959	4 AAM79473	Aam79473 Human pro
24	122.5	4.3	164	2 AAY31144	Aay31144 Human CAR
25	122.5	4.3	164	4 AAB20083	Aab20083 Human CAR
26	122.5	4.3	164	5 AAB31079	Abg31079 Human cas
27	122.5	4.3	164	5 AAO22135	Aao22135 Protein o
28	122.5	4.3	164	6 ABUS6297	Abu56297 Human Cas
29	122.5	4.3	249	2 AAY31143	Aay31143 Human CAR
30	122.5	4.3	249	4 AAB20082	Aab20082 Human CAR
31	122.5	4.3	249	5 AAB31078	Abg31078 Human cas
32	122.5	4.3	249	5 AAO22134	Aao22134 Protein o
33	122.5	4.3	249	6 ABUS6296	Abu56296 Human Cas
34	122.5	4.3	409	6 ABUS6299	Abu56299 Human Cas
35	122.5	4.3	779	4 AAB35610	Aab35610 Human pro
36	122.5	4.3	953	2 AAY31141	Aay31141 Human CAR
37	122.5	4.3	953	3 AAB15552	Aab15552 Apoptosis
38	122.5	4.3	953	4 AAB20080	Aab20080 Human CAR
39	122.5	4.3	953	4 AAM78489	Aam78489 Human pro
40	122.5	4.3	953	5 AAO22111	Aao22111 Protein o
41	122.5	4.3	953	6 ABUS6273	Abu56273 Human Cas
42	122.5	4.3	953	7 ABJ72227	Abj72227 Human nuc
43	121.5	4.2	953	5 AAB31076	Abg31076 Human cas
44	119	4.1	100	5 AAO22112	Aao22112 Human CAR
45	119	4.1	100	6 ABUS6274	Abu56274 Human CAR

#### ALIGNMENTS

RESULT 1

AAY59406  
ID AAY59406 standard; protein; 284 AA.

XX AC AAY59406;

XX XX

DT 21-MAR-2000 (first entry)

XX DE Human RICK protein sequence residues 248-531.

XX KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DRBP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease.

XX OS Homo sapiens.

XX XX

XX PN WO9955134-A2.

XX XX

PD 04-NOV-1999.

XX XX

PF 27-APR-1999; 99WO-US009183.

XX XX

PR 27-APR-1998; 98US-00069023.

XX XX

XX PA (UNMI ) UNIV MICHIGAN.

XX XX

XX PI Nunez G, Inohara N, Koseki T;

XX XX

XX DR WPI; 2000-072163/06.

XX XX

PT Compositions for identifying apoptosis signaling pathway inhibitors  
PT useful for treating diseases.

XX PS Claim 6; Page; 93pp; English.

XX CC This sequence is a fragment of the human RICK (RIP-like interacting CLARP

CC CC kinase) protein of the invention. RICK acts as a positive regulator of

CC CC apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

CC CC during CD95 signalling. The invention provides methods for identifying

CC CC apoptosis signalling pathway inhibitors and activators, and methods and

CC CC compositions for screening compounds which will modulate the interactions

CC CC of the various compositions identified: RICK, and the CIDE family of

CC CC activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening

CC CC assays for agents, useful in the diagnosis, prognosis or treatment of

CC CC disease associated with excess cell growth and dysregulation of

CC CC apoptosis. Complexes containing RICK and CLARP can be used in drug

CC CC screening assays to identify inhibitor molecules blocking CD95-mediated

CC CC apoptosis. Overexpression of ARC in an in vitro cell system can be used

CC CC to identify inhibitors of the enzymatic activity of caspase-8.

CC CC Identification of ARC-like inhibitory compounds may be useful for gene

CC CC therapy treatment of disease with increased cell death in muscle tissue

CC CC and cardiac disorders. Therapeutic compositions of CIDEs can be used to

CC CC treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

CC CC ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies

CC CC can be used as reagents for the preparation or affinity chromatography

CC CC media, and for diagnostically measuring RICK levels. A specific inhibitor

CC CC of an essential step in the biochemistry of apoptosis is needed. RICK

CC CC interaction with intracellular factors such as CLARP and FADD appears to

CC CC be essential for apoptosis, inhibitors of RICK binding to intracellular

CC CC apoptosis factors are potential drug candidates. Note: This sequence was

XX CC created using information given in the specification

SQ Sequence 284 AA;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
2.52e-119	1182.00	284	227
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.56%	Mismatches:	0
Query Match:	41.04%	Indels:	0
DB:	3	Gaps:	0

US-09-771-161A-2 (1-1669) x AAY59406 (1-284)

QY	332	CAGTTACAGAGTGTTCAGTCCATTACCTATGTCAGAGAGAAATGAAATATCT	391
DB	57	LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	76
QY	392	CTGACATACCTGTAATCATCGTCCACAGAGGATCATGTGGATCTCTCAGCTCCAT	451
DB	77	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	96
QY	452	GAATAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTT	511
DB	97	GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	116
QY	512	TTATCTAGAAAAGCTCAAGACTGTATTTATGAGCTGCATCATCTGCTCGGAATCATC	571
DB	117	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	136
QY	572	AGTTGGATGACCACTTTCTGGATCTCAAGGGCTGCATCTGTGATCACAAGACCACT	631
DB	137	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	156
QY	632	CAATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACCTCAGAACCTCTGCAG	691
DB	157	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	176
QY	692	CTGTGTATAGCCAGAGTGGATCCAGACAAAGGAGACATTTGTGACCAATGACA	751
DB	177	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	196
QY	752	GAAGCTGCTTAAACAGTGCCTAGATGCCCTTCTCTCCAGGACCTTGATCATGAAAGAG	811
DB	197	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	216

QY	812	GACTATGAACCTTGTAGTACCAAGCCTCAAGACCTCAAACTCAGACAAATTACTAGAC	871
DB	217	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	236
QY	872	ACTACTGACATCAAGAGAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAAC	931
DB	237	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	256
QY	932	AAACAATGGCTTCTCAGCTTACCCGGAATACTTGTGTTTCTAGATCACCACCTTTTA	991
DB	257	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	276
QY	992	AATTTACTTCAAAATAAAGCATG	1015
DB	277	AsnLeuLeuGlnAsnLysSerMet	284
RESULT 2			
ID	AAY59405		
XX	AAY59405 standard; protein; 478 AA.		
XX	AAY59405;		
XX	21-MAR-2000 (first entry)		
XX	Human RICK protein sequence residues 54-531.		
XX	RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;		
XX	caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;		
XX	CIDE-A; CIDE-B; DRP-1; diagnosis; cell growth; apoptosis dysregulation;		
XX	gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;		
XX	aplastic anaemia; ischaemic injury; toxin-induced liver disease.		
OS	Homo sapiens.		
XX	WO9955134-A2.		
XX	04-NOV-1999.		
XX	27-APR-1999; 99WO-US009183.		
XX	27-APR-1998; 98US-00069023.		
XX	(UNMI) UNIV MICHIGAN.		
XX	Nunez G, Inohara N, Koseki T;		
XX	WPI; 2000-072163/06.		
XX	Compositions for identifying apoptosis signalling pathway inhibitors		
XX	useful for treating diseases.		
XX	Claim 6; Page; 93pp; English.		
XX	This sequence is a fragment of the human RICK (RIP-like interacting CLARP		
XX	kinase) protein of the invention. RICK acts as a positive regulator of		
XX	apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10		
XX	during CD95 signalling. The invention provides methods for identifying		
XX	apoptosis signalling pathway inhibitors and activators, and methods and		
XX	compositions for screening compounds which will modulate the interactions		
XX	of the various compositions identified: ARC, RICK, and the CIDE family of		
XX	activators (CIDE-A, CIDE-B and DRP-1). RICK is useful in screening		
XX	assays for agents, useful in the diagnosis, prognosis or treatment of		
XX	disease associated with excess cell growth and dysregulation of		
XX	apoptosis. Complexes containing RICK and CLARP can be used in drug		
XX	screening assays to identify inhibitor molecules blocking CD95-mediated		
XX	apoptosis. Overexpression of RICK and CLARP can be used in drug		
XX	screening assays to identify inhibitor molecules blocking CD95-mediated		
XX	apoptosis. Overexpression of ARC in an in vitro cell system can be used		
XX	to identify inhibitors of the enzymatic activity of caspase-8.		
XX	Identification of ARC-like inhibitory compounds may be useful for gene		
XX	therapy treatment of disease with increased cell death in muscle tissue		
XX	and cardiac disorders. Therapeutic compositions of CIDEs can be used to		
XX	treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,		
XX	ischaemic injury, and toxin-induced liver disease. AntiRICK antibodies		





Db 304 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 323  
QY 392 CTGAACATACCTTAATCATGTGCACAAAGAGAAATCATGTGCATCTCTCAGCTCCAT 451  
Db 324 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 343  
QY 452 GAAATAGTGGTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511  
Db 344 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 363  
QY 512 TTATCTAGAAAGCTCAAGACGTGTTATTTATCAAGCTGCATCTCTGGAATCAC 571  
Db 364 LeuSerArgLysAlaGlnAspCysfyrPheMetLysLeuHisCysProGlyAsnHis 383  
QY 572 AGTTGGATAGACACCATTTCTGCATCTCAAGGGCTGCATTTCTGATCACAAGACCAT 631  
Db 384 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 403  
QY 632 CCATGCTCTTACCAATATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
Db 404 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 423  
QY 692 CTTGTATAGCCAGCAGTGGATCCAGACGAAAGGAGACATTTGTGAACCAATGACA 751  
Db 424 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 443  
QY 752 GAAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAAGAG 811  
Db 444 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 463  
QY 812 GACTATGAATCTTTAGTACCAAGCTTACAAGACCTCAAGACCTCAAAAGTCAGACAAATCTAGAC 871  
Db 464 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 483  
QY 872 ACTACTGACATCCAAGGAGAAATTTGCCAAGTTATAGTACAAATAATTGAAGATAC 931  
Db 484 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 503  
QY 932 AAACAAATGGTCTTACCGCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991  
Db 504 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 523  
QY 992 AATTACTTCAAAATAAAGCATG 1015  
Db 524 AsnLeuLeuGlnAsnLysSerMet 531

RESULT 4  
AAW92795  
XX AC AAW92795 standard; protein; 540 AA.  
XX AC AAW92795;  
XX DT 07-MAY-1999 (first entry)  
XX DE Human B1 protein.  
XX KW B1 protein; intracellular mediator; modulator; inflammation; cell death;  
XX KW cell survival pathway; intracellular signalling; AIDS; cancer; human.  
XX OS Homo sapiens.  
XX PN WO985507-A2.  
XX PD 10-DEC-1998.  
XX PF 01-JUN-1998; 98WO-IL000255.  
XX PR 05-JUN-1997; 97IL-00121011.  
XX PR 30-JUN-1997; 97IL-00121199.  
XX PR 11-SEP-1997; 97IL-00121746.  
XX PA (YEDA ) YEDA RES & DEV CO LTD.  
XX

PI Wallach D, Boldin M, Malinin N;  
XX WPI; 1999-070258/06.  
DR N-PSDB; AAX02558.  
XX New B1 protein regulates cell death and cell survival pathways -  
PT derivatives, DNA and antibodies, also regulate intracellular inflammation  
PT ; for treating AIDS, cancer.  
XX  
PS Claim 4; Fig 3A; 90pp; English.  
XX  
CC This invention describes the isolation of a novel human B1 protein which  
CC can interact with, intracellular mediators or modulators of inflammation,  
CC cell death and/or cell survival pathways, directly or indirectly. Cells  
CC can be modulated or mediated in inflammation, cell death or cell survival  
CC pathways or another intracellular signalling activity using B1.  
CC Conditions such as AIDS and cancer can be treated using B1. Antibodies,  
CC oligonucleotides and ribozymes can also be used to regulate the above  
CC pathways  
XX  
SQ Sequence 540 AA;  
Alignment Scores:  
Pred. No.: 3,3e-119 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 2 Gaps: 0  
US-09-771-161A-2 (1-1669) x AAW92795 (1-540)  
QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCATTCACCTATGTGACAGAGAAATGAATATCT 391  
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
QY 392 CTGAACATACCTGTTAAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451  
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352  
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511  
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372  
QY 512 TTATCTAGAAAGCTCAAGACGTGTTATTTATGAAGCTGCATCCTCTCTGGAATCAC 571  
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
QY 572 AGTTGGATAGACCATTTCTGCATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 631  
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 412  
QY 632 CCATGCTCTTACAGCAATATAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691  
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTTGTATAGCCAGCAGTGGATCCAGACGAAAGGAGACAAATGATTCGACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAATCTTTAGTACCAAGCTCACAAGGACCTCAAAAGTCAGACAAATTTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCCAAGGAGAAATTTGCCAAGTTATAGTACAAATAATTGAAGATAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAAATGGTCTTACCGCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991

|||||  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 532  
Qy 992 AATTTACTTCAAAATAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
RESULT 5  
AAV68774  
ID AAV68774 standard; protein; 540 AA.  
XX AC AAV68774;  
XX DT 16-MAY-2000 (first entry)  
XX DE Amino acid sequence of a human phosphorylation effector PHSP-6.  
XX KW Human; phosphorylation effector; PHSP; proliferative disorder;  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
XX Region. 18..287  
FT Modified-site /note= "protein kinase family signature sequence"  
FT Modified-site 23  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 34  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 58  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 100  
FT Modified-site /note= "potential glycosylation site"  
FT Modified-site 102  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 180  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 183  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 207  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 224  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 267  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 296  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 301  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 360  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 374  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 391  
FT Modified-site /note= "potential glycosylation site"  
FT Modified-site 401  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 428  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 442  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 457  
FT Modified-site /note= "potential glycosylation site"  
FT Modified-site 478  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 484  
FT Modified-site /note= "potential phosphorylation site"  
FT Modified-site 537  
FT Modified-site /note= "potential glycosylation site"  
XX PN W0200006728-A2.

XX PD 10-FEB-2000.  
XX PF 28-JUL-1999; 99WO-US017132.  
XX PR 28-JUL-1998; 98US-0155213P.  
XX PR 14-SEP-1998; 98US-0155213P.  
XX PR 14-OCT-1998; 98US-0155239P.  
XX PR 03-NOV-1998; 98US-0106889P.  
XX PR 19-NOV-1998; 98US-0109093P.  
XX PR 22-DEC-1998; 98US-0113796P.  
XX PR 12-JAN-1999; 99US-0155233P.  
XX FA (INCY-) INCYTE PHARM INC.  
XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;  
XX WPI; 2000-183125/16.  
XX DR N-PSDB; AAZ46143.  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
XX and prevention of proliferative, immune and neuronal disorders.  
XX Claim 1; Page 84-85; 142pp; English.  
XX AAV68769-95 and AAV68797-99 represent human phosphorylation effectors  
XX (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
XX given in the specification). The sequences were isolated from cDNA  
XX libraries prepared from various human tissues. The PHSP proteins are  
XX useful for the diagnosis, treatment and prevention of proliferative  
XX disorders, immune disorders and neuronal disorders. The PHSP proteins  
XX form pharmaceutical compositions which useful for treating or preventing  
XX disorders associated with decreased PHSP expression/activity. PHSP  
XX antagonists are useful for treating or preventing disorders associated  
XX with increased PHSP expression/activity  
XX SQ Sequence 540 AA;  
Alignment Scores:  
Pred. No.: 3.3e-119 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 3 Gaps: 0  
US-09-771-161A-2 (1-1669) x AAV68774 (1-540)  
Qy 332 CAGTTACAGAGTGTTCAGTCCATTCACCTATGTGACAGAGAAATGGAATTATCT 391  
Db 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332  
Qy 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCAT 451  
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
Qy 452 GAAATAGTGTCTCTCTGAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATTTT 511  
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372  
Qy 512 TTATCTAGAAAAGCTCAAGACTGTATTATTAAGCTGCATCATCTGTCTGGAATCAC 571  
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
Qy 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 631  
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412  
Qy 632 CCATGCTTTCAGCAATAAATAATCCACTCTCACTCAGAACTCAGAACGCTGCGAG 691  
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432





US-09-771-161A-2 (1-1669) x AAE27882 (1-540)

QY 332 CAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGAATATCT 391

Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

QY 392 CTGAACATACCTGTAATCATGGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451

Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352

QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 511

Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372

QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTGCTCTGGAATATC 571

Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392

QY 572 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 631

Db 393 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412

QY 632 CATGCTCTTCAGCAATATAATCCACTCTCACTGAGGAACTCAGAACGCTCTGCAG 691

Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751

Db 433 ProGlyIleAlaGlnGlnIleGlnSerLysArgLysAlaValAsnGlnMetThr 452

QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTCCAGGACTTGATCATGAAGAG 811

Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

QY 812 GACTATGACTGTGTAGTACCAAGCTCAGAGCACTCAAGAGCTCAAGTGCAGAACTAGAC 871

Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

QY 872 ACTACTGACATCCAGGAGGAAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931

Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

QY 932 AAACAAATGGTCTTCAGCTTACCCGAAATACCTTGTGGTTCCTAGATCACCATCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532

QY 992 AATTTACTTCAAAATAAAGCATG 1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9

AAB43570

ID AAB43570 standard; protein; 544 AA.

XX AC AAB43570;

XX DT 08-FEB-2001 (first entry)

XX DE Human cancer associated protein sequence SEQ ID NO:1015.

XX KW Human; cancer associated gene; cancer antigen; detection; cancer;

KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;

KW antiinflammatory; antithrombotic; antirheumatic; antiarthritic; antiviral;

KW antiinflammatory; antithrombotic; antirheumatic; antirheumatic; antiviral;

KW dermatological; neuroprotective; thrombolytic; coagulant; neurotropic;

KW vasotrophic; antiproliferative; angiogenic; gene therapy; inflammation;

KW immune disorder; haematopoietic cell disorder; autoimmune disorder;

KW allergic reaction; graft versus host disease; organ rejection;

KW haemostatic; thrombolytic; cardiovascular disorder; infection;

XX KW neurological disease; drug screening.

OS Homo sapiens.

XX WO200055350-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005882.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587533/55.

XX N-PSDB; AAC77779.

XX Novel isolated nucleic acids comprising sequences encoding peptides

PT useful for treating or diagnosing e.g. cancer.

XX Claim 11; Page 1595-1597; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in

CC AAB43398 to AAB44239. The proteins can have activities based on the

CC tissues and cells the genes are expressed in. Example of activities

CC include: cytostatic; proliferative; vulnerable; immunomodulator;

CC antiinflammatory; antithrombotic; antirheumatic; antirheumatic;

CC dermatological; neuroprotective; thrombolytic; coagulant;

CC vasotrophic; antiproliferative; angiogenic; gene therapy; inflammation;

CC polynucleotides and polypeptides can be used for preventing, treating or

CC ameliorating medical conditions and diagnosing pathological conditions.

CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from

CC the present invention may be used to treat immune disorders by activating

CC or inhibiting the proliferation, differentiation or mobilisation of

CC immune cells, to treat disorders of haematopoietic cells, autoimmune

CC disorders, allergic reactions, graft versus host disease and organ

CC rejection, modulate haemostatic or thrombolytic activity, modulate

CC inflammation, cancers, cardiovascular disorders, neurological diseases and

CC bacterial or viral infections. The peptides, nucleotides, antibodies,

CC agonists and antagonists may be also used in drug screens. AAC78449 to

CC AAC78457 and AAB44240 represent sequences used in the exemplification of

CC the present invention

XX SQ Sequence 544 AA;

Alignment Scores:

Pred. No.: 3,31e-119 Length: 544

Score: 1182.00 Matches: 227

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.56% Mismatches: 0

Query Match: 41.04% Indels: 0

DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x AAB43570 (1-544)

QY 332 CAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGAATATCT 391

Db 317 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 336

QY 392 CTGAACATACCTGTAATCATGGTCACAAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451

Db 337 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 356

QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 511

Db 357 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 376

QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTGCTCTGGAATATC 571

Db 377 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 396

QY 572 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAC 631

Db 397 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisIleThrThr 416  
 QY 632 CCATGCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACTGTCGAG 691  
 Db 417 ProCysSerSerAlaIleAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 436  
 QY 692 CCGTATAGCCACAGTGGATCCAGACCAAGGGAAGACATTTGTCAACCAATGACA 751  
 Db 437 ProGlyIleAlaGlnGlnTrpIleGlnSerIleArgGluAspIleValAsnGlnMetThr 456  
 QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTCATCATGAAAGAG 811  
 Db 457 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLeuGlu 476  
 QY 812 GACTATGAAGTGTGTAGTACCAAGCTTCAAGGACTCAAGAGTCCAGCAATATTACTAGAC 871  
 Db 477 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 496  
 QY 872 ACTACTGATCCCAAGGAGAGAAATTCGCCAAGTTATAGTACAAAATTTGAAGATTAAC 931  
 Db 497 ThrThrAspIleGlnGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 516  
 QY 932 AAACAATGGGTCTTCAGCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTA 991  
 Db 517 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 536  
 QY 992 AATTACTTCAAAATAAAGCATG 1015  
 Db 537 AsnLeuLeuGlnAsnLysSerMet 544  
 RESULT 10  
 ID AAY311140 standard; protein; 540 AA.  
 AC AAY311140;  
 XX 25-OCT-1999 (first entry)  
 DE Human CARD-3 protein.  
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
 KW caspase activation; detection; screening; therapy; diagnosis; disease;  
 KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
 KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
 KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
 KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
 KW human.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..300  
 FT Domain /note= "predicted kinase domain"  
 FT Domain 301..431  
 FT Domain /note= "predicted linker domain"  
 FT Domain 432..540  
 FT Domain /note= "predicted CARD domain"  
 FN WO9940102-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 05-FEB-1999; 99WO-US002544.  
 XX  
 PR 06-FEB-1998; 98US-00019942.  
 PR 17-JUN-1998; 98US-00099041.  
 PR 08-DEC-1998; 98US-00207359.  
 XX  
 FA (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;  
 FI WPI; 1999-494269/41.  
 DR N-PSDB; AAZ09246.  
 XX  
 PT Novel CARD-3 and CARD-4 genes and polypeptides used or treating  
 PT regulation of cellular proliferation and differentiation and cell  
 PT survival.  
 XX  
 PS Example 2; Fig 2; 181pp; English.  
 XX  
 CC This invention describes the isolation of novel human caspase recruitment  
 CC domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial  
 CC murine CARD-4L protein and genes. The genes and proteins of the invention  
 CC are involved in the regulation of caspase activation. The caspase  
 CC recruitment domain (CARD) polynucleotides, polypeptides, homologues and  
 CC antibodies can be used in screening assays, detection assays, predictive  
 CC medicine and therapeutic and prophylactic methods of treatment. The  
 CC methods may be used to diagnose and treat patients which are suffering  
 CC from a disorder associated with abnormal level or rate of apoptotic cell  
 CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the TNF receptor complex, or abnormal activity of a caspase.  
 CC Diseases that may be treated include cancer (particularly follicular  
 CC lymphoma, carcinomas associated with mutations in p53 and hormone-  
 CC dependent tumours), autoimmune disorders (e.g. systemic lupus  
 CC erythematosus, immune-mediated glomerulonephritis), viral infections,  
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
 CC retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration,  
 CC anaemia, myelodysplastic syndrome, myocardial infarction, and stroke.  
 CC CARD-3 protein interacts with other cellular proteins, and so can be used  
 CC for regulation of cellular proliferation and differentiation and cell  
 CC survival. The CARD proteins may also be used to for screen drugs or  
 CC compounds which modulate their activity. The CARD-4 gene can express a  
 CC long transcript that encodes CARD-4L, a short transcript that encodes  
 CC CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence  
 CC represents the human CARD-3 protein described in the method of the  
 CC invention  
 XX  
 SQ Sequence 540 AA;  
 Alignment Scores:  
 Pred. No.: 1.49e-118 Length: 540  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 40.83% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-771-161A-2 (1-1669) x AAY311140 (1-540)  
 QY 332 CAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT 391  
 Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAAATCATGTGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352  
 QY 452 GAAATATAGTGTCTCTCTGAAACTTCAAGGTCCCTGCAGCTCTCAGACAAATGATTTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
 QY 512 TTATCTAGAAAGCTCAAGACTGTATTATTTATGAAGCTGATCATCTCTGGAAATCAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTCATTTCTGTGATCAAGACCACT 631  
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
 QY 632 CCATGCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACTGTCGAG 691





QY 992 AATTTACTTCAAAATAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12

ABG31075  
 ID ABG31075 standard; protein; 540 AA.

AC ABG31075;

XX 21-OCT-2002 (first entry)

DE Human caspase recruitment domain protein CARD-3.  
 KW Human; caspase recruitment domain; CARD-3; CARD-4; LRR;  
 KW leucine rich repeat; LPS; lipopolysaccharide; NF-kB;  
 KW nuclear factor-kappa B; cancer; viral infection; autoimmune disorder;  
 KW systemic lupus erythematosus; immune-mediated glomerulonephritis;  
 KW arthritis; immune disorder; multiple sclerosis; Hashimoto's thyroiditis;  
 KW atopic condition; asthma; allergy; psoriasis; contact dermatitis;  
 KW gastrointestinal allergy; insulin-dependent diabetes;  
 KW bacterial infection; tuberculosis; lepromatous leprosy;  
 KW cell signalling disorder; tissue disorder.

XX Homo sapiens.

XX WO200253765-A1.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-US049798.

XX 29-DEC-2000; 2000US-0258724P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J, Philpott D, Sansonetti P, Girardin S;

XX WPI; 2002-583627/62.

XX N-PSDB; ABK89280.

Identifying modulators of long form of caspase recruitment domain, CARD-4L useful for treating cancer, infections, and immune disorders, by contacting test compound with CARD-4L and determining effect of the compound.  
 Example 2; Fig 2; 139pp; English.  
 The invention relates to identifying (MI) a compound which modulates a human or murine caspase recruitment domain (CARD)-4L (long form) polypeptide with a by contacting the polypeptide with a test compound and determining the effect of the test compound on the activity of the polypeptide to identify a compound which modulates the polypeptide. The method may be adapted for identifying a compound which binds to the LRR (leucine rich repeat) domain of CARD-4. Also included is a method of identifying a candidate compound for modulating LPS (lipopolysaccharide)-mediated activation of nuclear factor-kappa B (NF-kB), by providing a cell expressing a polypeptide comprising the LRR domain of CARD-4 and harbouring LPS, exposing the cell to a test compound and measuring NF-kB activation, where altered NF-kB activation polypeptide in the presence of the test compound compared to the binding in the absence of the test compound indicates that the test compound is a candidate compound for modulating LPS-mediated activation of NF-kB. Modulators identified by (MI) are useful for treating a disorder characterised by aberrant CARD-4 protein or nucleic acid. Compounds that modulate the activity of CARD-4L are useful to treat or diagnose disorders such as cancer, viral infections, autoimmune disorders e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis and arthritis, immune disorders, such as multiple sclerosis, Hashimoto's thyroiditis, atopic conditions such as asthma, allergy, psoriasis, contact dermatitis, gastrointestinal allergies, insulin-dependent diabetes, bacterial infections, including tuberculosis, and lepromatous leprosy, disorders of cell signalling and

CC disorders of tissues. The present sequence represents human CARD-3

CC protein

XX Sequence 540 AA;

Alignment Scores:

Pred. NO.: 1.49e-118 Length: 540  
 Score: 1176.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 1  
 Best Local Similarity: 99.12% Mismatches: 1  
 Query Match: 40.83% Indels: 0  
 DB: 5 Gaps: 0

US-09-771-161A-2 (1-1669) x ABG31075 (1-540)

QY 332 CAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGCAATTTATCT 391  
 Db 313 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 332  
 QY 392 CTGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451  
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
 QY 452 GAAATAGTGGTCTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 511  
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
 QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGTGCATCACTGTCTCTGGAATACAC 571  
 Db 373 LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis 392  
 QY 572 AGTTGGATAGCACCATTCTCGGATCTCAAGGGCTCATTTCTGTATGATCAAGACCACT 631  
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412  
 QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCACTCAGAGAACTCAGAACGCTGCGAG 691  
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
 QY 692 CTTGGTATAGCCACGAGTGGATCCAGAGCAAGGAAGACATTTGTGAACCAATGACA 751  
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
 QY 752 GAAGCTGCTTAACCAAGTCCGATAGTGCCTTCTGTCCAGGGACTTGTATCATCAAGAG 811  
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 472  
 QY 812 GACTATCAACTTGTAGTACCAAGCTTCAAGGACCTCAAGACCTCAAGACCAATTTACTAGAC 871  
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
 QY 872 ACTACTCACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
 QY 932 AAACAAATGGTCTCTACGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 991  
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532  
 QY 992 AATTACTTCAAAATAAAGCATG 1015  
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13

AAO22107  
 ID AAO22107 standard; protein; 540 AA.

XX AC AAO22107;

XX DT 27-SEP-2002 (first entry).

XX Protein of human CARD-3 SEQ ID No 2.  
 XX

Cytostatic; virucide; immunomodulatory; neuroprotective; antialzheimer's; cerebroprotective; antiparkinsonian; antisclerotic; ophthalmological; neurotropic; antihaemic; Caspase Recruitment Domain; CARD; CARD-41; P53; cancer; CARD-4S; follicular lymphoma; carcinoma; autoimmune disorder; hormone-dependent tumour; breast cancer; prostate cancer; ovarian cancer; systemic lupus; herpes virus; poxvirus; adenovirus; neurological disease; anaemia; neutropenia; myelodysplastic syndrome; human.

**Homo sapiens.**

US6369196-B1.

09-APR-2002.

05-FEB-1999; 99US-00245281.

06-FEB-1998; 98US-00019942.

08-DEC-1998; 98US-00207359.

(MILL-) MILLENNIUM PHARM INC.

Bertin J;

WPI; 2002-391988/42.

100

-4S) useful for diagnosing an

Example 2; Fig 2; 116pp; English.

The invention relates to novel is

be used to treat disorders associated with decreased CARD expression by supplementing the patient's own production of CARD. Disorders associated with the expression and activity of CARD include cancers (particularly follicular lymphomas, carcinomas associated with mutations in p53, and hormone-dependent tumours such as breast cancer, prostate cancer, and ovarian cancer), autoimmune disorders (such as systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (such as those caused by herpes viruses, poxviruses, and adenoviruses), neurological diseases (such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) retinitis pigmentosa, spinal muscular atrophy, and various forms of cerebellar degeneration), anaemia associated with chronic disease, aplastic anaemia, chronic neutropenia, and the myelodysplastic syndromes. This sequence represents a human CARD protein relating to the invention.

Sequence 540 AA:

Instrument Scores:

Length:	540
Matches:	226
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0
1.49e-118	
1176.00	
99.56%	
99.12%	
40.83%	
5	

09-771-161A-2 (1-1669) x AAO22107 (1-540)

332 CAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAGAGAAATGGAATTATCT 391

313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

392 CTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352

452 GAAATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 511

353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372

512	QY	TTATCTGAAAAGCTCAAGACTGTTATTTATGAAGCTCATCACTGCTCTCGAAATCAC	571
373	Db	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392
572	QY	AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCGATTCTGTGATCACAAGACCACT	631
393	Db	SerTrpaspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle	412
632	QY	CCATGCTCTTCAGCAATPAATAATCCACTCTCAACTGCGAGGAAATCTCAGAACGCTCTGCAG	691
413	Db	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
692	QY	CCTGGTATAGCCAGCAGTGGATCCAGAGCAGAAGGGAAGACATTCGTAAACCAATGACA	751
433	Db	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
752	QY	GAAGCGCTGCCTTAACCAAGTCGCTAGATGCGCCCTCTGTCCAGGACATTCATGATGAAGAG	811
453	Db	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
812	QY	GACTATGAACCTTGTTAGTACAAGCCCTACAAGGACCTCAAAAGTCAGACAATTACTAGAC	871
473	Db	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
872	QY	ACTACTGATCAATCCGAGGAGAGAAATTCGCCAAAGTTATAGTACAAAATTTGAAAGATAAC	931
493	Db	ThrThrAspIleGlnGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
932	QY	AAACAAATGGGCTCTTCAGCCCTTACCCGGAATAATCTTGTGGTTCTTAGATCACCAATCTTTA	991
513	Db	IuacGluMetGluGlnProThrProGluIleLeuValValSerArgSerProSerLeu	532

RESULT 14

ABU56269

ID	ABU56269 standard; protein; 540 AA.
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100	100

XX  
AC AB1156269.XX  
XX  
1507050074

DT 30-APR-2003 (first entry)

XX Human Caspase recruitment domain protein, CARD-3.  
 XX  
 XX Human; caspase recruitment domain; CARD; CARD-3; CARD-4; CARD-4L;  
 KW CARD-4S; CARD-4Y; CARD-4Z; apoptosis; cancer; AIDS; autoimmune disorder;  
 KW systemic lupus erythematosus; viral infection;  
 KW immune related glomerulonephritis; acquired immunodeficiency syndrome;  
 KW neurological disease; Alzheimer's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa;  
 KW spinal muscular atrophy; cerebellar degeneration; haematological disease  
 KW anaemia; neutropenia; myelodysplastic syndrome; myocardial infarction;  
 KW stroke; chromosome 7.  
 KW

OS Homo sapiens.

XX

PN US6469140-B1.

XX  
PD  
22-OCT-2002

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 104

PF 08-DEC-1998; 98US-00207359.

[illegible]

PR 06-FEB-1998; 98US-000199942.  
PR 17-JUN-1998; 98US-00099041.

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PA (MILL-) MILLENNIUM PHARM INC.

DR N-PSDB; ABX75869, ABX74870.

XX Novel isolated human caspase recruitment domain (CARD)-4Y or CARD-4Z

PT polypeptide, or murine CARD-4L polypeptide, useful in screening assays,

PT detection assays, predictive medicine, and in therapeutic applications.

XX

XX Example 2; Fig 2; 99pp; English.

XX The invention relates to an isolated polypeptide, comprising at least 25

CC contiguous amino acids of a human caspase recruitment domain (CARD)-4Y,

CC human CARD-4Z or murine CARD-4L (all splice variants of CARD-4)

CC polypeptide. Also included is an isolated fusion protein, comprising the

CC CARD polypeptide covalently linked by a peptide bond to a heterologous

CC polypeptide. The CARD polypeptide is useful in screening assays,

CC detection assays (e.g. chromosomal mapping, tissue typing and forensic

CC biology), predictive medicine (e.g. diagnostic assays, prognostic assays,

CC monitoring clinical trials and pharmacogenomics), and in therapeutic and

CC prophylactic treatments (in diseases associated with apoptotic cell death

CC e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and

CC immune related glomerulonephritis), viral infections, AIDS (acquired

CC immunodeficiency syndrome), neurological disease (e.g. Alzheimer's

CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis

CC pigmentosa, spinal muscular atrophy and cerebellar degeneration),

CC haematological diseases (e.g. anaemia, neutropenia and myelodysplastic

CC syndromes), myocardial infarction and stroke). The CARD polypeptide is

CC useful as bait protein in a two-hybrid assay or three hybrid assay to

CC identify other proteins, which bind to or interact with other CARD

CC proteins. Also disclosed are CARD-3 proteins and cDNAs. The gene for

CC human CARD-4 is located on chromosome 7. The present sequence is a human

CC CARD protein

XX

SQ Sequence 540 AA;

Alignment Scores:

Pred. No.: 1.49e-118 Length: 540

Score: 1176.00 Matches: 226

Percent Similarity: 99.56% Conservative: 1

Best Local Similarity: 99.12% Mismatches: 1

Query Match: 40.83% Indels: 0

DB: 6 Gaps: 0

US-09-771-161a-2 (1-1669) x ABUS6269 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCTACCTACCTATGTGACAGAGAAATGAATATCT 391

DB :::: 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

QY 392 CTGACATACCTGTAATCATGCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

DB :::: 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352

QY 452 GAAATAGTGGTTCCTGAACTTCAAGGTCCTCCAGCTCCTCAAGACAATGATTTT 511

DB :::: 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspHe 372

QY 512 TTATCTAGAAAGCTCAAGCTGTTATTTATGAGCTGCATCATGTCTCGGAATCAC 571

DB :::: 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392

QY 572 AGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCACAAGACCACT 631

DB :::: 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412

QY 632 CCATCTCTTTCAGCAATAATAATCCACTCTCACTCAGGAAATCTCAGAACGCTCGAG 691

DB :::: 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CCTGTATAGCCAGAGTGGATTCAGAGCAAAAGGAGACATTTGTGAACAAATGACA 751

DB :::: 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452

QY 752 GAAGCCTCCCTTAACAGTCGCTAGATCCCTCTCTCCAGGACTTCATCATGAAAGAG 811

DB :::: 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

QY 812 GACTATGAACCTGTGTAGTACCAAGCCCTACAGAGCCTCAAAAGTCAGACAATTACTAGAC 871

DB :::: 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATTATAGTACAAAATTTGAAAGATTAAC 931

DB :::: 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

QY 932 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATTCTTTA 991

DB :::: 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValValSerArgSerProSerLeu 532

QY 992 AATTACTTCAAAATAAAGCATG 1015

DB :::: 533 AsnLeuLeuGlnAsnLysSerMet 540

Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

Qy 812 GACTATGAACCTGTGTAGTACCAAGCCCTACAGAGCCTCAAAAGTCAGACAATTACTAGAC 871

Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

Qy 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTATTATAGTACAAAATTTGAAAGATTAAC 931

Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

Qy 932 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATTCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValValSerArgSerProSerLeu 532

Qy 992 AATTACTTCAAAATAAAGCATG 1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 15

ADB81362

ID ADB81362 standard; protein; 540 AA.

XX

AC ADB81362;

DT 04-DEC-2003 (first entry)

XX

DE Human caspase recruitment domain 3 (CARD-3) protein.

XX

KW human; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75;

KW tumour necrosis factor; TNF; neutrophin receptor; cancer;

KW autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;

KW viral infection; neurological; retinitis pigmentosa; haematologic;

KW chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAK.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

Domain 1..300

FT /label = Kinase\_domain

FT Domain 301..431

FT /label = Linker\_domain

FT Domain 432..540

FT /label = CARD

FT /note = Caspase recruitment domain

XX

PN US2002061833-A1.

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PD 23-MAY-2002.

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PF 26-DEC-2000; 2000US-00748537.

XX

PR 06-FEB-1998; 98US-00019942.

PR 17-JUN-1998; 98US-00099041.

XX

PA (BERT/) BERTIN J.

PA (CHAO/) CHAO M V.

PI Bertin J, Chao MV;

XX

DR WPI: 2003-657125/62.

DR N-PSDB; ADB81363.

XX

PT Detecting compounds which alter binding of the caspase recruitment domain

PT (CARD) of CARD-3 polypeptide to the neurotrophin receptor p75 is useful

PT to provide compounds for treating CARD-3 mediated disorders.

XX

PS Disclosure; Fig 1; 40pp; English.

XX

CC This invention relates to two novel genes CARD-3 and CARD-4 (caspase

CC recruitment domains), which are mediators of apoptosis and are useful in

CC the identification of compounds that modulate apoptosis. Specifically,

CC CARD-3 (also known as RIP2, RICK and CARDIAK) is known to be a mediator

CC of p75 (a member of the tumour necrosis factor (TNF) family), and is

CC believed to provide the switch for cell survival and cell death decisions  
CC mediated by this p75 neurotrophin receptor. Accordingly these genes, and  
CC the proteins encoded thereof, are linked to certain disorders associated  
CC with an increased number of cells surviving and proliferating when  
CC apoptosis is inhibited. These include cancer, autoimmune disorders e.g.  
CC systemic lupus and immune mediated glomerulonephritis, viral infections  
CC such as those caused by the herpesvirus, neurological disorders such as  
CC retinitis pigmentosa, haematologic diseases including chronic  
CC neutropenia, as well as myocardial infarction and strokes. The present  
CC invention further describes a novel method for determining whether a test  
CC compound alters the binding of CARD-3 to p75, which comprises measuring  
CC the binding of a polypeptide containing the CARD domain of CARD-3 to a  
CC polypeptide comprising the death domain of p75 in the presence and  
CC absence of the test compound, and determining if binding is altered. This  
CC polypeptide is the human CARD-3 protein sequence of the invention.

XX  
SQ Sequence 540 AA;

Alignment Scores:  
Pred. No.: 1.49e-118 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 7 Gaps: 0

US-09-771-161A-2 (1-1669) x ADB81362 (1-540)

QY	332	CAGTTACAGAGTCTTTCAAGTGCATTCACCTATGTGACAAAGAAATGGAATATCTCT	391
DB	313	LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	332
QY	392	CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	352
QY	452	GAATAATAGTCTCTCTCTGAAACTTCAAGTCTCCTCCAGCTCCTCAAGACAAATGATTTT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372
QY	512	TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTCTGGAATCAC	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392
QY	572	AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCTTCTGTGATCACAGACCACT	631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrIle	412
QY	632	CCATGCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACCTCTGCAG	691
DB	413	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
QY	692	CTGGTATAGCCAGCTAGTCCAGAGCAAAAGGAGACATTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
QY	752	GAAGCCCTGCTTACCAAGTCCGTAGATGCCCTTCTGTCAGGGACTTGATCATCAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu	472
QY	812	GACTATGAACCTGTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
QY	872	ACTACTGACATCCAGAGAGAGATTTGCCAAGTTATAGTACAAAATGAAAGATAAC	931
DB	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
QY	932	AAACAAATGGGTCTTACGCCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA	991
DB	513	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	532
QY	992	AATTACTTCAAAATAAAGCATG	1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540  
Search completed: March 29, 2004, 14:19:30  
Job time : 93.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:16:28 ; Search time 24.5 Seconds  
(without alignments)  
7033.775 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

Sequence: 1 accagttattaccagata.....caacagcgtgtgtgtataaa 1669

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 77828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1182	41.0	284	4	US-09-069-023-5
2	1182	41.0	478	4	US-09-069-023-4
3	1182	41.0	530	4	US-09-069-023-3
4	1182	41.0	531	4	US-09-069-023-1
5	1182	41.0	540	4	US-09-069-023-27
6	1182	41.0	540	4	US-09-345-473E-28
7	1176	40.8	540	3	US-09-019-942-1
8	1176	40.8	540	4	US-09-099-041A-2
9	1176	40.8	540	4	US-09-245-281-2
10	1176	40.8	540	4	US-09-470-271-1
11	1176	40.8	540	4	US-09-207-359B-2
12	1176	40.8	540	4	US-09-340-620A-2

13	1176	40.8	540	4	US-09-865-364-2	Sequence 2, Appli
14	1176	40.8	540	4	US-09-748-537-1	Sequence 1, Appli
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17	632	21.9	131	4	US-09-245-281-5	Sequence 5, Appli
18	632	21.9	131	4	US-09-207-359B-5	Sequence 5, Appli
19	632	21.9	131	4	US-09-340-620A-5	Sequence 5, Appli
20	632	21.9	131	4	US-09-865-364-5	Sequence 5, Appli
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26	149.5	5.2	109	4	US-09-340-620A-71	Sequence 71, Appl
27	122.5	4.3	164	4	US-09-245-281-41	Sequence 41, Appl
28	122.5	4.3	164	4	US-09-207-359B-41	Sequence 41, Appl
29	122.5	4.3	164	4	US-09-340-620A-41	Sequence 41, Appl
30	122.5	4.3	164	4	US-09-865-364-41	Sequence 41, Appl
31	122.5	4.3	249	4	US-09-245-281-39	Sequence 39, Appl
32	122.5	4.3	249	4	US-09-207-359B-39	Sequence 39, Appl
33	122.5	4.3	249	4	US-09-340-620A-39	Sequence 39, Appl
34	122.5	4.3	249	4	US-09-865-364-39	Sequence 39, Appl
35	122.5	4.3	409	4	US-09-207-359B-46	Sequence 46, Appl
36	122.5	4.3	409	4	US-09-865-364-46	Sequence 46, Appl
37	122.5	4.3	953	4	US-09-099-041A-8	Sequence 8, Appli
38	122.5	4.3	953	4	US-09-245-281-8	Sequence 8, Appli
39	122.5	4.3	953	4	US-09-207-359B-8	Sequence 8, Appli
40	122.5	4.3	953	4	US-09-340-620A-8	Sequence 8, Appli
41	122.5	4.3	953	4	US-09-865-364-8	Sequence 8, Appli
42	119	4.1	100	4	US-09-099-041A-10	Sequence 10, Appl
43	119	4.1	100	4	US-09-245-281-10	Sequence 10, Appl
44	119	4.1	100	4	US-09-207-359B-10	Sequence 10, Appl
45	119	4.1	100	4	US-09-340-620A-10	Sequence 10, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Alignment Scores:  
Pred. No.: 6,75e-132 Length: 284  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-5 (1-284)

QY 332 CAGTTACAGAGTGGTTTCAAGTGGCCATTACCTATGTGACAGAGAAATGAATTATCT 391  
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Db 57 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 76  
QY 392 CTGAACATACCTGTAATCATGCTGCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

77	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	96
452	GAATAATAGTGGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCTCAAGACAAATGATTTT	511
97	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	116
512	TTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCAGCTCTCTCTGGAATCATC	571
117	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis	136
572	AGTTGGCATAGACACCATTTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCACCT	631
137	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr	156
632	CGATGCTCTTCAGCAATATAATCCACTCTCAACTGCAGGAAACTCAGAACCTCTGCGAG	691
157	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	176
692	CTGTGTTATGCCCAGCAGTGGATCCAGACGAAAAAGGAAGACATTGTGAACCAAAATGACA	751
177	ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	196
752	GAGAGCTGCCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGAGCTTGATCATGAAAGAG	811
197	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	216
812	GACTATGAATCTTTAGTACCAGGCTTACAAGGACTCAAGGACTCAAAAGTCAGACAAATTACTAGAC	871
217	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	236
872	ACTACTGACATCCAAGGAGAGAAGATTGGCAAGTTATAGTACAAAATTTGAAGAGATAAC	931
237	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	256
932	AAACAAATGGTCTTCTCAGGCTTACCCGGAATACTTGTGGTTCTTAGATCATCACATCTTTA	991
257	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	276
992	AATTTACTCTCAAAATAAAAGCATG	1015
277	AsnLeuLeuGlnAsnLysSerMet	284

RESULT 2

US-09-069-023-4

; Sequence 4, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-4

Alignment Scores:

Pred. No.:

Score:

Percent Similarity: 100.00%

Best Local Similarity: 99.56%

Query Match: 41.04%

DB:

Length: 478

Matches: 227

Conservative: 1

Mismatches: 0

Indels: 0

Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-4 (1-478)

QY	332	CAGTTACAGAGTGTTTCAAGTGCATTACCTATTGTGACAAAGAAATGGAATTACT	391
Db	251	LyseuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer	270
QY	392	CTGAACATACCTGTAAATCATGGTCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT	451
Db	271	LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis	290
QY	452	GAATAATAGTGGTCTCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT	511
Db	291	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	310
QY	512	TTATCTAGAAAGCTCAAGACTGTTTATTATGAAGCTGCATCAGTGTCTTGGAAATCAC	571
Db	311	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	330
QY	572	AGTTGGGATAGCACCATTTCTGGATCTCAAAAGGCTTGCATTCTGTGATCACAAAGACCACT	631
Db	331	SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrThr	350
QY	632	CCATGCTCTTCAGCAATAATAATCAACTCTCACTGCGAGGAACCTCAGAAAGCTGCGAG	691
Db	351	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	370
QY	692	CCTGGTATAGCCACGAGTGGATCCAGAGCAAAGGGAAGACATTGTGAACCAAAATGACA	751
Db	371	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	390
QY	752	GAAGCCTGCCTTAACCAAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG	811
Db	391	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	410
QY	812	GACTATGAACTTGTTAGTACCAGCCCTACAAGGACCTCAAAAAGTCAGACAAATTTACTAGAC	871
Db	411	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	430
QY	872	ACTACTGATCTCCAAGGAGAGAATTTGCCAAGTTATAGTACAAAAATTGAAGATAC	931
Db	431	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	450
QY	932	AAACAAATGGGTCTTCAGCCCTTACCCGGAATACCTGTGGTTTCTAGATCACCATCTTTTA	991
Db	451	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu	470
QY	992	AATTACTTCAAAATAAAAGCATG 1015	
Db	471	AsnLeuLeuGlnAsnLysSerMet 478	

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RESULT 3
US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takayoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-3

Alignment Scores:
Fred. No.:
Score:

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Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-3 (1-530)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTCCATTACCTATGTGACAAAGAAATGAATATCT 391
DB 303 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 322
QY 392 CTGAACATACCTGTAATCATCGTCCACAAAGAGGATCATGTGGATCCTCAGTCCAT 451
DB 323 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 342
QY 452 GAAATAGTGGTTCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCAT 511
DB 343 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 362
QY 512 TTATCTAGAAAGCTCAAGTGTATTATTTATGAAGCTGCATCATGTCTCGAATATCAT 571
DB 363 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 382
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAGGCTGCTATCTGTGATCACAAGACCAT 631
DB 383 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 402
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
DB 403 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 422
QY 692 CTGTGTATAGCCAGCAGTGTGATCCAGACCAAGGAAAGACATGTGTGAACCAATGACA 751
DB 423 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 442
QY 752 GAAGCTGCTTAACAGTCCGTAGTGCCTTCTCTCCAGGACTTGATCATGAAGAG 811
DB 443 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 462
QY 812 GACTATGAATCTGTGTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAGGACCTCAAGGAC 871
DB 463 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 482
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATGAAGATATAC 931
DB 483 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 502
QY 932 AAACAATGGGTCTTCAGCCTTACCGGAAATCTGTGTGTCTGTGTGTGTGTGTGTGTGT 991
DB 503 LysGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeu 522
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
DB 523 AsnLeuLeuGlnAsnLysSerMet 530
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## RESULT 4

US-09-069-023-1

; Sequence 1, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 531

; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-069-023-1

Alignment Scores:

Pred. No.: 9 27e-132 Length: 531  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-1 (1-531)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTCCATTACCTATGTGACAAAGAAATGAATATCT 391
DB 304 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 323
QY 392 CTGAACATACCTGTAATCATCGTCCACAAAGAGGATCATGTGGATCCTCAGTCCAT 451
DB 324 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 343
QY 452 GAAATAGTGGTTCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCCTCAAGTCCAT 511
DB 344 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 363
QY 512 TTATCTAGAAAGCTCAAGTGTATTATTTATGAAGCTGCATCATGTCTCGAATATCAT 571
DB 364 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 383
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAGGCTGCTATCTGTGATCACAAGACCAT 631
DB 384 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 403
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
DB 404 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 423
QY 692 CTGTGTATAGCCAGCAGTGTGATCCAGACCAAGGAAAGACATGTGTGAACCAATGACA 751
DB 424 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 443
QY 752 GAAGCTGCTTAACAGTCCGTAGTGCCTTCTCTCCAGGACTTGATCATGAAGAG 811
DB 444 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 463
QY 812 GACTATGAATCTGTGTAGTACCAAGCTCAAGGACCTCAAGGACCTCAAGGACCTCAAGGAC 871
DB 464 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 483
QY 872 ACTACTGACATCAAGGAGAGAAATTTGCCAAGTTATAGTACAAAAATGAAGATATAC 931
DB 484 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 503
QY 932 AAACAATGGGTCTTCAGCCTTACCGGAAATCTGTGTGTCTGTGTGTGTGTGTGTGTGT 991
DB 504 LysGlnMetGlyLeuGlnProThrProGluIleLeuValValSerArgSerProSerLeu 523
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
DB 524 AsnLeuLeuGlnAsnLysSerMet 531
```

## RESULT 5

US-09-069-023-27

; Sequence 27, Application US/09069023A

; Patent No. 6348573

; GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof

; FILE REFERENCE: 35800/183781

; CURRENT APPLICATION NUMBER: US/09/345,473E

; CURRENT FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-345-473E-28

Alignment Scores:  
Pred. No.: 9,35E-132 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-345-473E-28 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCT 391  
Db 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
QY 392 CTGAACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGATCCTCTCAGCTCCAT 451  
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGGTCCCTCCAGCTCCCTCAAGACAAATGATTTT 511  
Db 353 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
QY 512 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGTGCATCATCTCTCTGGAATATCAC 571  
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
QY 572 AGTTGGGATAGCACCATTCTGGATCTCAAAAGGCTGCATCTCTGTGATCACAAGACCACT 631  
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 412  
QY 632 CCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACTGCTGCGAG 691  
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCTTAACCAAGTCCAGTGCCTAGATGCCCTTCTCTCCAGGACTTGCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAAGTGTGTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAAATCTTGTGGTTCTAGATCACCATTCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 7  
US-09-019-942-1  
; Sequence 1, Application US/09019942

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-27

Alignment Scores:  
Pred. No.: 9,35E-132 Length: 540  
Score: 1182.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.56% Mismatches: 0  
Query Match: 41.04% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-27 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCT 391  
Db 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332  
QY 392 CTGAACATACCTGTAATCATGTGTCACAAAGAGGAATCATGTGATCCTCTCAGCTCCAT 451  
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352  
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTCCAGCTCCCTCAAGACAAATGATTTT 511  
Db 353 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372  
QY 512 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGTGCATCATCTCTCTGGAATATCAC 571  
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392  
QY 572 AGTTGGGATAGCACCATTCTGGATCTCAAAAGGCTGCATCTCTGTGATCACAAGACCACT 631  
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 412  
QY 632 CCATGCTCTTCAAGCAATAATAATCCACTCTCAACTGCAGAAACTCAGAACTGCTGCGAG 691  
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432  
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGACA 751  
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452  
QY 752 GAAGCCTGCTTAACCAAGTCCAGTGCCTAGATGCCCTTCTCTCCAGGACTTGCATGAAAGAG 811  
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472  
QY 812 GACTATGAAGTGTGTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC 871  
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492  
QY 872 ACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512  
QY 932 AAACAAATGGTCTTCCAGCCTTACCCGGAAATCTTGTGGTTCTAGATCACCATTCTTTA 991  
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532  
QY 992 AATTTACTTCAAAATAAAAGCATG 1015  
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 6  
US-09-345-473E-28  
; Sequence 28, Application US/09345473E  
; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin



Patent No. 6033855  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
DOMAIN POLYPEPTIDES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,942  
FILING DATE: 06-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-019-942-1

Alignment Scores:  
Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-019-942-1 (1-540)

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QY 332 CAGTTACAGAGTGTTCAGTCCATTCACCTATGTGACAGAAGAAATGAATTATCT 391
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGATCATGTGGATCTCTCAGCTCCAT 451
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTGAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 511
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATTAAGAGCTGCATCTGCTCGAAATACAC 571
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGACCAATTTCTGGATCTCAAGGGCTGCATCTGTGATCACAAGACCACT 631
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTACGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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QY 692 CCTGTATAGCCACAGTGGATCCAGACAAAGGAGACATTGTGAACCAATGACA 751
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTGTAGTACCAAGCTCAAGGACTCAAAAGTCAGACAAATTTACTAGAC 871
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCAGCCTTACCAGGAAATACCTTGTTGTTCTAGATCACCATCTTTA 991
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTTACTTCAAAATAAAAGCATG 1015
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 533 AsnLeuLeuGlnAsnLysSerMet 540
RESULT 8
US-09-099-041A-2
; Sequence 2, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-2
Alignment Scores:
Pred. No.: 4,85e-131 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 4 Gaps: 0
US-09-771-161A-2 (1-1669) x US-09-099-041A-2 (1-540)
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RESULT 9

US-09-245-281-2

Sequence 2, Application US/09245281

Patent No. 6369196

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

FILE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 07334/118001

CURRENT APPLICATION NUMBER: US/09/245,281

EARLIER FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: US 09/207,359

EARLIER FILING DATE: 1998-12-08

EARLIER APPLICATION NUMBER: US 09/099,041

EARLIER FILING DATE: 1998-06-17

EARLIER APPLICATION NUMBER: US 09/019,942

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 540

TYPE: PRT

ORGANISM: Homo sapiens

US-09-245-281-2

Alignment Scores:

Pred. No.: 4, 85e-131

Score: 1176.00

Length: 540

Matches: 226

Percent Similarity: 99.56%

Conservative: 1

Best Local Similarity: 99.12%

Mismatches: 1

Query Match: 40.83%

Indels: 0

DB: Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-245-281-2 (1-540)

QY

332

CAGTTACAGAGTGTTCAGTCCATTACCTATGTGACAGAAAGAAATGGAATATCT

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QY

632

CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACTGTCGAG

691

Db

413

ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln

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692

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751

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QY

992

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Db

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RESULT 10

US-09-470-271-1

Sequence 1, Application US/09470271

Patent No. 6410689

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

FILE OF INVENTION: DOMAIN POLYPEPTIDES

TITLE OF INVENTION: DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/470,271

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/019,942

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-470-271-1

Alignment Scores:  
Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-470-271-1 (1-540)

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QY 392 CTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCAAACTTCAAGTCCCTGCGAGCTCCTCAAGACAAATGATTT 511
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DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
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DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCAATCTGTGATCACAAGACCCT 631
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DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATATAATCCACTCTCAACTGCGAGGAACCTCAAGACGCTGCGAG 691
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RESULT 11

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; Sequence 2, Application US/09207359B  
; Patent No. 6469140

; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; CURRENT FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-207-359B-2

Alignment Scores:

Pred. No.: 4,85e-131 Length: 540  
Score: 1176.00 Matches: 226  
Percent Similarity: 99.56% Conservative: 1  
Best Local Similarity: 99.12% Mismatches: 1  
Query Match: 40.83% Indels: 0  
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-207-359B-2 (1-540)

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QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCTTCACTATGTGACAGAGAAATGGAATTATCT 391
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QY 392 CTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
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QY 452 GAAATAGTGGTTCCTGAAACTTCAAGTCCCTGCGAGCTCCTCAAGACAAATGATTT 511
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DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTGCTCGAATATCATC 571
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QY 632 CCATGCTCTTCAGCAATATAATCCACTCTCAACTGCGAGGAACCTCAAGACGCTGCGAG 691
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QY 812 GACTATGAACTTGTAGTACCAAGCCTCAAGACCTCAAAAGTTCAGCAATTACTAGAC 871
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QY 872 ACTACTGACATCCAAGGAGAAATTTGCCAAGTTATAGTACAAAAATGGAAGATAC 931
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[illegible]

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Job time : 36.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

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11492.462 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

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Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delopt 7.0

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 2130338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1182	41.0	540	9	US-09-771-161A-184	Sequence 184, Appl
3	1182	41.0	540	9	US-09-862-027-28	Sequence 28, Appl
4	1182	41.0	540	10	US-09-981-397A-14	Sequence 14, Appl
5	1182	41.0	544	9	US-09-925-301-1015	Sequence 1015, Ap
6	1176	40.8	540	9	US-09-748-537-1	Sequence 1, Appl
7	1176	40.8	540	9	US-09-728-721-2	Sequence 2, Appl
8	1176	40.8	540	13	US-10-133-780-1	Sequence 1, Appl
9	1176	40.8	540	13	US-10-105-931-2	Sequence 2, Appl
10	1176	40.8	540	13	US-10-118-984-2	Sequence 2, Appl
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12	632	21.9	131	9	US-09-728-721-5	Sequence 5, Appl
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14	632	21.9	131	13	US-10-118-984-5	Sequence 5, Appl
15	632	21.9	131	14	US-10-295-981-5	Sequence 5, Appl
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22	461	16.0	92	14	US-10-314-506-21	Sequence 21, Appl
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28	122.5	4.3	164	9	US-09-728-721-41	Sequence 41, Appl
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38	122.5	4.3	953	14	US-10-013-477-12	Sequence 12, Appl
39	122.5	4.3	953	14	US-10-295-981-8	Sequence 8, Appl
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43	119	4.1	100	13	US-10-105-931-10	Sequence 10, Appl
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45	119	4.1	100	14	US-10-295-981-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-09-771-161A-93  
; Sequence 93, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 93  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-93

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Alignment Scores:
1.63e-116      Length:      232
1206.00       Matches:      232
Score:        Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches:    0
Indels:        0
41.88%        Gaps:        0
9
DB:
9

US-09-771-161A-2 (1-1669) x US-09-771-161A-93 (1-232)

320  ATGTATTCAATTACAGAGTGTTCGAAGTGCCATTACCTATGTGACACAGAGAAA  379
      |||||
      1 MetTySerLeuGinLeuGinSerValSerAlaIleHisLeuCyeAspIysIys  20
      |||||
      380  ATGGAATTATCTCGAACTACTCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCC  439
      |||||
      QY

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Db	21	MetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGlnIleuSerCysuSer	40
Qy	440	TCTCAGCTCCATGAAATAGTGTTCTCTCGTAAACTTCAAGTCCCTCGCAGCTCCTCAA	499
Db	41	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln	60
Qy	500	GACAAATATTTTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACACT	559
Db	61	AspAsnAspPheLeuSerArgLysAlaGlnAspCysTrpPheMetLysLeuHisCys	80
Qy	560	CCTGGAATACAGTTGGGATAGACACATTTCTGGATCTCAAGGGCTGCATTTCTGTGAT	619
Db	81	ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysasp	100
Qy	620	CACAGACACTCCAGTCTTTAGCAATATAAATCCACTCTCAACTCAGGAACTCA	679

[illegible][illegible]

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1 FILE REFERENCE: 802620-2005.1
2
3 CURRENT APPLICATION NUMBER: US/09/771,161A
4
5 CURRENT FILING DATE: 2001-01-26
6
7 PRIOR APPLICATION NUMBER: 09/724,676
8
9 PRIOR FILING DATE: 2000-11-28
10
11 PRIOR APPLICATION NUMBER: 136776
12
13 PRIOR FILING DATE: 2000-06-15

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PRIOR APPLICATION NUMBER: 135619



; TITLE OF INVENTION: No. US2002014248A1e1 Kinases and Uses Thereof  
 ; FILE REFERENCE: 35800/234862  
 ; CURRENT APPLICATION NUMBER: US/09/862,027  
 ; CURRENT FILING DATE: 2001-05-21  
 ; PRIOR APPLICATION NUMBER: US 09/345,473  
 ; PRIOR FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 82  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-862-027-28

Alignment Scores:  
 Pred. No.: 6.64e-114 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-862-027-28 (1-540)

QY	332	CAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT	391
DB	313	LyLeuGlnSerValSerAlaIleHisLeuCyAspLysLysMetGluLeuSer	332
QY	392	CTGAACATACCTGTAATCATGTCCACAGAGGATCATGTGGATCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluGlySerCysGlySerGlnLeuHis	352
QY	452	GAAATAGTGGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372
QY	512	TTATCTAGAAAGCTCAAGAGTGTATTTATTAAGTCCATTCACCTATGTGACAAAGAAATG	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392
QY	572	AGTTGGATAGCACCATTCTGATCTCAAGGGCTGCTTCTGATCACAAGACCAT	631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThr	412
QY	632	CCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG	691
DB	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
QY	692	CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
QY	752	GAAAGCTGCTTAACCCAGTCCGATGATGCTTCTGATCAGGAGCTTGTATGATGAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
QY	812	GACTATGAACTTGTAGTACCAAGCTTCAAGGAACTCAGAAAGTCAAGAAATGATAGAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
QY	872	ACTATGAACTTGTAGTACCAAGCTTCAAGGAACTCAGAAATGATGAAGAAATAC	931
DB	493	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
QY	932	AAACAATGGTCTTCCAGCTTACCGGAAATCTTGTGTTCTAGATCACCATTCTTA	991
DB	513	LysGlnMetGlyLeuGlnProThrArgThrSerLysValArgGlnLeuLeuAsp	532
QY	992	AATTTACTTCAAAATAAAGCATG	1015
DB	533	AsnLeuLeuGlnAsnLysSerMet	540

RESULT 4

US-09-981-397A-14  
 ; Sequence 14, Application US/09981397A  
 ; Publication No. US20030082519A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axxina Pharmaceuticals AG  
 ; APPLICANT: Schubart, Daniel  
 ; APPLICANT: Habenberger, Peter  
 ; APPLICANT: Stein-Gerlach, Matthias  
 ; APPLICANT: Bevec, Dorian  
 ; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
 ; TITLE OF INVENTION: Inhibition  
 ; FILE REFERENCE: AXM-004.1 US  
 ; CURRENT APPLICATION NUMBER: US/09/981,397A  
 ; CURRENT FILING DATE: 2002-06-28  
 ; PRIOR APPLICATION NUMBER: 60/240,750  
 ; PRIOR FILING DATE: 2000-10-16  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 14  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-981-397A-14

Alignment Scores:  
 Pred. No.: 6.64e-114 Length: 540  
 Score: 1182.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.56% Mismatches: 0  
 Query Match: 41.04% Indels: 0  
 DB: 10 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-981-397A-14 (1-540)

QY	332	CAGTTACAGAGTGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT	391
DB	313	LyLeuGlnSerValSerAlaIleHisLeuCyAspLysLysMetGluLeuSer	332
QY	392	CTGAACATACCTGTAATCATGTCCACAGAGGATCATGTGGATCTCTCAGCTCCAT	451
DB	333	LeuAsnIleProValAsnHisGlyProGlnGluGlySerCysGlySerGlnLeuHis	352
QY	452	GAAATAGTGGTTCCTCAAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT	511
DB	353	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	372
QY	512	TTATCTAGAAAGCTCAAGAGTGTATTTATTAAGTCCATTCACCTATGTGACAAATCAC	571
DB	373	LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis	392
QY	572	AGTTGGATAGCACCATTCTGATCTCAAGGGCTGCTTCTGATCACAAGACCAT	631
DB	393	SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThr	412
QY	632	CCATGCTCTTCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG	691
DB	413	ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln	432
QY	692	CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	751
DB	433	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	452
QY	752	GAAAGCTGCTTAACCCAGTCCGATGATGCTTCTGATCAGGAGCTTGTATGATGAAGAG	811
DB	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
QY	812	GACTATGAACTTGTAGTACCAAGCTTCAAGGAACTCAGAAATGATGAAGAAATAC	871
DB	473	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	492
QY	872	ACTATGAACTTGTAGTACCAAGCTTCAAGGAACTCAGAAATGATGAAGAAATAC	931
DB	493	ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512

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QY 932 AAACAAATGGTCTTACAGCCTTACCGGAAATACCTGTGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 5
US-09-925-301-1015
; Sequence 1015, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1015
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1015

Alignment Scores:
Pred. No.: 6,66e-114 Length: 544
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-925-301-1015 (1-544)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTATCT 391
Db 317 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 336
QY 392 CTGAACATACCTGTAATCATGTCGACAGAGAAATCATGTGGATCTCTCAGCTCCAT 451
Db 337 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 356
QY 452 GAAATAGTGGTTCCTCGAAACTTCAAGGTCCTCCAGCTCCTCAAGACAATGATTTT 511
Db 357 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 376
QY 512 TTATCTAGAAAGCTCAGACTGTTATTTATGAGCTGCATCACTGCTCGGAAATCAC 571
Db 377 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 396
QY 572 AGTTGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCGTGTGATCACAAGACCACT 631
Db 397 SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrThr 416
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAATCTGAGGAACTCAGACGCTGCGAG 691
Db 417 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 436
QY 692 CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATATGACA 751
Db 437 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 456
QY 752 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 811
Db 457 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 476
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QY 812 GACTATGAACCTGTTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAATGAC 871
Db 477 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 496
QY 872 ACTACTGACATCCAAAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAGATAAC 931
Db 497 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 516
QY 932 AAACAAATGGTCTTACAGCCTTACCGGAAATACCTGTGTTCTAGATCACCATCTTTA 991
Db 517 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 536
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 537 AsnLeuLeuGlnAsnLysSerMet 544

RESULT 6
US-09-748-537-1
; Sequence 1, Application US/09748537
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THEREK
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACTATGTGACAGAGAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCGACAGAGAAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTCGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAGACTGTTATTTATGAGCTGCATCACTGCTCGGAAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTGATCTCAAGGGCTGCATTCGTGTGATCACAAGACCACT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGAACTCAGAACTGCTGCGAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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QY 692 CCTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGACCAAAATGACA 751
Db 433 ProGlyleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCCAGCAAAATGAAAGTAAC 931
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGAGAGAAATTTGCCAAGTTATAGTACAAAATGAAAGTAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGCTTCCAGCCTTACCCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 7
US-09-728-721-2
; Sequence 2, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-2

Alignment Scores:
Pred. No.: 2.8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-728-721-2 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCT 391
Db 313 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 332
QY 392 CTGAACATCCTGTAATCATGTGTCACAGAGGAATCATGTGATCCCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352
QY 452 GAAATATAGTGTTCCTCGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAGCTGCATCATGTCTCGAAATCAC 571
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Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGCACCATTCTCGATCTCAAGGGCTGCATTCTGTGATCACAAGACCACT 631
Db 393 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTCGTGCAG 691
Db 413 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGCTATAGCCAGCAGTGGATCCAGACCAAAAGGGAAGACATTGTGACCAAAATGACA 751
Db 433 ProGlyleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCCAGCAAAATGAAAGTAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGCTTCCAGCCTTACCCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 8
US-10-133-780-1
; Sequence 1, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELE: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-133-780-1

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 0
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-133-780-1 (1-540)
QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGCCAAGAGAAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGTTCCTCAAGTCCCTCCAGGCTCCCTCAAGACCAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTCTCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGCACCATTCTGGAATCTCAAGGCTGCATCTGTGATCAAGACCACT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnAAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAAATCAACTCTCAAGTCCAGGAACTCAGAACGCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751
Db 433 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 452
QY 752 GAAGCTCCCTTAACCACTGCTAGATGCCCTTCTGCTCCAGGACTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTGTAGTACCAAGCTTACCAAGCTTATAGTACAAAATTCAGAAAGTAAAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGATCCAGAGGAGAAATTCGCAAGTATAGTACAAAATTCAGAAAGTAAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACGCTTACCCGGAAATACCTGTGGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
;

; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-931-2

Alignment Scores:
Pred. No.: 2,8e-113 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 0
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-2 (1-540)
QY 332 CAGTTACAGAGTGTTCCTCAAGTCCCAATTCACCTATGTGACAAAGAAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGCCAAGAGAAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGTTCCTCAAGTCCCTCCAGGCTCCCTCAAGACCAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTGTCTCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGCACCATTCTGGAATCTCAAGGCTGCATCTGTGATCAAGACCACT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnAAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAAATCAACTCTCAAGTCCAGGAACTCAGAACGCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGTTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751
Db 433 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 452
QY 752 GAAGCTCCCTTAACCACTGCTAGATGCCCTTCTGCTCCAGGACTTGATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTGTGTAGTACCAAGCTTACCAAGCTTATAGTACAAAATTCAGAAAGTAAAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGATCCAGAGGAGAAATTCGCAAGTATAGTACAAAATTCAGAAAGTAAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTACGCTTACCCGGAAATACCTGTGGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10
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QY 692 CTTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGAGAGACATTGTGAAACAAATGACA 751
Db 433 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTAAACAGTCGTAGATGCCCTTCTGTCAGGAGCTTGTATCATGATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTAGTACCAAGCCTCAAGAGCCTCAAAAGTCCAGAAATCTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAGAGAGAAATTCGCAAGTTATAGTACAAAAATGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATTCTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12
US-09-728-721-5
; Sequence 5, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-5
Alignment Scores:
Pred. No.: 8,848-57 Length: 131
Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-728-721-5 (1-131)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 391
Db 13 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 32
QY 392 CTGACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAATATAGTGGTTCTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 511
Db 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATCAAGCTGCATCATCTGCTGGAATCAC 571
Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCAAGACCAT 631
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688
Db 113 ProCysSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 14
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5
Alignment Scores:
Pred. No.: 8,848-57 Length: 131
Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-5 (1-131)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 391
Db 13 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 32
QY 392 CTGACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAATATAGTGGTTCTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 511
Db 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATCAAGCTGCATCATCTGCTGGAATCAC 571
Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCAAGACCAT 631
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688
Db 113 ProCysSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 14
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
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Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCAAGACCAT 631
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688
Db 113 ProCysSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 13
US-10-105-931-5
; Sequence 5, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5
Alignment Scores:
Pred. No.: 8,848-57 Length: 131
Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-5 (1-131)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGCAAGAGAAATGGAATTATCT 391
Db 13 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 32
QY 392 CTGACATACCTGTAATCATGTGCCAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAATATAGTGGTTCTCCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACATGATTTT 511
Db 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATCAAGCTGCATCATCTGCTGGAATCAC 571
Db 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCGTGATCAAGACCAT 631
Db 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTCG 688
Db 113 ProCysSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 14
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
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; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5

Alignment Scores:
Pred. No.:      8,84e-57      Length:      131
Score:          632.00      Matches:      117
Percent Similarity: 99.16%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 1
Query Match:      21.94%      Indels:      0
DB:              13          Gaps:          0

US-09-771-161A-2 (1-1669) x US-10-118-984-5 (1-131)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAGAGAAATGGAATTATCT 391
DB 13 LysLeuGlnSerValSerSerAlaHisLeuHisCysAspLysLeuMetGluLeuSer 32
QY 392 CTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 52
QY 452 GAAATAGTGGTTCCTGAAACTTCAAGTCCCTCCAGCTCCCTCAAGACAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCCTGCTCGAAATCAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCATTCTGTGATCACAGACCACT 631
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATTAATTAATCCACTCTCAACTGCAGGAACTCAGAACTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

RESULT 15
US-10-295-981-5
; Sequence 5, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-5

Alignment Scores:
Pred. No.:      8,84e-57      Length:      131
Score:          632.00      Matches:      117
Percent Similarity: 99.16%      Conservative: 1
Best Local Similarity: 98.32%      Mismatches: 1
Query Match:      21.94%      Indels:      0
DB:              14          Gaps:          0

US-09-771-161A-2 (1-1669) x US-10-295-981-5 (1-131)
QY 332 CAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAGAGAAATGGAATTATCT 391
DB 13 LysLeuGlnSerValSerSerAlaHisLeuHisCysAspLysLeuMetGluLeuSer 32
QY 392 CTGAACATACCTGTAATCATGGTCCACAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 52
QY 452 GAAATAGTGGTTCCTGAAACTTCAAGTCCCTCCAGCTCCCTCAAGACAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 72
QY 512 TTATCTAGAAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCCTGCTCGAAATCAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTCTCGGATCTCAAAGGGCTGCATTCTGTGATCACAGACCACT 631
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATTAATTAATCCACTCTCAACTGCAGGAACTCAGAACTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

Search completed: March 29, 2004, 14:28:31
Job time : 86 secs
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:15:32 ; Search time 31.5 Seconds  
(without alignments)  
10193.248 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880  
Sequence: 1 acctagttataccagata.....caacagcgtgatgtgtaaaa 1669

Scoring table: BLASUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O=/cpn2.1/USPTO spool\_p/US09771161/runat\_29032004.124825.13694/app\_query.fasta\_1.1863  
-DB=PIR\_78 -QFMT=fstasn -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOFCLE=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blasmus62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09771161 @CN 1.1.44 @runat\_29032004.124825.13694 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.5	3.5	943	2 S44636	f22b7.5 protein -
2	99.5	3.5	830	2 T00029	Miranda protein -
3	98	3.4	618	2 S68450	apoptosis inhibito
4	95	3.3	731	2 A99106	hypothetical prote
5	93	3.2	692	2 T32980	hypothetical prote
6	90.5	3.1	956	2 T40953	hypothetical prote
7	90	3.1	597	2 F82935	DNA polymerase III
8	90	3.1	708	2 JQ1148	killer toxin KHS p
9	90	3.1	1205	2 T41987	hypothetical prote
10	90	3.1	2288	2 T29999	hypothetical prote
11	89.5	3.1	2368	2 S46005	BSR1 protein - yea
12	89	3.1	242	2 S71757	MADS box protein D
13	89	3.1	283	2 B81996	RNA polymerase sig
14	89	3.1	1360	2 T33922	hypothetical prote

15	89	3.1	1944	2 A55117	tsg24 protein - mo
16	88	3.0	133	2 H71190	hypothetical prote
17	88	3.0	358	2 JC5964	apoptosis inhibito
18	88	3.1	397	2 E82876	hypothetical prote
19	88	3.1	524	2 S35551	transcription fact
20	88	3.1	1019	2 E90097	hypothetical prote
21	88	3.1	1135	2 T30561	Scythe protein - A
22	88	3.1	1758	2 T30560	resistance protein
23	87.5	3.0	340	2 T27389	hypothetical prote
24	87.5	3.0	406	2 S44842	K06H7.2 protein -
25	87	3.0	147	2 F84869	hypothetical prote
26	87	3.0	294	2 T21474	hypothetical prote
27	87	3.0	340	2 E70121	hypothetical prote
28	86.5	3.0	407	2 S27774	transforming protei
29	86.5	3.0	528	2 T52092	DNA-binding protei
30	86.5	3.0	1203	2 T17415	mycellial surface a
31	86	3.0	371	2 E88986	protein C50H11.13
32	86	3.0	721	2 S11824	gene Mx protein -
33	86	3.0	3169	2 T00296	toxin B - Escheric
34	85.5	3.0	212	2 G75458	conserved hypothet
35	85.5	3.0	455	1 JC4338	tryptophan dimethy
36	85.5	3.0	1095	2 T20528	hypothetical prote
37	85.5	3.0	3898	1 GNWVHC	genome polyprotein
38	85	3.0	690	2 A24545	triacylglycerol li
39	85	3.0	721	2 S31820	gene Mx protein -
40	85	3.0	721	2 A37472	interferon-inducib
41	85	3.0	1121	2 F71613	hypothetical prote
42	84.5	2.9	224	2 S23728	MADS box protein T
43	84.5	2.9	362	2 E71637	hypothetical prote
44	84.5	2.9	644	2 A42220	helix-loop-helix p
45	84.5	2.9	810	2 S69652	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S44636

f22b7.5 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Dec-1997

C:Accession: S44636

R:Anderson, K.

submitted to the ENBL Data Library, March 1993

A:Description: Sequence of the C. elegans cosmid F22B7.

A:Reference number: S44628

A:Accession: S44636

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-943 <AND>

A:Cross-references: EMBL:L12018; NID:g156298; PID:g156307

C:Genetics:

A:Introns: 83/2; 250/2; 453/1; 484/2; 519/1; 553/3; 580/3; 632/3; 729/3; 830/2; 905/1

C:Superfamily: dnaJ amino-terminal homology

F:531-595/Domain: dnaJ amino-terminal homology <DNJ>

##### Alignment Scores:

Pred. No.:	0.376	Length:	943
Score:	100.50	Matches:	45
Percent Similarity:	38.36%	Conservative:	44
Best Local Similarity:	39.40%	Mismatches:	84
Query Match:	3.49%	Indels:	59
DB:	2	Gaps:	10

US-09-771-161A-2 (1-1669) x S44636 (1-943)

QY 392 CTGAACATACCTGTAATCATGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

DB 349 IIEASVALAlaMetAsnGlnGluArgSerGluThrAlaThrAspClnAspValCysLeu 368

QY 452 GAAATAGTGGTTCCTCGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 511

DB 369 AlAlieAspSerSerProAspProThrSerSer-----AsnAspMet 382

QY 512 TTATCTAGAAAAAGCTCAAGACCTGTTATTATTAAGAAGCTGCATCATCTGTCCTCGAAATCAC 571  
    |||||  
 Db 383 ILeAsnLys-----PheValValGluLeuGluHisAlaThrAsnValGlu 397  
    |||||  
 QY 572 AGTTGGATAGCACCATTTCCTGA- 595  
    |||||  
 Db 398 ThrTrpGluMetIleValAsnGlyllelleAspAspGlnLysProValalaileGlu 417  
    |||||  
 QY 596 -----TCTCAAAGGGCTGCA 610  
    |||  
 Db 418 LysLysGluAsnGluGluProValAspMetMetAspLeuIlePheSerMetSerArg 437  
    |||  
 QY 611 TTCGTGTATCACAGACCACTCCATCTCTTCAGCAATAAATA-----AATCCACTCTCA 664  
    |||||  
 Db 438 MetAspAspGlnArgThrGluLeuProAlaAlaArgPheIleProProArgProValSer 457  
    |||||  
 QY 665 ACTGCAGGA-----AACTCAGAACGTCCTGCAGCCTGGTATAGCCCCAGCAGTG 712  
    |||||  
 Db 458 SerAlaSerLysLysThrThrLysSerHisArgIleLeuProGlyLeuArgAlaAsnTrp 477  
    |||||  
 QY 713 ATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACAGAGCCTGCTTAAACGACGTG 772  
    |||  
 Db 478 ThrLysValGlnSerMetLysValLeuGlyMetPheVal-----LeuAsnArgSer 494  
    |||  
 QY 773 CTAGATGCCCTCTGTCAGGACTTGATCATGAAAGAGGACTATGAACCTTGTAGTACC 832  
    |||  
 Db 495 ---SerGlyLeuIleHisArgSerValProLeuLeuAlaGln-----ValSerThr 510  
    |||  
 QY 833 AAGCCTACAGAGGACCTCAAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGAGAA 892  
    |||  
 Db 511 ProThrThrSerThrThrLysLeuAlaGlnLeuHisThrThrHisAlaLeuSerLysGlu 530  
    |||  
 QY 893 GAATTTCCCAAGTTATA---GTACAAAATTGAAAGATAACAA- 934  
    |||  
 Db 531 AspTyrtyrLysThrLeuGlyValAspLysLysSerAspAlaLysAlaIleLysLysAla 550  
    |||  
 QY 935 -----CAAAATGGTCTTCAGCCCTTACCCCGGAAATA 964  
    |||  
 Db 551 TyrPheGlnLeuAlaLysLysTyrHisProaspVal 562  
    |||

RESULT 2  
 T00029  
 Miranda protein - fruit fly (*Drosophila melanogaster*)  
 C:Species: *Drosophila melanogaster*  
 C>Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 17-Nov-2000  
 C:Accession: T00029  
 R:Ikeshimu-Kataoka, H.; Skeath, J.B.; Nabeshima, Y.; Doe, C.Q.; Matsuzaki, F.  
 Nature 390, 625-629, 1997  
 A>Title: Miranda directs Prospero to a daughter cell during *Drosophila* asymmetric division  
 A:Reference number: Z14067; MUID:98065952; PMID:9403694  
 A:Accession: T00029  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <IKX>  
 A:CROSS-references: EMBL:AB005661; NID:g2749776; PIDN:BAZ24111.1; PID:g2749777  
 A:Experimental source: strain Canton-S  
 C:Genetics:  
 A:CROSS-references: FlyBase:FBgn0021776  
 A:Map position: 92B-C

Alignment Scores:	
Pred. No.:	0.462
Score:	Length: 830
	Matches: 59
Percent Similarity:	Conservative: 49
Best Local Similarity:	Mismatches: 111
Query Match:	Indels: 69
DB:	Gaps: 10

US-09-771-161A-2 (1-1669) x T00029 (1-830)  
 QY 353 GCATTTCACCTATGTGCAAGAAGAAAATGGAATTTATCTCGAACATACCTGTAATCAT 412  
    |||||  
 Db 354 AlaValaPheAlaSer-Ser-LysGluAlaIlysGluPheAlaIlePro----- 80

QY	413	GGTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAAGTGGTTCTCTCCTGAA	472
Db	81	---LysGluAspLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln	99
QY	473	ACTTCAAGTCCCTCGCAGCTCCTCAAGACAATAGATTTTATCTAGAAAAGCTCAAGAC	532
Db	100	ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly	117
QY	533	TGTTATTTTATGAAGCTGCATCACTCTCTCGGAATCAAGTTGGGATAGCACCATTCT	592
Db	118	-----Ser	118
QY	593	GGATCTCAAAAGGCTGCATTTCTGTGATCAAGAAGCACCATCCATGCTCTTCAGCAATAATA	652
Db	119	GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr	133
QY	653	AATCCACTCTCAACTCGAGAACTCAGAACGCTCTCAGCCTGGTATAGCCAGCAGTGG	712
Db	134	ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnThr	153
QY	713	---ATCCAGAGCAAAAGGAAGACATTGTCAACCAAAATCACAAAGCC---TGCCTTAAC	766
Db	154	GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg	173
QY	767	CAGTCGCTAGATGCCCTCTGTCCAGGGACTTGATCATGAAGAGACTATGAACCTGTT	826
Db	174	ArgHisValAspGlnLeuLysGluAlaGluAlaLysLeuArgGluGluHisGluLeuAla	193
QY	827	AGTACCAAGCTACAAG-----ACCTCAAAAGTCAGACAATTTACTAGAC	871
Db	194	ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla	213
QY	872	ACTACTCATCAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC	931
Db	214	LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaAlaMet	232
QY	932	AAACAATGGGTCTTACGCTTACCCGGAA-----ATACCTTGCGTTTCT	976
Db	233	GluGlnGlnLeuGlnGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla	252
QY	977	AGATCACCATCTTTA-----AATTACTTCAAAATAAAGCATGTAAAGTGACT	1024
Db	253	GluSerGluAlaLeuArgLeuAlaAsnGluLeuLeuGlnThrAlaAsnGluAspArgGln	272
QY	1025	GTTTTCAAGAGAAATGTGTTTCATAAAAGGATATTATATCTCTGTTGCTTGACTTT	1084
Db	273	LysValGluGluGln-----	277
QY	1085	TTTTATATAAATCCGTGAGTATTAAAGCTTTATTGAAGTTCTTTGGGTAAATATTAGT	1144
Db	278	-----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla	290
QY	1145	CTCCCTCCATGACACTGCAGTATT	1168
Db	291	GlnAlaArgGluHisCysSerLeu	298
RESULT 3			
S68450			
apoptosis inhibitor hiap-2 - human			
C:Species: Homo sapiens (man)			
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000			
C:Accession: S68450			
R:Jubston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.;			
Nature 379, 349-353, 1996			
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related fami			
A:Reference number: A58182; MUID:96149249; PMID:8552191			
A:Accession: S68450			
A>Status: nucleic acid sequence not shown			
A:Molecule type: mRNA			
A:Residues: 1-618 <LIS>			
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:AAAC50372.1; PID:g1184318			
C:Function:			

A:Description: apoptotic suppressor  
 C:Superfamily: RING finger homology  
 C:Keywords: apoptosis; zinc finger  
 F:567-611/Domain: RING finger homology <RNG>

## Alignment Scores:

Pred. No.:	0.623	Length:	618
Score:	98.00	Matches:	31
Percent Similarity:	44.78%	Conservative:	29
Best Local Similarity:	23.13%	Mismatches:	58
Query Match:	3.40%	Indels:	16
DB:	2	Gaps:	3

US-09-771-161A-2 (1-1669) x S68450 (1-618)

QY	713	ATCCAGAGCAAAAGGAGACACATTTGTGAACCAATGACAGAAAGCCCTTAAACAGTCG	772
DB	461	IleArgLysAsnArgMetAlaLeuPheGlnLeuThr-----CysValLeuProIle	478
QY	773	CTAGATGCCCTTCTGTCCAGGACTGTATCATGAAGAGGACTATGAACCTTGTAGTACC	832
DB	479	LeuAspAsnLeuLeuLysAlaAsnValIleAsnLysGlnGluHisAspIleIleLysGln	498
QY	833	AAAGCTTACAAAGACCTCAAAAGTCACAAATTAAGACACTACTACATCCAAAGAGAA	892
DB	499	LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleTrpValLysGlyAsn	518
QY	893	GAATTTGCCAAAGTTATAGTACAAAATTTGAAAGAT-----	928
DB	519	AlaAlaAlaAsnIlePheLysAsnCysLeuLysGluIleAspSerThrLeuTyrlsAsn	538
QY	929	-----AACAAACAAATGGTCTTACGCTTACCCGGAATATCTGTGTTTCTAGA	979
DB	539	LeuPheValAspLysAsnMetLysTyrlleProThrGluAspValSerGlyLeuSerLeu	558
QY	980	TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAAGTCACTGTTTTCAGAGAA	1039
DB	559	GluGluGlnLeuArgArgLeuGlnGluGluArgThrCysLysValCysMetAspLysGlu	578
QY	1040	ATGTGTTTCATAT-----AAAGGATATTTATATCTCTGT	1072
DB	579	ValSerValValPheIleProCysGlyHisLeuValValCys	592

## RESULT 4

A99106  
 Hypothetical protein orf731 [imported] - Guillardia theta nucleomorph  
 C:Species: nucleomorph Guillardia theta  
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C:Accession: A99106  
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif, N.  
 Nature 410, 1091-1096, 2001  
 A:Title: The highly reduced genome of an enslaved algal nucleus.  
 A:Reference number: A99082, PMID:11323671, PMID:11323671  
 A:Accession: A99106  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-731 <DOU>  
 A:Cross-references: GB:AJ010592; NID:g12580677; PIDN:CAC26995.1; GSPDB:GN00151  
 C:Gene: orf731  
 A:Map position: 2  
 A:Genome: nucleomorph  
 C:Keywords: nucleomorph

## Alignment Scores:

Pred. No.:	1.22	Length:	731
Score:	95.00	Matches:	109
Percent Similarity:	37.47%	Conservative:	78
Best Local Similarity:	21.84%	Mismatches:	179
Query Match:	3.30%	Indels:	133
DB:	2	Gaps:	23

US-09-771-161A-2 (1-1669) x A99106 (1-731)	
QY	206 CTCAACTCTTTATATATTTCTTTTCATATGATTTTGTACAAACATATAAAATGTGTAGATT
DB	118 LeuAsnIleIlePheAspThrLysMetTyrllePhe-----ArgPheAsnLeuArgIleLeu
QY	266 GTATTTTACTTCTATAAATTTCTTAATCATCTCC-----AGTTAAAGTGTATATATA
DB	136 LysSerPheIleHisPheLeuLeuThrSerAlaIleSerAsnIleAsnTyrllePhe
QY	317 TTTATGTTATTCATACAGTTCACAGAGTGTTCACAGTCCATTACCTATGTGCACAGAAG
DB	156 PheIleTyrlsLeuSerTyrlsAsnGlnGlnLeuLysLysIleCysPheLysLys
QY	377 AAAATGGAATTTATCTCTGAACATACCTGTAATCATGTGCCACAGAGGAATCATGTGGA
DB	176 PheIleIleIle-----
QY	437 TCCTCTCAGCTCCATGAATAAGTAGTGTCTCTGTAACCTTCAAGGTCTCTGCCAGCTCT
DB	180 -----LeuAsnGlnHisSerGlyLys-LeuSerPheGluLysSerAsnAsnIle--
QY	497 CAAGACAATGATTTTCTAGAAAAGCTCAAGACTG-----
DB	196 -----PheValPheTyrlle-PheSerSerValLeuLeuLeuPhePheAsnTyrl
QY	535 --TTATTTTATGAAGCTGCATCCTCTCGAAATCACAGTTGGGATAGCACCATTCT
DB	213 yrLeuPheTyrlsAsnLysPheIleLeuAspMetLysSerGlnLeuPheSerPhePhe
QY	593 GGATCTCAAAGGGTGCATTTCTGTGATCACAAGACCCTCCATGCTCTTCAGC-----
DB	233 heIleAspLysAsnIleIlePheSerIleProGlnSerAsnTyrlleIleAsnThrAsp
QY	646 --AATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCAGCCTCGTATAGCC
DB	253 leAsnAsnIleIleTyrlleLeuLeuLeuAsnPheThrAsnSerIleLeuPhe-SerLeu
QY	704 CAGCAGTGGATC-----CAGAGCAAAAGGGAAGACATTTGTAACCAATGACAGAACCC
DB	273 LysLysTyrllePheLeuLeuLysLysThrGluTyrlMetArgAsnAsnIleIleLeu
QY	758 TGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGAGCTTCATCATGAAAGAGACTAT
DB	293 LeuThrPheSerLysLeuSerAsnLysLeuAsnLysAsnVal-----Tyr
QY	818 GAACCTTGTGTAGTACCAAGGACCTCAAGGACCTCAAAAGTCAGACAAATTAAGACTACT
DB	309 AsnLeuPheAsnLeu-----LysValPheGluLeuLeuLysLysArg
QY	878 GACATCCAAAGGAGAGAATTTGCCAAGTTATAGTACAAAATTTGAAAGATAACAAACAA
DB	323 PheIleAspAsnAsnHisTyrlleThrArgLeuLeuPheAspPheIle-----
QY	938 ATGGGTCTTCAGCCTTACCCGGAATATCTGTGGTTTCTAGATCACCATTCTTAATTTA
DB	338 -----ValGluIleIleIleLysSerLysAsnTyrlsIle-IleAs
QY	998 CTTCAAAATAAAGCATGTAAGTGTCTTTTCAAGAGAAATGTTTTCATAAAGGA
DB	351 nGlnLysIleSerThr-IleAsnIleCysPheArgLeuPhePheIlePheHisGluLys-
QY	1058 TATTTATATCTGTGTGCTTTTGACTTTTTTATATAAATCCGTGAG-----T
DB	371 -----LeuIleLysIleAsnGluIleLysPheArgT
QY	1106 ATTAAGCTTTTATGAAGGTCTTTTGGGT-----AAATATTAGTCTCCCTCC-----
DB	381 yrPheGlyPheIleLysTrpLeuLeuAsnPheLysTyrlAsnAsnThrGluValLeuThrI
QY	1160 TGCAGTATTTTATTAATTAACAAGTAAAGATTTGCAATTTTCTACATAGTTCAAT-
DB	401 leTyrlPheIleLeuArgLeuLysPheLysTyrlleLysAspAsnLysPheSerLeu



Qy	76	GA	TTTCGAGGATGAAGCTCTGAGACACTGAGAGAGGTAAACCAATTAATATATGACCCAGGA	135
Db	262	Lys	PheGluAsnGluIleLeuTyThrAlaMetHisThrSerIlePheLysSerVal	281
Qy	136	TTCAAGAGTCTGGTTCNTAAAGTTATTTCCGGTCTTACACTGCTCTTTCTTC	189	
Db	282	PheAsnIleLeuGlySer	-----PheTyThrMetArgLeuLeuArgAsn	296
Qy	190	-----AGTTATATGTTATATTCTCAACTCTTTATATT	222	
Db	297	LysHisAspGlyAspSerTyGluLeuValPro	-----ValPheAlaLysAsnPro	313
Qy	223	-----TCCTTCATGATATTTGTACAAACATATAAAATG	258	
Db	314	SerLysThrProCysAsnAspAsnPheLysIlePheSerAspAspIle	-----LysLeu	332
Qy	259	TTAGATTGTTATTTACTTCTATATTTCCTAATCATCTCCAGTTAAAGTGATATATATT	318	
Db	333	IleGlyCys	-----LysIlePheAla	339
Qy	319	TATGTATTCAATTACAGTTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAAAGA	378	
Db	340	GlyVal	-----SerLeuAsnPheSerSerProLysProAlaHisArgPheTyGluLeuAsnLys	359
Qy	379	AATGGAATTATCTCTGAACATACCTCTGTAATAATCATGGTCCACAGAGGAATCATGTGCATC	438	
Db	359	ethrSerSerAsnLeuSerIleProValLeuGlnLysProSerAsnPheHisSerSerSe	379	
Qy	439	CTCTCAGCTCCATGAATAATAGTGGTTCTCTGAAACCTTCAAGGTCCCTGCCAGCTCTCTCA	498	
Db	379	rThrGluLeuSerAspAsn	-----SerIleHisGlnGlyArgArgAlaValAspProVal	397
Qy	499	AGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTGAAGCTGCATCAGT	558	
Db	397	lValAsnGlnAsnAsnProSerAsnPheGluGluMetIleMetAsnLysLeuAsnLysLeu	417	
Qy	559	TCCTGAAATCACTGGGTAGCACCATTTCTGGAGTCTCAAGGGCTGCATTTCTGTGA	618	
Db	417	uPro	-----ThrIleAspLysGlnIleLeuGlyThrSerSerLeuThrHisPheGlu	434
Qy	619	TCACAGACCACT	-----	631
Db	434	naAspLysThrThrAlaIleGluHisSerIleAsnLysSerAsnSerLysGlnProProAr	454	
Qy	632	-----CCATGCTCTTCAGCAATA	-----ATAAATCCA	658
Db	454	gPheLysPheGlnLeuProProArgProThrSerAsnThrLeuProLeuGluProGluG	474	
Qy	659	-----CTCTCAACTGTCAGGAAC	-----	676
Db	474	uGluLeuValThrArgTygSerValSerSerAspGlyAsnThrValAspGluAlaIleTh	494	
Qy	677	-----TCAGAACGCTCTGCACCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGA	729	
Db	494	rlYsGlnSerGlnThrPheGlnLeuValAsnSerAsnGluPheAsnGlnValAsnAlaAs	514	
Qy	730	AGACATTGTGAACCAATGACAGAAGCTTCGCTTAAACGATCGCTAGATGCCCTTCTGTC	789	
Db	514	naAspValHisLysSerLeuArgGlnAsnCysAlaLysLeuAspPheAspAspSerLysSe	534	
Qy	790	CAGGGACTTGATCATGAAGAGCACTATGAACCTTGTGTAGTACCAAGCCTCAAGGACCTC	849	
Db	534	rlYsAsnLeuLeuSerValGluCysLeuGluLeuAspLysGlySerAspCysSerThrPr	554	
Qy	850	AAAAGTCAGACAATTACTAGACACTACTGCATCCAAAGGAGAAATTTGCCAAAGATTAT	909	
Db	554	olYsSerGlySerLeuThrProSerIleAspMetLys	-----	566
Qy	910	AGTACAAAATTGAAAGATAACAACAATGGGTCTTCAGCCTTACCCGGAAATACTTGT	969	
Db	567	-PheLeuArgLeuGlnAspGluLysMetAspAspLeuGlyAspAsnTyrTyThrIleLeu	586	

Qy	970	GGTTTCTAGATACCA-----TCTTTAAATTTACTTCAAAATAA	1008
Db	586	uMetSerAsnProValSerSerTyrGlyValGlySerLeuTyrLeuPheGlnProLy	606
Qy	1009	AAGCATGTAAGTCACTGTTTTCAGAAGAAATGTGTTCATATAAAGGATATTATATCT	1068
Db	606	s-----II	607
Qy	1069	CTGTTGCTTTGACTTTTTTTTAT-----ATAAAATCCGTGAGTATTAAAGCTTT	1116
Db	607	eValCysSerGluLysTyrIleAsnHisGluGluIleAspAsnMetAsnLeuLysSerLe	627
Qy	1117	ATTGAAG-----	1123
Db	627	uHisArgTrpLeuSerArgSerLeuHisValLeuGlnSerPheSerGlyGluIleGluLe	647
Qy	1124	-----GTTCTTTGGGTAAATATTAGTCTCCCTCCATGACACTGCAG	1164
Db	647	uAsnLeuGluPheGlyValIleLeuTyrProAsnIleSerSerAspValSerAlaCysSe	667
Qy	1165	TATT-----TTTTTAAATTAATACAAG	1186
Db	667	rHisGlyPheMetAsnIleTyrLys	675
RESULT 7			
F82935			
DNA polymerase III gamma-tau subunits UU087 [imported] - Ureaplasma urealyticum			
C:Species: Ureaplasma urealyticum			
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000			
C:Accession: F82935			
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000			
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views			
A:Reference number: A82870			
A:Accession: F82935			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-597 <GLA>			
A:Cross-references: GB:AE002108; GB:AF222894; NID:g6899034; PIDN:AAF30492.1; GS			
A:Experimental source: serovar 3; biovar 1			
C:Genetics:			
A:Gene: dnax; UU087			
A:Genetic code: GGC3			
Alignment Scores:			
Pred. No.:	3.59	Length:	597
Score:	90.00	Matches:	67
Percent Similarity:	34.58%	Conservative:	53
Best Local Similarity:	19.31%	Mismatches:	98
Query Match:	3.12%	Indels:	129
DB:	2	Gaps:	15
US-09-771-161A-2 (1-1669) x F82935 (1-597)			
Qy	187	TTCAAGTTATATGTTATATTTCTCAACTCTTTATATTTTCTTCCATGTTATTTTGTACAAC	246
Db	266	PheIleTyrGluLeuTyrAsnGln-----GlyValAsnLeuGluAlaPheCysValGln	283
Qy	247	ATATAAATGCTGTAGATGCTATTTTACTTCTAT-----	280
Db	284	IleIleAsnValLeu-IleAspTyrIleuIleTyrLeuLysThrAsnAspIleAsnAsnLe	303
Qy	281	-----AATTT	285
Db	303	uLysLysValSerValAspGluLeuLysLysMetLeuLeuIleAsnPheAsnGlyAsnTy	323
Qy	286	CCTAATCATCTCCAGTTTAAAGTGTAT-----ATATT	318
Db	323	rLeuLeuAsnAsnPheIleSerLeuPheAsnAsnLeuLysLysSerLeuAsnGlnValPh	343
Qy	319	TATGTATTCAATACAGTTACAGAGTGTTCACGTCCATTCAC---CTATGTGACAAGAA	375
Db	343	eGluPheGluIleTyrLeuTyrValIleIleAsnAlaAsnAspLysLeuGluAsnLy	363





Db 862 LysLeuGluAsnGluLeuGluLysLeuArgAsnGluAsnLysGluValGlyLysGlu 881  
 QY 866 CTAGACACTACTGACATCCAGGAGAGAAATTT-----GCCAAGTTATAGTACAAAA 919  
 Db 882 AlaArgAlaArgAspAlaAlaAsnGlnGlnLeuSerArgAlaAsnLeuLeuAsnLysGlu 901  
 QY 920 TTCAAGATACAAACAA 937  
 Db 902 LeuGluAspThrLysGln 907  
 RESULT 11  
 S46005  
 ES1 protein - yeast (Saccharomyces cerevisiae)  
 N;Alternate names: MEC1 protein; protein YBR1012; protein YBR136W  
 C;Species: Saccharomyces cerevisiae  
 C;Date: 26-Aug-1994 #sequence revision 09-Sep-1994 #text\_change 29-Oct-1999  
 C;Accession: S46005; S46578; S46663; S47954; S84650  
 R;Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.  
 submitted to the Protein Sequence Database, August 1994  
 A;Reference number: S45995  
 A;Accession: S46005  
 A;Molecule type: DNA  
 A;Residues: 1-2368 <BEC>  
 A;Cross-references: EMBL:Z36005; NID:G536429; PIDN:CAA85094.1; PID:G536430; MIPS:YBR136W  
 A;Experimental source: strain S289C  
 R;Becam, A.M.; Cullin, C.; Graybowski, E.; Lacroute, F.; Nasr, F.; Ozier-Kalogeropoulos,  
 Yeast 10(Suppl.A), S1-S11, 1994  
 A;Title: The sequence of 29.7kb from the right arm of chromosome II reveals 13 complete  
 A;Reference number: S46569; MUID:94378717; PMID:8091856  
 A;Accession: S46578  
 A;Molecule type: DNA  
 A;Residues: 1-2368 <BE2>  
 A;Cross-references: EMBL:X75891; NID:G496856; PIDN:CAA53494.1; PID:G496866  
 A;Experimental source: strain S289C  
 R;Kato, R.; Ogawa, H.  
 submitted to the EMBL Data Library, May 1992  
 A;Description: An essential gene, ES1, is required for mitotic cell growth, DNA repair  
 A;Reference number: S46662  
 A;Accession: S46663  
 A;Molecule type: DNA  
 A;Residues: 1-196, 'D', 198-2368 <KAT>  
 A;Cross-references: EMBL:D11089; NID:G506874; PIDN:BAA01860.1; PID:d1002337; PID:G506876  
 R;Kato, R.; Ogawa, H.  
 Nucleic Acids Res. 22, 3104-3112, 1994  
 A;Title: An essential gene, ES1, is required for mitotic cell growth, DNA repair and me  
 A;Reference number: S47953; MUID:94344772; PMID:8065923  
 A;Accession: S47954  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 195-196, 'D', 198-322; 671-744; 848-1796; 1803-2003; 2004-2368 <KA2>  
 A;Cross-references: EMBL:D11088  
 R;Weinert, I.A.; Harlow, D.  
 submitted to the EMBL Data Library, July 1995  
 A;Reference number: S64650  
 A;Accession: S64650  
 A;Molecule type: DNA  
 A;Residues: 1-715, 'P', 717-1254, 'Q', 1256-1275, 'G', 1277-2368 <WE1>  
 A;Cross-references: EMBL:U31109; NID:G950172; PIDN:AAA74482.1; PID:G950173  
 C;Genetics:  
 A;Gene: SGD:ESR1; MEC1  
 A;Cross-references: SGD:S0000340; MIPS:YBR136W  
 A;Map position: 2R  
 C;Function:  
 A;Description: required for mitotic cell growth, DNA repair, and meiotic recombination  
 C;Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein  
 F;74-90/Domain: transmembrane #status predicted <TM1>  
 F;218-234/Domain: transmembrane #status predicted <TM2>  
 F;717-787/Domain: transmembrane #status predicted <TM3>  
 F;922-938/Domain: transmembrane #status predicted <TM4>  
 F;1152-1169/Domain: transmembrane #status predicted <TM5>  
 F;1288-1304/Domain: transmembrane #status predicted <TM6>  
 F;1315-1331/Domain: transmembrane #status predicted <TM7>

F;1682-1689/Region: nucleotide-binding motif A (P-loop)  
 F;1918-1934/Domain: transmembrane #status predicted <TM8>  
 F;2126-2142/Domain: transmembrane #status predicted <TM9>  
 F;1688/Binding site: ATP/GTP (Lys) #status predicted  
 Alignment Scores:  
 Pred. No.: 4.63 Length: 2368  
 Score: 89.50 Matches: 64  
 Percent Similarity: 36.36% Conservative: 44  
 Best Local Similarity: 21.55% Mismatches: 126  
 Query Match: 3.11% Indels: 63  
 DB: 2 Gaps: 13  
 US-09-771-161a-2 (1-1669) x S46005 (1-2368)  
 QY 359 CACCTATGTGCAAGAGAA-----ATGGAATTATCTGAACATACCT 403  
 Db 491 HisLeuCyAspIleGlyLysThrGlyAsnProPheValArgIleAsnProAsnArgPro 510  
 QY 404 GTAAATCATGTGTCACAGAGGAATCATGTGATCTCTCAG-----CTCCAT 451  
 Db 511 -----GluAlaAlaGlyLysSerGluIlePheArgIleLeuHis 523  
 QY 452 GAAATAGTGTCTCTCAAACTTCAAGTCCCTCCAGCTCCCTCAAGACATGATTT 511  
 Db 524 SerAsn-----PheLeuSerHisProAsnIleAspGluPhe 535  
 QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAC----- 556  
 Db 536 ---SerGluSerLeuLeuSerGlyIleLeuPheSerLeuHisArgIlePheSerHisPhe 554  
 QY 557 -----TGCTCTGGAATCACAGTGGGATAGCACCATTCTTGATCTCAA 601  
 Db 555 GlnProLysLeuThrAspGlyAsnGlyGlnIleAsnLysSerPheLysLeuValGln 574  
 QY 602 AGGGCTGCAATTCGTGATCACAAGACCCTCCATGCTCTTCAGCAATAATAATCCACATC 661  
 Db 575 LysCysPheMetAsnSerAsnArgTyrLeuArgLeuLeuSerThrArgIleLeuProLeu 594  
 QY 662 -----TCAACTGCAGGAAATCAGAACCTGTGCAGCCTGGTATATGCCAGAGTGG 712  
 Db 595 PheAsnIleSerAspSerHisAsnSerGluAspGluHisThrAlaThrLeuIleLysPhe 614  
 QY 713 ATCCAGAGCAAAAGGAGACATGTTG-----AACCAATG 748  
 Db 615 LeuGlnSerGlnLysLeuProValValLysGluAsnLeuValIleAlaTrpThrGlnLeu 634  
 QY 749 ACAGAGCCTGCCTTAACACAGTCGTAGATGCCCTTCTGTCCAGG-----GACTTGATC 802  
 Db 635 ThrLeuThrThrSerAsnAspValPheAspThrLeuLeuLeuLysLeuIleAspIlePhe 654  
 QY 803 ATGAAAGAGGACTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCAGACAA 862  
 Db 655 AsnSerAspAspTyrSerLeuArgIleMetThrLeuGlnIleLysAsnMetAlaLys 674  
 QY 863 TTACTAGACACTACTGACATCCAA---GGAGAGAATTTGCCAAAGTATTAGTACAAAAA 919  
 Db 675 IleLeuLysLysThrProTyrGlnLeuLeuSerProIleLeuProValLeuLeuArgGln 694  
 QY 920 TTCAAGATTAAC-----AAACAAATGGGTCTTCAGCCTTACCCTGGGAAATCTGTG 970  
 Db 695 LeuGlyLysAsnLeuValGluArgLysValGlyPheGlnAsnLeuIleGluLeuLeuGly 714  
 QY 971 GTTCTAGATCACCATCTTTAAATTTACTTTCAAAATAAAGAGCATGTAAGTGACTGTTTT 1030  
 Db 715 TyrSerLysThrIleLeuAspIlePheGlnArgTyrIleIleProTyrAlaIle 734  
 QY 1031 CAA-----GAAGAAATGTTTCATAAAAGGATATTTATATCTCTGT 1072  
 Db 735 GlnTyrLysSerAspValLeuSerGluIleAlaLysIle-----MetCys 749  
 QY 1073 TGCTTTGACCTTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGAAG 1123



Db 750 AspGlyAspThrSerLeuIleAsnGlnMetLysValAsnLeuLeuLysLys 766

## RESULT 12

S71757  
MADS box protein DRFH200 - garden snapdragon  
C:Species: Antirrhinum majus (garden snapdragon)  
C:Date: 11-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 20-Jun-2000  
C:Accession: S71757  
ENBO J. 15, 4330-4343, 1996  
R:Davies, B.; Egea-Cortines, M.; de Andrade Silva, E.; Saedler, H.; Sommer, H.  
A:Title: Multiple interactions amongst floral homeotic MADS box proteins.  
A:Reference number: S71756; MUID:97015133; PMID:8861961  
A:Accession: S71757  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-242 <DAV>  
A:Cross-references: EMBL:X95469; NID:g1239958; PIDN:CAA64743.1; PID:g1239959  
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
C:Keywords: DNA binding; transcription regulation  
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
F:94-159/Domain: domain K <KDO>

Alignment Scores:  
Pred. No.: 4.07 Length: 242  
Score: 89.00 Matches: 48  
Percent Similarity: 34.36% Conservative: 30  
Best Local Similarity: 21.15% Mismatches: 65  
Query Match: 3.09% Indels: 84  
DB: 2 Gaps: 7

US-09-771-161A-2 (1-1669) x S71757 (1-242)

```
QY 362 CTATGTGCAAGAAGAAATGGAATATCTCTCAACATACCTGTAATCATGGTCACAA 421
Db 38 LeuCysAsp-----AlaGluValAlaLeuIlePheSerAsnArgGlyLysLeu 54
QY 422 GAGGAATCATGTGGATCTCTCAGCTCCATGAA-----AAT 457
Db 55 TyrGluPheCysSerSerThrSerMetLeuAsnThrLeuGluArgTyrGlnLysCysAsn 74
QY 458 AGTGGTCTCTCAAGACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTTATCT 517
Db 75 TyrGlyProProGluThrAsnValSer----- 83
QY 518 AGAAAGCTCAAGACTGTTATTTTATGAAGTGCATCACTGCTCTGGAATCACAGTTGG 577
Db 83 ----- 83
QY 578 GATAGACCACTTCTGGATCTCAAGGGGTGCATCTCTGTGATCACAGACCCTCATGCC 637
Db 83 ----- 83
QY 638 TCTTCAGCAATAATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTCTGCAGCTGGT 697
Db 84 -----ThrArgGluAlaLeuGluLeuSer 91
QY 698 ATAGCCAGCAGTGGATCCAGAGCAAA---AGGGAAGACATTGTGAACCAAAATGACAGAA 754
Db 92 SerGlnGlnGluTyrLeuLysLysLysAlaAgtTyrGluAlaLeuGlnArgSerGlnArg 111
QY 755 GCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAGGAC 814
Db 112 AsnLeuLeuGlyGluAspLeuGlyProLeuAsnSerLysGluLeuSerLeuGluArg 131
QY 815 TATGAACCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874
Db 132 GlnLeuAspMetSerLeuLysGlnIleArgSerThrArgThrGlnAlaMetLeuAspThr 151
QY 875 ---ACTGACATCCAAAGGAGAAATTTGCC-----AAAGTTATAGTACAA 916
Db 152 LeuThrAspLeuGlnArgLysGluHisAlaLeuAsnGluAlaAsnArgSerLeuLysHis 171
QY 917 AAATTGAAGATAACAAACAAATGGGTCTTACGCTTACCCG-----GAAATACTT 967
```

Db 172 ArgLeuMetAspGlySerGlnIleSerLeuGlnTrpAsnProAsnAlaGluAspHisVal 191

QY 968 GTGGTTTCTAGATCACCACATCT 988

Db 192 GlyTyrGlyArgGlnProSer 198

## RESULT 13

B81996  
RNA polymerase sigma factor NMA0049 [imported] - Neisseria meningitidis (strain Z2491 ser  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: B81996  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: B81775; MUID:20222556; PMID:10761919  
A:Accession: B81996  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-283 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83366.1; PID:g7378824  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA0049

Alignment Scores:  
Pred. No.: 4.14 Length: 283  
Score: 89.00 Matches: 53  
Percent Similarity: 35.68% Conservative: 28  
Best Local Similarity: 23.35% Mismatches: 86  
Query Match: 3.09% Indels: 60  
DB: 2 Gaps: 9

US-09-771-161A-2 (1-1669) x B81996 (1-283)

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QY 500 GACAAATGATTTTATCTAGAAAAGCTCAAGAC-----TGT 535
Db 42 AspAsnProLeuLeuGluArgLysAspThrAspGluPheSerAspAlaGluPheSerHis 61
QY 536 TATTTTATGAAGTCATCACTGCTCTGGAATCACAGTTGGAT-----AGCACCATT 589
Db 62 TyrThrAlaProAlaArgGlnIleGlyGlyGlyGlyGluAspMetLeuSerAsnIle 81
QY 590 TCTGATCTCAA-----AGGGCTGCATCTCTGTGATCACAAGACCACT 631
Db 82 AlaGlyGluGlnAspPheLysGlnTyrLeuHisAlaGlnValCysGluHisProLeuSer 101
QY 632 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCGAGGAACTCAGAACGTCGTGCAG 691
Db 102 AspGlnGluSerAlaCysValHisIleLeuIleAspPheLeuAspGlu----- 117
QY 692 CTGTGTATAGCCACAGTCAGTGGATCCAGACCAAAAGGAGACATTGTGAAC----- 742
Db 118 -----GlnGlyTyrLeuThrAspSerIleGluAspIleLeuAspHisThrPro 133
QY 743 -----CAAATGACAGAACGCTGCTTACCACTGCTAGTCGCTT----- 784
Db 134 LeuGluTrpMetLeuAspGluAlaMetLeuLysGlnAlaLeuThrAlaLeuLysLysPhe 153
QY 785 -----CTGTCCAGGACTTCATCATGAAA---GAGGAC 814
Db 154 AspProAlaGlyValAlaAlaAlaAspLeuAsnGluSerLeuIleLeuGlnIleGluArg 173
QY 815 TATGAACCTGTTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874
Db 174 SerGlyGluCysAlaAlaLysProSerAlaLeuHisIleValArgAsnAlaLeuAspSer 193
QY 875 ACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATACAAA 934
Db 194 IleAspGlyAsnArgSerGlnThrLeuAlaArgLysLysLeuArgLeuProGlnThrAsp 213
```

QY 935 CAA-----ATGGGTCTTCAGCTTACCGGAATA 964  
 Db 214 SerGlyThrLeuGluAlaLeuAspLeuIleAlaSerLeuAsnProPheProAlaVal 233  
 QY 965 CTTGTGGTTTCTAGATCACCATCT-----TTAAATTACTTCAA 1003  
 Db 234 GlyPheAlaSerThrProThrProTyrSerAspGluAlaLeuAlaAsnLeuLeuAla 253  
 QY 1004 AATAAAGCATGTAAAGTACT 1024  
 Db 254 PheArgGlyMetGluValSer 260  
 RESULT 14  
 T33922  
 Hypothetical protein Y8A9A.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T33922  
 R:Courtney, L.; Langston, Y.; Drone, K.; Mead, K.  
 submitted to the EMBL Data Library, February 1999  
 A:Description: The sequence of C. elegans cosmid Y8A9A.  
 A:Reference number: Z21439  
 A:Accession: T33922  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1360 <COU>  
 A:Cross-references: EMBL:AF125461; PIDN:AAD12852.1; GSPDB:GNO0020; CESP:Y8A9A.2  
 A:Experimental source: strain Bristol N2; clone Y8A9A  
 C:Genetics:  
 A:Gene: CESP:Y8A9A.2  
 A:Map position: 2  
 A:Introns: 43/3; 69/3; 134/3; 174/1; 604/2; 643/3; 718/3; 787/3; 848/2; 944/2; 1044/2; 1  
 Alignment Scores:  
 Pred. No.: 4.87 Length: 1360  
 Score: 89.00 Matches: 39  
 Percent Similarity: 33.68% Conservative: 25  
 Best Local Similarity: 20.53% Mismatches: 68  
 Query Match: 3.09% Indels: 58  
 DB: 2 Gaps: 7  
 US-09-771-161A-2 (1-1669) x T33922 (1-1360)  
 QY 341 AGTGTTCACAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCTCTGAACATA 400  
 Db 972 ThrValSerGlyThrGlnHisLeuCysGlyProGlnPro-----AsnTyr 985  
 QY 401 CCTGTAAATCATGTGTCACAGAGAGATCATGTGGATCCCTCAGCTCCATGAAAT--- 457  
 Db 987 ThrThrProTyrAlaProTyrAspProThrCysThrAspAsnCysCysProGluThrGly 1006  
 QY 458 -----AGTGGTTCCTCGTAAACTTCAAGGTCCTCCAGCTCCCTCAAGAC 502  
 Db 1007 IleTrpSerAspTrpThrSerThrProAsnGlnCysArgAspTyrCysGlySerCysGly 1026  
 QY 503 AATGATTTTTTATCTAGAAAAGCTCAAGAC----- 532  
 Db 1027 AsnGlnThrArgThrArgThrCysThrSerAspAlaAspGlyCysProCysGlnGlyPro 1046  
 QY 533 -----TGTTATTTTATGAAGCTGCATCACTGT 559  
 Db 1047 ThrThrIleThrGluProCysGlyThrGlyValCysTyrPheProArgLeuSerCysCys 1066  
 QY 560 CTTGGAATACAGTGTGGATGACCACTTTCTGGATCTCAAGGGCTGCATCTGTGTAT 619  
 Db 1067 ProGly-----TyrThrAlaThrValGluGlyAsnGln----- 1077  
 QY 620 CACAGACCATCTCCATGTCTTCCAGCAATATAATCCA-----CTCTCACTCCAGGA 673  
 Db 1078 HisIleCysGlyProLeuThrThrAlaValAlaAspProAspLysLeuAsnThrCysGly 1097  
 QY 674 AACTCAGACGCTCTGAGCTTGGTATAGCCAGCAGTGGATCCAG----- 718

Db 1098 ValSerCysCysProSerAlaGlyIleTrpGlyGluTrpValSerValSerGlyCysAsn 1117  
 QY 719 -----AGCAAAAGGGAAGACATTGTGCAACCAATG 748  
 Db 1118 AspThrCysGlySerCysGlyGlnGluThrArgLysArgLysCysLeuSerLeuGlnTyr 1137  
 QY 749 ACAGAAGCTGCTTTAACCAACGTCGCTAGAT 778  
 Db 1138 GlyCysAlaCysThrGlyAsnAlaThrAsp 1147  
 RESULT 15  
 A55117  
 tsq24 protein - mouse  
 N:Alternate names: bime protein homolog  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 17-Mar-2000  
 C:Accession: A55117  
 R:Starborg, M.; Brundell, E.; Gell, K.; Hooeog, C.  
 J. Biol. Chem. 269, 24133-24137, 1994  
 A:Title: A novel murine gene encoding a 216-kDa protein is related to a mitotic checkpoint  
 A:Reference number: A55117; MUID:95014147; PMID:7929068  
 A:Accession: A55117  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1944 <STR>  
 A:Cross-references: GB:X80169; NID:g562764; PIDN:CAA56450.1; PID:g642252  
 C:Genetics:  
 A:Gene: tsq24  
 C:Superfamily: bime protein  
 Alignment Scores:  
 Pred. No.: 5.06 Length: 1944  
 Score: 89.00 Matches: 52  
 Percent Similarity: 37.56% Conservative: 25  
 Best Local Similarity: 25.37% Mismatches: 72  
 Query Match: 3.09% Indels: 56  
 DB: 2 Gaps: 10  
 US-09-771-161A-2 (1-1669) x A55117 (1-1944)  
 QY 326 TCATTACAGTTACAGAGTGTTCCTCAAGTGCAT---CACCTATGTGACAGAGAA 379  
 Db 291 ThrLeuGlnAsnAlaThrThrSerSerLeuThrAlaHisLeuArgSerLeuSerLys 310  
 QY 380 ATGGAATTATCTCTGAACATACCTGTAATCAT-----GGTCCACAAGAGGAA 427  
 Db 311 GlyGluSerProValAlaSerProPheGlnAsnTyrSerSerIleHisSerGlnSerArg 330  
 QY 428 TCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTTCCTCTGAAACTTCAAGGTCCTG 487  
 Db 331 SerThrSerSerProSerLeuHisSerArgSer----- 341  
 QY 488 CCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAG 547  
 Db 342 ProSerIleSerAsnMetGlyValLeuSerArgAla----- 353  
 QY 548 CTGCATCACTGTCT-----GGAAATCACAGTTGGATAGACCATTTCTGGATCTCAA 601  
 Db 354 -----HisSerProAlaLeuGlyValHisSerPhe-----SerGlyAlaGln 367  
 QY 602 AGGCTGCATTCGTGATCACAAGACCATCTCCATGCTCTTCAGCAATATAATATCCACTC 661  
 Db 368 ArgPheAsnLeuSerHisSerGlnSerProLysArgHisSerIleSerHisSerPro 387  
 QY 662 TCAACTCCAGAAACTCAGAACCTCTCAGCTGGTATAGCCCGCAGTCGATCCAGAGC 721  
 Db 388 SerGlySerPheAsnAspSerPheLeuAlaPro----- 398  
 QY 722 AAAAGGAAGACATTTGTGAACCAAAATGACAGAACCTCTGCTTAACCAAGTCGTAGATGCC 781  
 Db 399 GluThrGluProIleVal-----ProGluLeuCysIle----- 409  
 QY 782 CTTCTGTCCAGGACTTGTATCATGAAGAGAGACTATGAACTTGTATTACCAACGCTTACA 841

```

Db      410 -----AspHisLeuTrpThrGluThrLeuProAsnIleArgGluLysAsnSer 425
QY      842 AGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGAGAGAGAATTGCCC 901
Db      426 GlnAlaSerLysVal-----PheIleThrThrAspLeuCysGlyGlnLysPheLeu 442
QY      902 AAAGTTATAGTACAA 916
Db      443 CysPheLeuValGlu 447

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Search completed: March 29, 2004, 14:24:54  
Job time : 50.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:14:22 ; Search time 20.5 Seconds  
(without alignments)  
8478.545 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880  
Sequence: 1 acctgtttatccagata.....caacagcgtgtgtgtataaa 1669

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cpn2\_1/USPTO\_spool\_p/US09771161/runat\_29032004\_124824\_13664/app\_query.fasta\_1.1863  
-DB=SwissProt\_42 -OPMT=fastan -SUFFIX=n2p\_rsp -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	41.0	540	1 RIK2_HUMAN	O43353 h receptor-
2	839.5	29.1	539	1 RIK2_MOUSE	P58801 mus musculus
3	122.5	4.3	953	1 CAR4_HUMAN	Q9Y239 homo sapien
4	100.5	3.5	943	1 YLW5_CAEEL	P34408 caenorhabdi
5	98	3.4	618	1 BIR2_HUMAN	Q13490 homo sapien
6	96.5	3.4	953	1 CAR4_MOUSE	Q8bnb0 mus musculus
7	94	3.3	357	1 REP1_ZYGBA	P13776 zygosacchar
8	92	3.2	612	1 BIR2_MOUSE	Q62210 mus musculus
9	90	3.1	708	1 KHS1_YEAST	P39690 saccharomyc
10	89.5	3.1	2368	1 ESR1_YEAST	P38111 saccharomyc
11	89.5	3.1	3130	1 DPOZ_HUMAN	O60573 homo sapien
12	89	3.1	1944	1 ANCI_MOUSE	P53995 mus musculus
13	88	3.1	358	1 PIAP_PIG	O62640 sus scrofa
14	88	3.1	524	1 T2FA_XENLA	Q04870 xenopus lae
15	88	3.1	8797	1 SNE1_HUMAN	Q8nf91 homo sapien
16	87.5	3.0	406	1 YMX2_CAEEL	P34510 caenorhabdi
17	87	3.0	341	1 Y173_BORBU	O51195 borrelia bu
18	87	3.0	400	1 RT0A_DICDI	P54681 dictyostell

19	86.5	3.0	365	1 SYAP_MOUSE	Q9d5v6 mus musculu
20	86.5	3.0	407	1 MYC_ASTVU	Q17103 asterias vu
21	86.5	3.0	976	1 YBS4_YEAST	P38244 saccharomyc
22	86.5	3.0	1088	1 MRTB_HUMAN	Q9ulh7 homo sapien
23	85.5	3.0	513	1 MATK_CYRRA	Q8wlv4 cyrilla rac
24	85.5	3.0	3898	1 POLG_HCVA	P19712 hog cholera
25	85	3.0	627	1 ABPX_YEAST	Q08641 saccharomyc
26	85	3.0	690	1 LIP_STAAN	P10335 staphylococ
27	85	3.0	721	1 MX_ANAPL	P32338 anas platyr
28	84.5	2.9	224	1 AGI9_LYCES	Q42464 lycopersico
29	84.5	2.9	733	1 ACE1_TRIE	Q9p8w3 trichoderma
30	84	2.9	690	1 LIP_STAAN	Q8nyv2 staphylococ
31	83.5	2.9	266	1 KUR5_MOUSE	Q60852 mus musculu
32	83.5	2.9	486	1 ZASA_HUMAN	Q15172 h serine/th
33	83.5	2.9	604	1 BIR3_HUMAN	Q13489 homo sapien
34	83.5	2.9	805	1 HIPA_XENLA	Q918a9 xenopus lae
35	83.5	2.9	1822	1 SC72_SCHPO	Q9p7v5 schizosacch
36	83.5	2.9	2567	1 M18B_HUMAN	Q8iug5 homo sapien
37	83.5	2.9	2813	1 VWF_CANFA	Q28295 canis famli
38	83	2.9	853	1 AHR_RAT	P41738 rattus norv
39	83	2.9	1113	1 PHG1_HUMAN	Q9u1l1 homo sapien
40	83	2.9	1499	1 PGF1_HUMAN	Q9y4g8 homo sapien
41	82.5	2.9	374	1 HAT1_YEAST	Q12341 saccharomyc
42	82.5	2.9	495	1 ACH3_BOVIN	Q07263 bos taurus
43	82.5	2.9	647	1 L1K1_RAT	P53669 rattus norv
44	82	2.8	489	1 YEN5_YEAST	P39970 saccharomyc
45	82	2.8	933	1 N106_SCHPO	O14310 schizosacch

#### ALIGNMENTS

##### RESULT 1

ID	RIK2_HUMAN	STANDARD;	PRT;	540 AA.
AC	O43353			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)			
DE	(RIP-like interacting CLARP kinase) (Receptor-interacting protein 2)			
DE	(RIP-2) (CARD-containing interleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICE-kinase).			
GN	RIPK2 OR RICK OR RIP2 OR CARDIAC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=98307936; PubMed=9642260;			
RA	McCarthy J.V., Ni J., Dixit V.M.;			
RT	"RIP2 is a novel NF-kappaB-activating and cell death-inducing kinase.";			
RL	J. Biol. Chem. 273:16968-16975 (1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.			
RX	MEDLINE=98381580; PubMed=9705938;			
RA	Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,			
RT	Mattmann C., Tschoopp J.;			
RT	"Identification of CARDIAC, a RIP-like kinase that associates with caspase-1.";			
RL	Curr. Biol. 8:885-888(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Ozersky P., Holmes A., Broy M.;			



Db 533 AnLeuLeuGlnAsnLysSerMet 540

RESULT 2

ID\_RIK2\_MOUSE STANDARD; PRT; 539 AA.

AC P58801; 332 CAGTTACAGAGTGTTCAGAGTCCATTCACATATCTGACAGAGAGAAATGAATATCT 391

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).

GN RIK2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RX MEDLINE=21891093; PubMed=11894097;

RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;

RT "Involvement of receptor-interacting protein 2 in innate and adaptive

immune responses.";

RL Nature 416:190-194(2002).

CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates

CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.

CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and

CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40

CC receptor complex (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

CC -!- PTM: Autophosphorylated (By similarity).

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -----

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CC -----

DR EMBL; AF461040; AAL96436.1; -

DR MGD; MGI:1891456; Rikp2.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR Pfam; PF00619; CARD; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot kinase; 1.

DR SMART; SM00114; CARD; 1.

DR PROSITE; PS0209; CARD; 1.

DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Phosphorylation; Apoptosis.

FT DOMAIN 18 294 PROTEIN KINASE.

FT DOMAIN 431 533 CARD.

FT NP\_BIND 24 32 ATP (BY SIMILARITY).

FT BINDING 47 47 ATP (BY SIMILARITY).

FT ACT\_SITE 146 146 BY SIMILARITY.

SQ SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;

Alignment Scores:

Pred. No.: 5,29e-68 Length: 539

Score: 839.50 Matches: 164

Percent Similarity: 80.70% Conservative: 20

Best Local Similarity: 71.93% Mismatches: 43

Query Match: 29.15% Indels: 1

DB: 1 Gaps: 1

US-09-771-161a-2 (1-1669) x RIK2\_MOUSE (1-539)

QY 332 CAGTTACAGAGTGTTCAGAGTCCATTCACATATCTGACAGAGAGAAATGAATATCT 391

DB 313 LysileGlnSerSerSerThrIleHisLeuCysAsp---LysLysMetAspLeuSer 331

QY 392 CTGAACATACCTGTAATAATCATGTGTCACCAAGAGGAATCATGTGGATCTCTCAGCTCCAT 451

DB 332 LeuAsnIleProAlaAsnHisProGlnGluSerCysGlySerSerLeuLeuSer 351

QY 452 GAAATAGTGTTCCTCGAAACTTCAAGGTCCTCCAGCTCCCTCAAGACAAATATTT 511

DB 352 ArgAsnThrGlySerProGlyProSerArgSerLeuSerAlaProGlnLysGlySer 371

QY 512 TTATCTAGAAAAGCTCAAGAGCTGTTATTTTATTAAGCTGTCATCTGCTGCTGGAATCAC 571

DB 372 LeuSerGlyAlaProGlnAspCysSerSerLeuLysAlaHisCysProGlyAsnHis 391

QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 631

DB 392 SerTrpAspGlyIleValSerValProGlyAlaAlaPheCysAspArgAlaSer 411

QY 632 CATGCTCTTCAGCAATATAATCACTCTCAACTGCAGGAAACTCAGAAGCTCTGCAG 691

DB 412 SerCysSerLeuAlaValIleSerProPheLeuValGluLysGlySerGluArgPro 431

QY 692 CCTGTATAGCCAGCAGTGCATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACA 751

DB 432 IleGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAlaIleValSerGlnMetThr 451

QY 752 GAAGCTCTCCCTTAACCACTGCTAGATCCCTCTCTGTCAGGAGCTTGATCATGAAAGAG 811

DB 452 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 471

QY 812 GACTATGAAGTGTGTAGTACCAAGCTCAAGAGCTCAAAAGTCAGACAATTACTAGAC 871

DB 472 AspTyrGluLeuIleSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 491

QY 872 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAC 931

DB 492 ThrSerAspIleGlnGlyGluGluPheAlaLysValValGlnLysLeuLysAspAsn 511

QY 932 AAACAATGGTCTTTCAGCTTACCCGGAATATCTGTTGTTCTAGATCACCATTCTTTA 991

DB 512 LysGlnLeuGlyLeuGlnProTyrProGluValProValLeuSerLysAlaProProSer 531

QY 992 AATTACTTCAAATAAAGCATG 1015

DB 532 AsnPheProGlnAsnLysSerLeu 539

RESULT 3

CAR4\_HUMAN

ID\_CAR4\_HUMAN STANDARD; PRT; 953 AA.

AC Q9V239; Q9V239;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caspase recruitment domain protein 4 (Nod1 protein).

GN CARD4 OR NOD1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Endothelial cells;

RA MEDLINE=99240667; PubMed=10224040;

RA Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R.,

RA Grant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,

RA Glucksman M.A., DiStefano P.S.;

RT "Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

that activates NF-kappaB.";  
J. Biol. Chem. 274:12955-12958(1999).  
[2]  
SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.  
TISSUE=Breast;  
MEDLINE=99262599; PubMed=10329646;  
RA Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R.,  
RA Merino J., Liu D., Ni J., Nunez G.;  
RA "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-  
RT kappaB".  
J. Biol. Chem. 274:14560-14567(1999).  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences".  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[4]  
FUNCTION.  
MEDLINE=21264704; PubMed=11058605;  
RA Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;  
RA "Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";  
J. Biol. Chem. 276:2551-2554(2001).  
CC -/- FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-  
CC B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers  
CC responsiveness to intracellular bacterial lipopolysaccharides  
CC (LPS).  
CC -/- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD  
CC interaction.  
CC -/- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -/- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal  
CC muscle, pancreas, spleen and ovary. Also detected in placenta,  
CC lung, liver, kidney, thymus, testis, small intestine and colon.  
CC -/- SIMILARITY: Contains 1 CARD domain.  
CC -/- SIMILARITY: Contains 1 NOD1 domain.  
CC -/- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.  
-----  
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CC ENBL; AF126484; AAD29125.1; -  
CC ENBL; AF149774; AAD3922.1; -  
CC ENBL; AF113925; AAD28350.1; -  
CC ENBL; BC040339; AAD40339.1; -  
CC Genew; HGNC:16390; CARD4.  
CC MIN; 605980; -  
CC GO; GO:0008656; F: caspase activator activity; TAS.  
CC GO; GO:0006915; P: apoptosis; TAS.  
CC GO; GO:0007165; P: signal transduction; TAS.  
CC InterPro; IPR001315; CARD



RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craston M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins J., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Wieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkins-Sproat J.,  
RA Wohldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
CC -!- SIMILARITY: Contains 1 GoLoco domain.  
CC -!- SIMILARITY: Contains 1 J domain.  
CC -----  
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CC -----  
CC EMBL; L12018; AA65459.1; --  
CC PIR; S44636; S44636.  
CC WSP; P08622; 1XBL.  
DR WormPep; F22B7.5; CE00158.  
DR InterPro; IPR002939; DnaJ C.  
DR InterPro; IPR001305; DnaJ\_CXXCXXGXG.  
DR InterPro; IPR001623; DnaJ N.  
DR InterPro; IPR003109; GoLoco.  
DR InterPro; IPR008971; HSP40\_DnaJ\_pap.  
DR InterPro; IPR003095; Hsp\_DnaJ.  
DR InterPro; IPR008941; TPR-like.  
DR Pfam; PF00226; DnaJ; 1.  
DR Pfam; PF01556; DnaJ C; 1.  
DR Pfam; PF00684; DnaJ\_CXXCXXGXG; 1.  
DR Pfam; PF02188; GoLoco; 1.  
DR PRINTS; PR00625; DNAJPROTEIN.  
DR SMART; SM00271; DnaJ; 1.  
DR SMART; SM00390; GoLoco; 1.  
DR PROSITE; PS00636; DnaJ 1; 1.  
DR PROSITE; PS00076; DnaJ 2; 1.  
DR PROSITE; PS50877; GOLOCO; 1.  
KW Hypothetical protein.  
FT DOMAIN 424 445 GOLOCO.  
FT DOMAIN 531 595 J-DOMAIN.  
SQ SEQUENCE 943 AA; 105926 MW; 9847F95977E0418E CRC64;  
Alignment Scores:  
Pred. No.: 0.394 Length: 943  
Score: 100.50 Matches: 45  
Percent Similarity: 38.36% Conservative: 44  
Best Local Similarity: 19.40% Mismatches: 84  
Query Match: 3.49% Indels: 59  
DB: 1 Gaps: 10  
US-09-771-161a-2 (1-1669) x YLW5\_CABEL (1-943)  
QY 392 CTGAACATACCTGTAAATCATGTGCACAAAGGAATCATGTGGATCTCTCAGCTCCAT 451  
Db 349 IieAspValAlaWeCAsnGlnGluArgSerGluThrAlaThrAspGlnAspValCysLeu 368  
QY 452 GAAATAGTGGTCTCTCTGAACTTCAAGGTCCTCCAGCTCCCTCAAGACATGATTTT 511  
Db 369 AlAlieAspSerSerProAspProThrSerSer-----AsnAspMet 382  
QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGTGCATCATCTGCTCGAATCATC 571

Db 383 IieAsnLys-----PheValValGluLeuGluHieAlaThrAsnValGlu 397  
QY 572 AGTTGGATAGCACCATTCTTGGG----- 595  
Db 398 ThrTrpGluMetIleValAsnGlyIleIleAspAspGlnLysLysProValAlaIleGlu 417  
QY 596 -----TCTCAAAGGCTGCA 610  
Db 418 LysLysGluAsnGluGluProValAspMetMetAspLeuIlePheSerMetSerArg 437  
QY 611 TTCTGTGATCACAAGACACCTCCATGCTCTTCAGCAATAATA-----AATCCTCTCA 664  
Db 438 MetAspAspGlnArgThrGluLeuProAlaAlaArgPheIleProProArgProValSer 457  
QY 665 ACTGCAGGA-----AATCTCAGAACCTCTGCAGCCTGTGTATAGCCCCAGCAGTGG 712  
Db 458 SerAlaSerLysLysThrThrLysSerHisArgIleLeuProGlyLeuArgAlaAsnTrp 477  
QY 713 ATCCAGACAAAGGAAGACATTGTGAACCAATGACAGAACCTGCTTAACAGTGG 772  
Db 478 ThrLysValGlnSerMetLysValLleuGlyMetPheVal-----LeuAsnArgSer 494  
QY 773 CTAGATGCCCTTCTCTCCAGGACTTGATCATGAAAGAGGACTATGAACCTGTTAGTACC 832  
Db 495 ---SerGlyLeuIleHisArgSerValProLeuLeuAlaGln-----ValSerThr 510  
QY 833 AAGCCTACAAGGACCTCAAAAGTACAGACAACTTACTAGACACTTACTGACATCCAGGAGAA 892  
Db 511 ProThrThrSerThrThrLysLeuAlaGlnLeuHisThrThrHisAlaLeuSerLysGlu 530  
QY 893 GAATTGGCCAAAGTTATA---GTACAAAATTTGAAGATAACAAA----- 934  
Db 531 AspTyrTyrLysThrLeuGlyValAspLysLysSerAspAlaLysAlaIleLysLysAla 550  
QY 935 -----GAAATGGTCTTTCAGCCTTACCGGAAATA 964  
Db 551 TyrPheGlnLeuAlaLysLysTyrHisProAspVal 562  
RESULT 5  
BIR2 HUMAN  
ID BIR2 HUMAN STANDARD; PRT; 618 AA.  
AC Q13450; Q16516;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Baculoviral IAP repeat-containing protein 2 (Inhibitor of apoptosis  
DE protein 2) (HIAP2) (IAP-2) (C-IAP1) (TNFR2-TRAF signaling complex  
DE protein 2) (IAP homolog B).  
GN BIR2 OR API1 OR IAP2 OR MIH6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96128127; PubMed=8548810;  
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;  
RT "The TNFR2-TRAF signaling complex contains two novel proteins related  
RT to baculoviral inhibitor of apoptosis proteins.";  
RL Cell 83:1243-1252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96149249; PubMed=8552191;  
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,  
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
RT "Suppression of apoptosis in mammalian cells by NAIP and a related  
RT family of IAP genes.";  
RL Nature 379:349-353(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal liver;

RX MEDLINE=96209843; PubMed=8643514;  
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;  
 RT "Cloning and expression of apoptosis inhibitory protein homologs that  
 RT function to inhibit apoptosis and/or bind tumor necrosis factor  
 RL receptor-associated factors";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis, and Uterus;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Krausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP STRUCTURE BY NMR OF 266-363.  
 RX MEDLINE=9932054; PubMed=10404221;  
 RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;  
 RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)  
 RT repeat";  
 RL Nat. Struct. Biol. 6:648-651(1999).  
 CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS  
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO  
 CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR  
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -!- SUBUNIT: Interacts with SMAC and with PRSS25; these interactions  
 CC inhibit apoptotic suppressor activity.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -!- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.  
 CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,  
 CC AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD  
 CC LEUKOCYTES.  
 CC -!- SIMILARITY: Belongs to the IAP family.  
 CC -!- SIMILARITY: Contains 3 BIR repeats.  
 CC -!- SIMILARITY: Contains 1 CARD domain.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; L49431; AAC41942.1; --  
 CC EMBL; U45879; AAC50372.1; --  
 CC EMBL; U37547; AAC50508.1; --  
 CC EMBL; BC016174; AAH16174.1; --  
 CC EMBL; BC028578; AAH28578.1; --  
 CC PIR; S68450; S68450.  
 CC PDB; 1QBH; 20-OCT-99.  
 CC Genew; HGNC:590; BIRC2.  
 CC MIM; 601712; --  
 CC DR GO; 0008189; F:apoptosis inhibitor activity; TAS.  
 CC DR GO; 0007166; P:cell surface receptor linked signal transdu. . . ; TAS.  
 CC DR InterPro; IPR001370; BIR.

DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF00653; BIR; 3.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR SMART; SMO0238; BIR; 3.  
 DR SMART; SMO0114; CARD; 1.  
 DR SMART; SMO0184; RING; 1.  
 DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
 DR PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS0518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 KW Apoptosis; Zinc-finger; Repeat; 3D-structure.  
 FT REPEAT 46 113  
 FT BIR 1.  
 FT REPEAT 184 250  
 FT BIR 2.  
 FT REPEAT 269 336  
 FT BIR 3.  
 FT DOMAIN 453 543  
 FT CARD-TYPE.  
 FT ZN FING 571 606  
 FT RING-2.  
 FT CONFLICT 157 157  
 FT S -> P (IN REF. 2).  
 FT CONFLICT 308 308  
 FT C -> G (IN REF. 2).  
 FT CONFLICT 414 414  
 FT Q -> L (IN REF. 2).  
 FT CONFLICT 514 514  
 FT L -> W (IN REF. 2).  
 FT TURN 259 270  
 FT STRAND 309 309  
 FT HELIX 322 325  
 FT TURN 326 328  
 FT STRAND 333 333  
 FT TURN 334 343  
 FT STRAND 344 351  
 FT HELIX 353 354  
 FT TURN 353 354  
 SQ SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

Alignment Scores:  
 Pred. No.: 0.64 Length: 618  
 Score: 98.00 Matches: 31  
 Percent Similarity: 44.78% Conservative: 29  
 Best Local Similarity: 23.13% Mismatches: 58  
 Query Match: 3.40% Indels: 16  
 DB: 1 Gaps: 3  
 US-09-771-161a-2 (1-1669) x BIR2\_HUMAN (1-618)  
 QY 713 ATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACAGAGCCCTGCTTACCACTCG 772  
 Db 461 ILAAGLYSAsnArgMetAlaLeuPheGlnLeuThr-----CysValLeuProIle 478  
 QY 773 CTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAGGACTATGAACTTTGTAGTACC 832  
 Db 479 LeuAspAsnLeuLeuValIleAsnValIleAsnValIleGlnGlnIleLysGln 498  
 QY 833 AAGCTACAAAGGACCTCAAAAGTCAGACATTTACTAGACACTACTGACATCCAAAGAGAA 892  
 Db 499 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleLeuValLysGlyAsn 518  
 QY 893 GAATTTCCCAAGTTATAGTACAAAATTTGAAAGAT----- 928  
 Db 519 AlaAlaAlaAsnIlePheLysAsnCysLeuLysGluIleAspSerThrLeuYrLysAsn 538  
 QY 929 -----AACAAACAATAGGGTCTTACGCTTACCCGGAATACTTGTGTTCTTAGA 979  
 Db 539 LeuPheValAspLysAsnMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 558  
 QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTCAGAGAGAA 1039  
 Db 559 GluGluGlnLeuArgArgLeuGlnGluGluGluGluGluGluGluGluGluGluGlu 579  
 QY 1040 ATGTGTTTCATA-----AAAGGATATTATATCTCTCTGT 1072



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RESULT 7
REPI_ZYGBA STANDARD; PRT; 357 AA.
AC REPI_ZYGBA
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Trans-acting factor B (REP1).
GN B.
OS Zygosaccharomyces baillii.
OC Plasmid PSB2.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
OX NCBI_TaxID=4954;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1047;
RX MEDLINE=88059763; PubMed=3680169;
RA Utatsu I., Sakamoto S., Imura T., Toh-E A.;
RT "Yeast plasmids resembling 2 micron DNA: regional similarities and
RL J. Bacteriol. 169:5537-5545 (1987)."
CC -!- FUNCTION: PLASMID PARTITION REQUIRE REP1, REP2, AND A CIS-ACTING
CC DNA SEQUENCE (KNOWN AS STB). REP 1 MAY ACT BY INTERCALATING IN
CC THE YEAST NUCLEAR MATRIX AND BINDING STB EITHER DIRECTLY OR VIA
CC REP2.
CC -!- SIMILARITY: TO THE P GENE PRODUCT OF PSR1.
CC
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CC
CC EMBL: M18274; AAA35283.1;
DR InterPro; IPR008897; Yeast_TAF.
DR Pfam; PF05797; Yeast_TAF; 1.
KW Plasmid; Trans-acting factor.
SQ SEQUENCE 357 AA; 40752 MW; 7DF4C06359D4BA35 CRC64;

Alignment Scores:
Pred. No.: 1.41 Length: 357
Score: 94.00 Matches: 61
Percent Similarity: 29.72% Conservative: 53
Best Local Similarity: 21.25% Mismatches: 100
Query Match: 3.26% Indels: 73
DB: 1 Gaps: 12

US-09-771-161A-2 (1-1669) x REPI_ZYGBA (1-357)
QY 275 TTCTATATTTCTTAATCATCTCCAGTTAAAGTGATATATATTTATGATTCATTACAG 334
DB 95 PheGlnAspHisLysLeuPheAlaAsnLysAsnAlaAspValTyValGluArgLeuGln 114
QY 335 TTACAGAGGTGTTCAAGTGCCATTCCTATGTCAGCAAGAAAGAAATGGAATTATCTGTG 394
DB 115 ---AsnAlaIleAlaSerGlyIleLysLeuProGluSerLysLys- 128
QY 395 AACATACCTGTAATCATGTCCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 454
DB 129 ---AsnGlu 130
QY 455 AATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCCACAGACAATGATTTTGA 514
DB 131 ArgLeuGlyGlnProLysLysThrLysAsnValThrLysGluIleGluThrPheIle 150
QY 515 -----TCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGTCTCT 562
DB 151 AspAlaThrAsnAlaArgLysGluLeuAspGluTyPheArgLysLeuGln----- 167
QY 563 GGAAATCACAGTGGGATAGACCACTTCTGGATCTCAAAGGGCTGCATCTGTGATCAC 622

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Db 168 -----AspGlyThrLeuThrGlyAspLeuGluGlyGlyLeuCysLysVal 182
QY 623 AAGACCTCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAATCTCAGAA 682
Db 183 LysThrLeuIleSerCysLysAlaLeuPhe-----GlyGlyHisThrGln 197
QY 683 CGTCTGCAG-----CCTGGTATAGCCAGCAGCTGGATCCAGAGCAAAAGGAGAC 733
Db 198 GluLeuGlnPheMetAlaThrAsnValArgLysValTrpIle-----GlyGlu 213
QY 734 ATTGTGAACCAATACAGAACGCTGCTTAACCAAGTCGCTAGATGCCCTCTCTGTCCAGG 793
Db 214 IleValCysGlyMetVal-----SerAsnLysAsnAlaIleAspAsn 228
QY 794 GACTTGATCATCAAGAGGACTATGAACTTGTAGTACCAAGCCTTACAGAGCACTCAAAA 853
Db 229 AspLeu-----GluGluGluGluArgAsnAlaSerGlyGluGlnThrThrAlaArg 246
QY 854 GTCAGA---CAATTACTAGACACTACTGAC----- 880
Db 247 GluGluSerGluAlaLeuAspThrThrSerAsnGlyLeuAspAlaLeuAsnThrGlnIle 266
QY 881 -----ATCAAGGAGAGAAGATTCCCAAGTTATTAGTACAAAATTCGAAGATAACAA 934
Db 267 AsnAlaIleGluThrGluGluSerPheTrpGluAlaIleArgAlaLeuHisGlnGlu--- 285
QY 935 CAAATGGGTCTTCAGCCTTACCCGAAATACTTGTGTCTTCTAGATCCACTTTTAAAT 994
Db 286 -----LeuArgThrSerProThrGlnLeuGluGlyCysArgLysAlaValPhe 302
QY 995 TTACTTCAAATAAAGCATGTAAGTGAAGTGTGTTTTCAGAGAAGAAATGTGTTTCATAAA 1054
Db 303 LeuLeuGlyHisLysLysIleLeuGlnThr-PheThrLysGlnLysAspThrAlaArgAl 322
QY 1055 GGATATTTATATCTCTGTT 1073
Db 322 aLeuPheTyIleAsnLeu 328

RESULT 8
BIR2_MOUSE STANDARD; PRT; 612 AA.
ID_BIR2_MOUSE Q82210; O08864;
AC Q82210; O08864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2 (inhibitor of apoptosis
DE protein 2) (MIAP2) (MIAP-2).
DE BIRC2 OR BIRC3 OR IAP2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=8548810;
RA Rothe W., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503 (1997).
CC -!- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -!- SUBUNIT: Interacts with SMAC and with PRS25; these interactions

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QY 602 AGGGCTGCATTCGTGATCACAGACCACTCATCTCTTACGACATATAAATCCACTC 661
D 603 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 575 LysCysPheMetAsnSerAsnArgTyrLeuArgLeuLeuSerThrArgIleLeuLeu 594
QY 662 -----TCACTGCAGGAACACGACGCTGCAGCCTGGTATGCCAGAGTGG 712
D 663 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 595 PheAsnIleSerAspSerHisAsnSerGluAspGluHisThrAlaThrLeuIlePhe 614
QY 713 ATCCAGAGCAAAAGGAGACATTTGTG-----AACCAAAATG 748
D 714 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 615 LeuGlnSerGlnLeuLeuProValValLysGluAsnLeuValIleAlaTrpThrGlnLeu 634
QY 749 ACAGAGCGCTGCTTAACGAGTCGCTAGATGCCCTTCTGTCCAGG-----CACTTGATC 802
D 750 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 635 ThrLeuThrThrSerAsnAspValPheAspThrLeuLeuLeuLysLeuIleAspIlePhe 654
QY 803 ATGAAAGAGGACTATCACTTCTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAA 862
D 804 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 655 AsnSerAspAspTyrSerLeuArgIleMetThrLeuGlnIleLysAsnMetAlaLys 674
QY 863 TTACTAGACACTACTGACATCCAA---GGAGAAGAATTTGCCAAAGTTATAGTACAAAAA 919
D 864 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 675 IleLeuLysLysThrProTyrGlnLeuLeuSerProIleLeuProValLeuLeuArgGln 694
QY 920 TTGAAGATAAC-----AAACAATGGCTTTCAGCCTTACCGGAATATCTGTG 970
D 921 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 695 LeuGlyLysAsnLeuValGluArgLysValGlyPheGlnAsnLeuIleGluLeuGly 714
QY 971 GTTCTAGATCACCCTTTAAATTTACTTCAAAATAAAAGCATGTAGTGTCTTTT 1030
D 972 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 715 TyrSerSerLysThrIleLeuAspIlePheGlnArgTyrIleIleProTyrAlaIle 734
QY 1031 CAA-----CAAGAATGTCTTTTCATAAAAGGATATTATATCTCTGT 1072
D 1032 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 735 GlnTyrLysSerAspValLeuSerGlnIleAlaLysIle-----MetCys 749
QY 1073 TCGTTTGACTTTTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGAG 1123
D 1074 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 750 AspGlyAspThrSerLeuIleAsnGlnMetLysValAsnLeuLeuLysLys 766

RESULT 11
DPOZ HUMAN
ID DPOZ HUMAN STANDARD; PRT: 3130 AA.
AC O60673; O43214;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA polymerase zeta catalytic subunit (EC 2.7.7.7) (hREV3).
GN REV3L OR POLZ OR REV3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Fetal brain;
RX MEDLINE=92824025; PubMed=9618506;
RA Gibbs P.E.M., McGregor W.G., Maher V.M., Nisson P., Lawrence C.W.;
RT "A full-length cDNA of hREV3 is predicted to encode DNA polymerase
RL zeta for damage-induced mutagenesis in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6876-6880(1998).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Bone marrow, and Leukocyte;
RX MEDLINE=99202263; PubMed=10102035;
RA Lin W., Wu X., Wang Z.;
RT "A full-length cDNA of hREV3 is predicted to encode DNA polymerase
RL zeta for damage-induced mutagenesis in humans.";
RN [3]
RP SEQUENCE FROM N.A.
RA Murakumo Y., Rasio D., Roth T., Negrini M., Croce C.M., Fishel R.;

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Alignment Scores:

```

RT "Cloning and characterization of hREV3, the human homolog of S.
RL cerevisiae REV3.";
RN Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 79-3130 FROM N.A.
RA Roth T., Rasio D., Murakumo Y., Negrini M., Croce C.M., Fishel R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 79-3130 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99126315; PubMed=9925914;
RA Morelli C., Mungall A.J., Negrini M., Barbanti-Brodano G., Croce C.M.;
RT "Alternative splicing, genomic structure, and fine chromosome
RL localization of REV3L.";
RL Cytogenet. Cell Genet. 83:18-20(1998).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA} (N).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -!- DOMAIN: Its C-terminal part could serve as the catalytic domain
during nucleotide polymerization, while its N-terminal part could
provide sites for protein-protein interactions with other factors
during translation DNA synthesis.
CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.

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EMBL; AF058701; AAC24357.1; -
DR EMBL; AF071798; AAC24009.1; -
DR EMBL; AF157476; AAD40184.1; -
DR EMBL; AF179428; AAG09402.1; -
DR EMBL; AF179429; AAG09403.1; -
DR EMBL; AF035537; AAB88486.1; -
DR EMBL; AF078695; AAC28460.1; -
DR Genbank; HGNC:9568; REV3L.
DR MIM; 602776; -
DR GO; GO:0003894; F:zeta DNA polymerase activity; TAS.
DR GO; GO:0006261; P:DNA dependent DNA replication; TAS.
DR InterPro; IPR006172; DNA pol_B.
DR InterPro; IPR006134; DNA pol_B dom.
DR InterPro; IPR006133; DNA pol_B_exo.
DR InterPro; IPR004578; Pol2.
DR Pfam; PF00136; DNA_pol_B; 1.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLB; 1.
DR TIGRFAMs; TIGR00592; pol2; 1.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; DNA repair; Nuclear protein; Zinc-finger; Polymorphism.
FT ZN_FING 3042 3057
FT ZN_FING 3086 3104
FT ZN_FING 231 231
FT VARIANT 231 231
FT VARIANT 389 389
FT VARIANT 1540 1540
FT VARIANT 2607 2607
FT VARIANT 3064 3064
FT CONFLICT 237 237
FT CONFLICT 1156 1156
FT CONFLICT 3130 3130
SQ SEQUENCE 3130 AA; 352782 MM; 1C0700900F10BB14 CRC64;

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Pred. No.: 4.29 Length: 3130
Score: 89.50 Matches: 68
Percent Similarity: 32.11% Conservatives: 28
Best Local Similarity: 22.74% Mismatches: 116
Query Match: 3.11% Indels: 87
DB: 1 Gaps: 14

US-09-771-161A-2 (1-1669) x DPOZ_HUMAN (1-3130)
QY 350 AGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTCTGACATACCTGTAAT 409
Db 1631 SerCysTyrSerLeuGluAspSerLeuSerProGluHisAsnTyrAsnPheAspIleAsn 1650
QY 410 CATGGTCCACAGAGGAATCATGT-----GGATCCTCTCAGCTCCATGAAAT 457
Db 1651 ThrIleGlnThrGlyPheCysSerPheTyrSerGlySerGlnPheValProAlaAsp 1670
QY 458 AGTGGTTCCTGAACTCAAGGTCCTCCAGCTCCTCAAGAC----- 502
Db 1671 GlnAsnLeuProGlnLysPheLeuSer---AspAlaValGlnAspLeuPheProGlyGln 1689
QY 503 -----AATGATTTTATCTAGAAAAGCTCAAGACTGTATTATGACAGCTG 550
Db 1690 AlaIleGlnLysAsnGluPheLeuSerHisAspAsnGlnLysCysAspGluAspLys 1708
QY 551 CATCACTGTCTCGAATACACAGTTGG----- 577
Db 1709 HisHisThrThrAspSerAlaSerTyrIleArgSerGlyThrLeuSerProGluIlePhe 1728
QY 578 ---GATAGACCAATTCCTGATCTCAAGGCGGTCATCTGTGATCAAGACCACTCCA 634
Db 1729 GluLysSerThrIleAspSerAsnGluAsnArgHisAsnGlnTyrLysAsnSer 1747
QY 635 TGCTCTTCAGCAATAAATCACTCACTCAACTCGACGGAACATCA----- 679
Db 1748 -----PheHisProLeuThrThrArgSerAsnSerIleMetAspSerPhe 1762
QY 680 -----GAAGCTCTG----- 688
Db 1763 CysValGlnGlnAlaGluAspCysLeuSerGluLysSerArgLeuAsnArgSerVal 1782
QY 689 -----CAGCTGGTATAGCCAGCGTGATCCAGAGC 721
Db 1783 SerLysGluValPheLeuSerLeuProGlnProAsn---AsnSerAspTyrIleGlnGly 1801
QY 722 AAAGGGAAGACATGTGTAACCAATGACAGAGCCCTGCTTAACCAAGTCGCTAGATGCC 781
Db 1802 HisThrArgLysGluMetGlyGlnSerLeuAspSerAla---AsnThrSerPheThrAla 1820
QY 782 CTTCTGTCCAGG-----GACTTG-----ATCATGAAAGAGGACTATGAACCTGTT 826
Db 1821 IleLeuSerSerProAspGlyGluLeuValAspValAlaCysGluAspLeuGluLeuTyr 1840
QY 827 AGTACCAAG-----CCTACAGGACCTCAAAAGTCACAGCAATCTACTA 868
Db 1841 ValSerArgAsnAsnAspMetLeuThrProAspSerSerProArgSerThrSer 1860
QY 869 GACACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAGAAAT 928
Db 1861 SerProSerGlnSerLysAsnGlySerPheThrProArgThrAlaAsnIleLeuLys--- 1879
QY 929 AACAAACAAATGGGCTCTTACGCTTACCCGGAATACTTGTGGTTCTAGATCACCATCT 988
Db 1880 -----ProLeuMetSerProProArgGluGluIle 1890
QY 989 TTAATTTACTTCAAAATAAAGCATGTAGTACTGCTTTTTCAGAGAAATGTGT 1045
Db 1891 MetAlaThrLeuLeuAspHisAspLeuSerGluThrIleTyrGlnGluProPheCys 1909

RESULT 12
ANCL MOUSE
ID ANCL_MOUSE STANDARD; PRT; 1944 AA.
AC P53995; Q8BP33; Q8C772;
```

```
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Anaphase promoting complex subunit 1 (APC1) (Cyclosome subunit 1)
DE (Protein Tsg24) (Mitotic checkpoint regulator).
GN ANAPC1 OR TSG24 OR MCPR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CBA; TISSUE=Testis;
RX MEDLINE=95014147; PubMed=7929068;
RA Starborg M., Brundell E., Gell K., Hosoe C.;
RT "A novel murine gene encoding a 216-kDa protein is related to a
RT mitotic checkpoint regulator previously identified in Aspergillus
RT nidulans."; RT
RL J. Biol. Chem. 269:24133-24137(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb, and Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmerond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -i- FUNCTION: Component of the anaphase promoting complex/cyclosome
CC (APC/C), a cell cycle-regulated ubiquitin ligase that controls
CC progression through mitosis and the G1 phase of the cell cycle (By
CC similarity).
CC -i- SUBUNIT: The APC/C is composed of at least 11 subunits (By
CC similarity).
CC -i- TISSUE SPECIFICITY: Abundantly expressed in proliferating
CC fibroblasts, juvenile testis, adult brain and epididymis.
CC -i- DEVELOPMENTAL STAGE: Uniformly expressed throughout interphase of
CC the cell cycle.
CC -i- SIMILARITY: Contains 4 PC repeats.
CC
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CC
CC EMBL; X80169; CAA56450.1; --
DR
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DR EMBL; AK052404; BAC34976.1; -.
DR EMBL; AK077847; BAC37032.1; -.
DR MGI; A55117; A55117.
DR MGI; MGI:103097; Mcpr.
DR InterPro; IPR002015; APC_proteasome.
DR Pfam; PF01851; PC rep; 5.
KW UbL conjugation pathway; Cell cycle; Cell division; Mitosis; Repeat.
FT REPEAT 1297 1325 PC 1.
FT REPEAT 1366 1404 PC 2.
FT REPEAT 1467 1501 PC 3.
FT REPEAT 1520 1552 PC 4.
FT CONFLICT 112 112 Q -> A (IN REF. 2).
FT CONFLICT 348 349 GV -> AA (IN REF. 2).
FT CONFLICT 643 643 N -> K (IN REF. 2; BAC34976).
FT CONFLICT 1036 1036 H -> D (IN REF. 2; BAC34976).
SQ SEQUENCE 1944 AA; 216086 MW; 48F1BEF01053E6C3 CRC64;

Alignment Scores:
Pred. No.: 4.58 Length: 1944
Score: 89.00 Matches: 52
Percent Similarity: 37.56% Conservative: 25
Best Local Similarity: 25.37% Mismatches: 72
Query Match: 3.09% Indels: 56
DB: 1 Gaps: 10

US-09-771-161a-2 (1-1669) x ANCI_MOUSE (1-1944)
QY 326 TCATTACAGTACACAGTCTTTCAAGTGCCATT-----CACCTATGTGACAAAGAA 379
Db ThrLeuGlnAsnAlaThrThrSerSerLeuThrAlaHisLeuArgSerLeuSerLys 310
QY 380 ATGGAATTATCTCTGAACACTACTGTAATCAT-----GGTCCACAAGAGAA 427
Db GlyGluSerProValAlaSerProPheGlnAsnTyrSerSerIleHisSerGlnSerArg 330
QY 428 TCATGTGGATCTCTCAGCTCCATGAATAGTGGTGTCTCTCTGAACTTCAAGTCCCTG 487
Db SerThrSerSerProSerLeuHisSerArgSer----- 341
QY 488 CCAGCTCTCTCAAGCAATGATTTTTTATCTCAAGAAAGCTCAAGACTGTTATTTTATGAAG 547
Db ProSerIleSerAsnMetGlyValLeuSerArgAla----- 353
QY 548 CTGCATCACTGCTCT-----GGAATACAGATGGGATAGCACCATTCTGCATCTCAA 601
Db HisSerProAlaLeuGlyValHisSerPhe-----SerGlyAlaGln 367
QY 602 AGGGTGCATTCTGTGATCACAAGACCCTCCATGCTCTTTCAGCAATAATAATCACTC 661
Db ArgPheAsnLeuSerSerHisSerGlnSerProLysArgHisSerIleSerHisSerPro 387
QY 662 TCAACTGCAGGAACCTCAGAACGCTCTGCAGCCTGGTATAGCCAGCAGTGGATCCAGAGC 721
Db SerGlySerPheAsnAspSerPheLeuAlaPro----- 398
QY 722 AAAAGGGAAGACATTGTGTGAACCAATAGCAGAGGCTGCTTAAACAGTCGTAGATGCC 781
Db GluThrGluProIleVal-----ProGluLeuCysIle----- 409
QY 782 CTTCTGTCAGGACTGTATCATGAAGAGGACTATGAACCTTTAGTACCAAGCTTACA 841
Db AsHisLeuThrThrGluThrLeuProAsnIleArgGluLysAsnSer 425
QY 842 AGGACCTCAAAAGTCAGAAATTAATAGACACTACTGACACTCAAGAGGAATTTGCC 901
Db GlnAlaSerLysVal-----PheIleThrThrAspLeuCysGlyGlnLysPheLeu 442
QY 902 AAAGTTATAGTACAA 916
Db CysPheLeuValGlu 447

RESULT 13
PIAP_PIG
```

```
ID AC 062640; STANDARD; PRT; 358 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative inhibitor of apoptosis.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98162622; PubMed=9501011;
RA Stehlik C., de Martin R., Binder B.R., Lipp J.;
RT "Cytokine induced expression of porcine inhibitor of apoptosis
RL Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -!- SIMILARITY: Belongs to the IAP family.
CC -!- SIMILARITY: Contains 2 BIR repeats.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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DR EMBL; U79142; AAC39171.1; -.
DR PIR; JC5964; JC5964.
DR HSSP; Q13490; 1QBH.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT DOMAIN 193 283 CARD.
FT ZN_FING 311 346 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Alignment Scores:
Pred. No.: 4.91 Length: 358
Score: 88.00 Matches: 72
Percent Similarity: 33.33% Conservative: 47
Best Local Similarity: 20.17% Mismatches: 135
Query Match: 3.06% Indels: 103
DB: 1 Gaps: 18

US-09-771-161a-2 (1-1669) x PIAP_PIG (1-358)
QY 76 GATTTTCGAGGATGAAGCTCTGACAGACTGACAGAGAGGTAACCAATTAATATGAGCCAGA 135
Db AspAlaMetThrGluHisLeuArgHis----- 63
QY 136 TTCAAAGTCTGTGGTTNCTNCTAAAGTTATTTCGGTTC----- 171
Db PheProAsnCys-----ProPheLeuGlyAsnGlnLeuGlnAspSer 77
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QY 172 -----TACACTGCTCTTTCTCCTCAGTTATATGTTATATCTCAACTCTTTATATTCTT 225
Db 78 SerArgTyrThrValSerAsnLeuSerMetGlnThrTyrAlaAla-----Arg 93
QY 226 TTCCATGTAATTTTGTACAAACATATATAAATGTGTTAGATTGTATTTTACTTCTATAATTT 285
Db 94 PheLysThrPheCys-----AsnTyrProSerSerIleProVal-----His 107
QY 286 CTTAATCATCTCCAGTTAAAGTGTATATATATATTTATTTATTTATTTATTTATTTATTTATTT 345
Db 108 ProGluGlnLeuAlaSerAlaGlyPheTyrTyrMetGlyHisSerAspValLysCys 127
QY 346 TTCAAGTGCCATTACCTATGTGACAAAGAAATGGAATTATCTCTGAACATACCTGT 405
Db 128 PheCysCys-----AspGlyGlyLeu----- 134
QY 406 AAATCATGTGTCACAGAGGAATCATGTGTGATCCTCTCAGCTCCATCAAAATAGTGGTTC 465
Db 135 ArgCysTrpGluSerGlyAspProTyrValGluHisAlaLys-----TrpPhe 151
QY 466 TCTGAACTTCAAGTCCCTGCTCCTCAAGCAATGATTTTATCTAGAAAGC 525
Db 152 -ProArg---CysGluTyrLeuIleArgIleLysGlyGlnGluPheIleSerArg---Va 169
QY 526 TCAAGACTGTATTTTATGAAGCTGCATCATCTGCTCGGAAATCAACAGTTGGGATAGCAC 585
Db 169 GlnAlaSerTyr-----ProHisLeuLeuGlnLe 180
QY 586 CATTTCTGGATCTCAAGGCTGCATTTCTGTGATCAACAGCACCTCCATGCTTTCAGC 645
Db 180 uLeuSerThrSerAsp----- 185
QY 646 AATAATAAATCCACTCTCAACTGCAGGAATCTCAGACGCTCTCAGCTGGTATAGCCCA 705
Db 186 -----AsnPro-----GluAspGluAsnAlaGluProProAsnAspLe 198
QY 706 GCAGTGTGATCAGACGAAAGGAAAGACATTTGTGTGAACCAATGACAGAACCTGCTTAA 765
Db 198 uSerLeuIleArgLysAsnArgMetAlaLeuPheGlnHisLeuThr-----CysValle 216
QY 766 CCAGTCTGCTAGATCCCTCTCTCCAGGACTGTGATCATGAAGAGGACTATGAACCTGT 825
Db 216 uProIleLeuAspSerLeuLeuIleAlaArgValIleSerGluGlnGluHisAspValII 236
QY 826 TAGTACCAAGCCTACAGAGACCTCAAAGTACAGCAATTTACTAGACACTACTGACATCCA 885
Db 236 eLysGlnLysThrGlnThrSerLeuGlnAlaArgGluLeuIleAspIleLeuVally 256
QY 886 AGGAGAAAGATTTTCCAAAGTTATAGTACAAAAATTTGAAAGAT-----AA 930
Db 256 sGlyAsnTyrAlaAlaThrIlePheLysAsnSerLeuGlnGluIleAspProMetLeuTy 276
QY 931 CAACAAATGGCTTCTCAG-----CCTTACCCGGAATATCTTGTGGT 972
Db 276 rLysHisLeuPheValGlnGlnAspIleLysTyrIleProThrGluAsnValSerAspLe 296
QY 973 TTCTTAGATCACCATTCTTAAATTTTACTTCAAAATTAAGATGTAAGTACTGTTTTCAT 1032
Db 296 uSerMetGluGlnLeuArgLeuGlnGlnGluArgThrCysLysValCysMetAs 316
QY 1033 AGAAGAAATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072
Db 316 pLysGluValSerIleValPheIleProCysGlyHisLeuValValCys 332
RESULT 14
T2FA_XENLA
ID T2FA_XENLA STANDARD; PRT; 524 AA.
AC Q04870;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Transcription initiation factor IIF, alpha subunit (TFIIF-alpha)
```

(Transcription initiation factor RAP74).

GN RAP74.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93126122; PubMed=1480494;

RA Gong D.-W., Hasegawa S., Wada K., Roeder R.G., Nakatani Y., Horikoshi M.;

RT "Elucidation of three putative structural subdomains by comparison of primary structure of Xenopus and human RAP74.";

RL Nucleic Acids Res. 20:6736-6736(1992).

CC -!- FUNCTION: TFIIF IS A GENERAL TRANSCRIPTION INITIATION FACTOR THAT BINDS TO RNA POLYMERASE II AND HELPS TO RECRUIT IT TO THE INITIATION COMPLEX IN COLLABORATION WITH TFIIB. IT PROMOTES TRANSCRIPTION ELONGATION.

CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.

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CC -----

DR EMBL; Z17426; CAA78999.1; -.

DR PIR; S35551; S35551.

DR TRANSFAC; T02171; -.

DR InterPro; IPR008851; TFIIF-alpha.

DR Pfam; PF05793; TFIIF-alpha; 1.

KW Transcription regulation; DNA-binding; Nuclear protein.

SQ SEQUENCE 524 AA; 58699 MW; 8CF3A74A3BF77BB0 CRC64;

Alignment Scores:

Pred. No.:	5 07	Length:	524
Score:	88.00	Matches:	54
Percent Similarity:	33.63%	Conservative:	22
Best Local Similarity:	23.89%	Mismatches:	90
Query Match:	3.06%	Indels:	60
DB:	1	Gaps:	9

US-09-771-161A-2 (1-1669) x T2FA\_XENLA (1-524)

QY 398 ATACCTGTAAATCANGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAAT 457

Db 290 LeuProGlyLysIleLysProAlaLysGluGluGluGlyProLysGlyLeuAspGluGln 309

QY 458 AGTGGTCTCTCTGAAACTTCA----- 478

Db 310 SerGluSerGluSerGluSerGluGluLysAlaGluGluGluGluGluGluGlu 329

QY 479 AGGTCTCTGCGAGCTCCTCAAGACAAATGATTTTTTATCTAGAAAAGCTCAAGACTGTTAT 538

Db 330 LysLysAlaProThrProGlnAspAsnLys-----LysLysLysLysGlyAsp----- 345

QY 539 TTTATGAAGCTGCATCCTGCTCTGGAATATCACAGTTGGGATAGCACCATTCTTGGATCT 598

Db 346 -----SerSerAspGluSerGluThrSerGluAspSerAspIleAspGlyAla 361

QY 599 CAAAGGGCTCATTTCTGTGATCACAAGACCACCTCCA----- 634

Db 362 SerSerLeuPheMetGlnLysLysThrProProLysLysAspLysLysGlyGly 381

QY 635 ---TGCTCTTCAGCAATAATAAAT-----CCACTCTCAACTGCAGGAAC 676

Db 382 SerAsnSerSerSerArgGlyAsnSerArgProGlyThrProSerProAspThrGlyAsn 401

QY 677 TCAGAACGTCCTGACGCTGGTATAGCCAGCAGCTGGATCCAGGAGAAAGGGAACATT 736  
Db 402 ThrSerSerThrLeuArgAlaalaaserLysLeuGluGlnSerLysArgGlyThrVal 421  
QY 737 GTGAACCAATCACAGACGCTGCCTTAACACAGCTCGCTAGATGCC----- 781  
Db 422 SerAsn-----ThrProAlaalaLysArgLeuLysMetGluAlaGlyProGlnAsnThr 439  
QY 782 -----CTTCTGTCCAGGACTTG 799  
Db 440 SerGlyLysSerThrProGlnProGlnSerGlyLysSerThrProSerSerGlyAspIle 459  
QY 800 ATCATGAAGAGAC-----TATGACTGTGTAGTACCAAGCTACAGGACCTCAAA 853  
Db 460 GlnLeuThrGluGluAlaValArgArgTyrLeuThrArgLysProMetThrThrLysAsp 479  
QY 854 GTCAGACAATTACTAGACACT-----ACTGACATCCAGGAGAGAATTTCCTCAAGTT 907  
Db 480 LeuLeuLysLysPheGlnThrLysLysThrGlyLeuSerSerGluGlnThrValAsnVal 499  
QY 908 ATAGTACAAAATTGAAA 925  
Db 500 LeuAlaGlnIleLeuLys 505  
RESULT 15  
SNEI\_HUMAN  
ID SNEI\_HUMAN STANDARD; PRT; 8797 AA.  
AC Q8NF91; Q8NF97; Q8TQCP1; Q8WWM6; Q8WWM7; Q8WKF6; Q96N17;  
AC Q9COA7; Q9H525; Q9H536; Q9NS316; Q9NU50; Q9UJ06; Q9UJ07; Q9ULF8;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Nesprin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic  
DE nuclear envelope protein 1) (Syne-1) (Myocyte nuclear envelope protein  
DE 1) (Wyne-1) (Enaptin).  
GN SYNE1 OR WYNE1 OR KIAA0796 OR KIAA1756 OR KIAA1262.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), CHARACTERIZATION, AND  
RP MUTAGENESIS OF 8758-LEU-CYS-8763.  
RC TISSUE=Heart, Spleen, and Testis;  
RX MEDLINE=21652858; PubMed=11792814;  
RA Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G.,  
RA Weissberg P.L., Ellis J.A., Shanahan C.M.;  
RT "Nesprins: a novel family of spectrin-repeat-containing proteins that  
RT localize to the nuclear membrane in multiple tissues.";  
RL J. Cell Sci. 114:4485-4498(2001).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.  
RC TISSUE=Heart, Spleen, and Testis;  
RX MEDLINE=22296983; PubMed=12408964;  
RA Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;  
RT "The nesprins are giant actin-binding proteins, orthologous to  
RT Drosophila melanogaster muscle protein MSP-300.";  
RL Genomics 80:473-481(2002).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.  
RA Braune S., Abraham S., Padmakumar V., Tunggal B., Noegel A.A.,  
RA Kornebaum E.;  
RT "The longest isoform of enaptin/Syne-1, a nuclear envelope associated  
RT protein, binds actin cytoskeleton via the alpha-actinin-like actin-  
RT binding domain.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).  
RA Zhang Q., Shanahan C.M.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Almeida J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M.,

Tracey A., Williams S.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 1-856 FROM N.A.  
RC TISSUE=Kidney;  
RA Gough I., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.;  
RT "Golgi localization of syne-1.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.  
RC TISSUE=Adrenal gland, and Testis;carcinoma;  
RA Nimmiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
RA Furuya I., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,  
RA Otsuka N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato K., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
RA Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,  
RA Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,  
RA Nagai K., Isogai T.;  
RT "NED0 human cDNA sequencing project.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE OF 443-8797 FROM N.A. (ISOFORM 5).  
RC TISSUE=Brain;  
RX MEDLINE=21082932; PubMed=11214970;  
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XIX.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 7:347-355(2000).  
RN [9]  
RP SEQUENCE OF 743-8797 FROM N.A. (ISOFORM 6).  
RC TISSUE=Brain;  
RA Anseorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).  
RC TISSUE=Brain;  
RX MEDLINE=20039619; PubMed=10574462;  
RA Nagase T., Iehikawa K.-I., Kikuno R., Hirose M., Nomura N.,  
RA Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:337-345(1999).  
RN [11]  
RP SEQUENCE OF 6922-8797 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99087487; PubMed=9872452;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,  
RA Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XI.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:277-286(1998).  
RN [12]  
RP REVISIONS.  
RC TISSUE=Brain;  
RX MEDLINE=22158633; PubMed=12168954;  
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
RT curation of 330 KIAA cDNA clones.";  
RL DNA Res. 9:99-106(2002).  
RN [13]  
RP SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=21659781; PubMed=11801724;  
RA Mislow J.M.K., Kim M.S., Davis D.B., McNally E.M.;  
RT "Wyne-1, a spectrin repeat transmembrane protein of the myocyte inner  
RT nuclear membrane, interacts with lamin A/C.";  
RL J. Cell Sci. 115:61-70(2002).  
RN [14]  
RP SEQUENCE OF 8406-8797 FROM N.A.



Search completed: March 29, 2004, 14:20:36  
Job time : 44.5 secs

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 29, 2004, 14:14:57 ; Search time 87.5 Seconds

(without alignments)  
12036.569 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

Sequence: 1 acctagttattaccagata.....caacagcctgtgtgtaaaa 1669

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2.1/USPTO scool\_p/US09771161/runat\_29032004\_124825\_13679/app\_query.fasta\_1.1863  
-DB=SPTREMBL\_25 -QFWT=fastcan -SUFFIX=n2p.ispt -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09771161 @CGN 1.1.95 @runat\_29032004\_124825\_13679 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: sp\_archea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rotent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvrius.\*  
16: sp\_bacteriap.\*  
17: sp\_archeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	335	11.6	584 13 Q8JHU4	Q8JHU4 brachydanio

ID	Q8JHU4	PRELIMINARY;	PRT;	584 AA.
AC	Q8JHU4;			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
GN	Protein kinase RICK.			
OS	RICK.			
OC	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98241596; PubMed=9575181;			
RA	Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;			
RT	"RICK", a novel protein kinase containing a caspase recruitment domain,			
RT	interacts with CIARP and regulates CD95-mediated apoptosis.";			
RL	J. Biol. Chem. 273:12296-12300(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,			
RA	Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.;			

#### ALIGNMENTS

#### RESULT 1

Q8JHU4

ID Q8JHU4 PRELIMINARY; PRT; 584 AA.

AC Q8JHU4;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

GN Protein kinase RICK.

OS RICK.

OC Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP MEDLINE=98241596; PubMed=9575181;

RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;

RT "RICK", a novel protein kinase containing a caspase recruitment domain,

interacts with CIARP and regulates CD95-mediated apoptosis.";

RL J. Biol. Chem. 273:12296-12300(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Muto A., Ruland J., McAllister-Lucas L.M., Lucas P.C., Yamaoka S.,

Chen F.F., Lin A., Mak T.W., Nunez G., Inohara N.;





Db 564 -----ThrProSerSerLeuLeuPheile 572

QY 656 CCACCTCACTCAAGTCAGGA-----AACTCAGAAAGCTCTG----- 688

Db 573 ProThrMetGluThrGlyLeuTyrrAsnArgPheLeuLeuAsnThrPheArgLeuProAla 592

QY 689 -----CAGCCTGGTATAGCCAGAGCGTGGATCCAGAGCAAAAGGAGACATTTGTGAAC 742

Db 593 AlaTrpGlnAspValPheAlaGluGluysValArgAla-----AspAspLeuPheAsn 610

QY 743 CAATGACAGAGCGCTGCTTAAACAGTCGCTAGATGCCCTTCTGCCAGGACCTGATC 802

Db 611 GluLeuSerMetArgPheAlaGlnMetAlaLeu----- 621

QY 803 ATCAAGAGGACTATGAACCTTGTAGTACCAAGCCTCACAAGGACCTCAAAAGTCAGACAA 862

Db 622 -----PheLeuLysAspSerProThrGlu----- 629

QY 863 TTACTAGACACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTG 922

Db 630 ---ValLysLeuThrAspThrGlnLysLysGluPheAsnArgValPheThrGlnLeuLeu 648

QY 923 AAAGATAACAACAATGGTCTTCCAGCTTACCCGGAATACTT---GTGGTTTCTAGA 979

Db 649 LysAspThrAspGlnLeuGly-----AsnAspAspLeuLeuGlyValValLysArg 665

QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCACAGAGAA 1039

Db 666 -----TyrGlyValLeuThrAlaArg 672

QY 1040 ATGTGTTTCAATA-----AAAGA----- 1057

Db 673 IleCysCysIlePheSerAlaIleAspLysGlyThrMetArgMetGluThrProGluVal 692

QY 1058 -----TATTATATCTCTGTTGCTGCTGCTT 1084

Db 693 TyrCysSerAspAlaHisPheLysAlaAlaLeuAlaIleValLeuCysCysPheGluHis 712

QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCT 1114

Db 713 SerLysLeuValSerThrSerValLysSer 722

RESULT 3

Q81JEB PRELIMINARY; PRT; 1309 AA.

AC Q81JEB;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Hypothetical protein.

GN PF10\_0250.

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3D7;

RX MEDLINE=22255705; PubMed=12368864;

RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

RA Chan M.-S., Nene V., Shallow J.J., Suh B., Peterson J., Angiuoli S.,

RA Perle M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., R.W.,

RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

RA Fraser C.M., Barrell B.;

RT "Genome sequence of the human malaria parasite Plasmodium

RT falciparum."

RL Nature 419:498-511(2002).

DR EMBL; AE014833; AN35447.1; --

KW Hypothetical protein.

SQ SEQUENCE 1309 AA; 158469 MW; 5FF6811DE127D910 CRC64;

Alignment Scores:

Pred. No.: 0.449 Length: 1309

Score: 101.50 Matches: 82

Percent Similarity: 38.46% Conservative: 73

Best Local Similarity: 20.35% Mismatches: 143

Query Match: 3.52% Indels: 105

DB: 5 Gaps: 18

US-09-771-161A-2 (1-1669) x Q81JEB (1-1309)

QY 176 CTGCTTTTCTCCTCAGTTATATATATCTCAACTCTTTATATTTCTTCTCC----- 229

Db 46 LeuCysTyrrAspLysMetIleMetPheTyrCysAsnThrPheAspTyrLeuLysAspAsn 65

QY 230 -----ATGTATTTTGTACAAACA-----TATAAAATGTTGTAGATTGTA 268

Db 66 ValValIleCysIleAspThrPheLeuGlnThrLysLysTyrMetLeuLysLysLeuIle 85

QY 269 TTTTACTTCTATAATTTCTCAATCATCTCCAGTTAAAGTGTATATATATTTATGATTCA 328

Db 86 ValAspLysLysAsnPheValTyrIleLys-----TyrGluTyrPheTyrLys 101

QY 329 TTACAGTTACAGAGTGTTCAGT---GCCATTACCTATGTGAC----- 370

Db 102 IleLysLeuSerSerTyrSerThrAspHisIleAsnIleCysAspLysIleCysAspAsp 121

QY 371 ---AAGAAAGAAATGGAATTATCTCGAATATCTCGAATATCTGTAATCATGTTCCACAAAGGAA 427

Db 122 GluLysAsnLysLysLys-Tyr-----IleMetLysAsnAs 133

QY 428 TCATGTGATCTCTCAGCTCCATCCATGAAATAGTGTCTCTGAAACTTCAAGGTCCTCG 487

Db 133 nHisIleAspAsn----- 137

QY 498 CCAGCTCTCTCAAGACAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAG 547

Db 138 -----PheIleAsnLysLeuLysLysPheAsnAsnGluAs 149

QY 548 CTGCATCACTGTCCTGGAA---ATCACAGTTGGGATAGCACCATTTCTCGATCTCAAAGG 604

Db 149 nCysTyrLeuIlePheGlnGlyValAspGlnAsnIleTyrThrIleLeuLysGlnAsnAs 169

QY 605 GCTGCATCTGTGATCAAGAACCACTCAATCTCTTACAGCAATAATAATAATCACTCTCA 664

Db 169 nLeuAsnArgile-----Tyr-IlePheLeuAsnAspIleAsnIleAs 184

QY 665 ACTGCAGGAATCTCAGACGCTGCGAGCTGTATAGCCACAGCTGGATCCAGAGCAAA 724

Db 184 snLeuAsnLysIleAsnThrHis-----TyrHisValIleMet-CysAsnTyrThr 200

QY 725 AGGGAAGACATTTGTAACCAATATGACAGAAGCTGCTTAACACAGTCGCTAGATGCCCTT 784

Db 201 LysGluAsnIleAsnLeuIleLysTyrTyrTyrGluLysGluLysGlnTyrVal 220

QY 785 CTGTCAGGAGCTTCATCATGAAGAGGACTAT----- 817

Db 221 GlnGlnAsnAspGluIleAsnGlnGluAspTyrGlnGluArgValMetAsnLeuTyrAsn 240

QY 818 GAACTGTGTAGTACCAAGCCTACAGGACCTCAAAGTACAGCAATTTACTAGACTACT 877

Db 241 GluCysLeuAsnAsnGluLysThrLysGluGluValValLysGluIleSerGluGluLys 260

QY 878 GACATCCAGGAGAA-----CAATTTTGCCAAA 904

Db 261 GluLysHisAsnGlnHisIleLysAsnSerAsnThrLysAspGluLysGluPheAlaLeu 280

QY 905 GTT-----ATAGTACAAAATTTGAAA---GATAACAAAATGGTCTTT 946

Db 281 IleTyrValPheTyrLeuLeuIleGluSerLeuLysTyrIleAsnGlnTyrTyrIle 300

QY 947 ---CAGCCTTACCCGGAATATCTTGGTTTCTAGATCACCATCTTTAATTTACTTCA 1003

301 CysAsnThrPhePheLeuLysIleValLysSerPheSerArgHisPheAsnIleMetAsn 320  
 1004 AATAAAGCANGTAAGTACTGTTTCAAGAAGAAATGTTTCAATAAAGGATATTTA 1063  
 321 AsnLys-----GlnAlaGluIle-----TyrIleLeuAsnTyrPhe 332  
 1064 TATCTCTGTTGCTTGCATTTTATATAAATCCGTGAGTA-----TT 1108  
 333 TyrPheTyrIleLeuSerLeuIleTyrAsnLysAspIle-LeuThrValAsnPheIleLeu 352  
 1109 AAAGCTTTATTAAGAGTCTTTCGGTAAATATTAGTCTCCCTCCATGACACATGATTT 1168  
 352 uSerIleTyrIleAspIlePheValAsnAsnLeuLysTyrLysAspIlePheLeuPh 372  
 1169 TTTTAAATTAACAAGTAAAGTTTGAATTTTCTCATAGTTCATTTTATGCTT 1228  
 372 ePheLysThrPheThrAsnGlnAsnLysGluLysCysIleLeuGlnLysTyrIleAsnLe 392  
 1229 C 1229  
 392 u 392

RESULT 4

Q811Z1 PRELIMINARY; PRT; 734 AA;  
 AC Q811Z1;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein, conserved.  
 GN PF00185C.  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP MEDLINE=2255708; PubMed=12369867;  
 RX Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies P., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphrey S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabbintowitsch E.,  
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G;  
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";  
 RL Nature 419:527-531(2002).  
 DR EMBL; AL034557; CAD49130.1;  
 DR GO; GO:0003824; P:catalytic activity; IBA.  
 DR InterPro; IPR000379; Ser\_estrs.  
 KW Hypothetical protein.  
 SQ SEQUENCE 734 AA; 83360 MW; 7ADBBD4F3D8F69EC CRC64;

Alignment Scores:

Pred. No.: 0.463 Length: 734  
 Score: 101.00 Matches: 76  
 Percent Similarity: 35.65% Conservative: 73  
 Best Local Similarity: 18.18% Mismatches: 163  
 Query Match: 3.51% Indels: 106  
 DB: 5 Gaps: 17

US-09-771-161A-2 (1-1669) x Q811Z1 (1-734)

QY 5 AGTTTATACCAGATATTTTATATATAGGTCATCTAGAACCATCTGCCATGTA 64  
 DB 249 SerValTyr---AspIleSerAsnIleAsnThrGlnLysLeuArgAsnMetPheIleLeu 267

QY 65 GGTAAATTGTTAGATTTTCGAGGATGAAGCTCTGAGACTGAGAGAGGTAACCAATTAAT 124  
 DB 268 AsnAsnThrGluLysLeuLysAspLysLeu-----LysGluLysIleGly 282  
 QY 125 ATGAGCCAGAGTCAAAAGTCTGTGTGTTCTAAAGTATTATCCCGTCTACACTGCTTTT 184  
 DB 283 AspLysGluLysLysAspLeuThrSerLysIleLysLysAsnGluLysValIleLeu 302  
 QY 185 CTTTCAGITATATGTTATATT-----CTCAACTCTTTATATTCTTTCCATGAT 235  
 DB 303 AsnAsnLysIleProLysLysLysAspValAsnSerTyrTyrSerSerMetGlu 322  
 QY 236 TTTGTA-----CAAAACATATAAATGTGTTAGATT-----GTATTTTACTTCTAT 280  
 DB 323 GlyIleGlySerSerThrGlnAsnIleCysLysValGlnSerSerThrGluSerSerTyr 342  
 QY 281 AATTTCCTTAATCATCTCCAGTTAAAGTGTATATATATTTATGTTATTCATTACAG----- 334  
 DB 343 AsnSerLeuThr-----SerValSerThrIleLeuAlaSerIleGluSerIle 358  
 QY 335 TTACAGAGTGTTCGAGTCCCATTCACCTATGTCACAGAGAAATGAATATATCTCTG 394  
 DB 359 MetLysGlyIleProAspSerAsnThrLeuCysGluLysAsnSerValGlnArgAsnAsn 378  
 QY 395 AACATACCTGTAAATCATCGTCCACAAGAG-----GAATCATGT----- 433  
 DB 379 AsnIleLysLysAsnAsnSerSerAsnGluIleTyrSerAspCysAsnProGlyTyrAsn 398  
 QY 433 ----- 433  
 DB 399 TyrTyrThrAsnAsnLysTyrAspAsnLeuTyrSerProAsnLysValThrSerIleAsn 418  
 QY 434 -----GGATCCTCTCTCAGCTCCAT 451  
 DB 419 AsnAsnLysMetAspGlnLysAsnLysAsnHisLysGlyAsnAsnLysSerSerAsnAsn 438  
 QY 452 GAAATAGTGTGTTCTCCTGAACTTCAAGTCTCCAGCTCCCTCAACACATGATTTT 511  
 DB 439 AsnAsnAsnAsnAsnAsnAsnAsnAsnSerSerSerSerSerSerSerSerSerMet 458  
 QY 512 ---TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCTCTCTGGAAT 568  
 DB 459 SerLeuAsnMetLysThrLeuSerSerTyrThrLeuLysAsnLysAsnThrGlnGlyAsn 478  
 QY 569 CACAGTTGGGATAGCACCACTTTCTGCATCTCAAAAGGCTGCATCTGTGATCAACAGACC 628  
 DB 479 SerAsnHisAspAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnSerAsnSerAsn 498  
 QY 629 ACTCCATGCTCTTCAGCAATAATAATCCACTCTCA-----ACTCGAGAAAC----- 676  
 DB 499 SerThrCysSerSerHisSerLysAsnAsnLeuSerTyrAsnAsnLysGlyAsnGlyLeu 518  
 QY 677 -----TCAGAACCTCTGCAGCTGTATAGCCAGCAGTGCAGTCCAG 718  
 DB 519 IleAsnThrAsnIleGlySerSerAsnValLysProAsnIle-----ArgIleLeuGln 536  
 QY 719 AGCAAAAGGAGAACATTT-----GTGAACCAATGACA 751  
 DB 537 ThrLysArgAsnSerTyrLysValAspLysValProArgIleAsnPheAspAsnMetLys 556  
 QY 752 GAAGCTGCTTAACCAAGTCCGTAGATGCCCTTCTGTCAGAGGACTTGATCATGAAAGAG 811  
 DB 557 LysAsnIleIleSerGluGlnIleAspSer-----AsnIleValTyrAsnAsn 572  
 QY 812 GACTATGAATCTGTTAGTACCAAGCCCTACAAAGGACCTCAAAAGTACAGACATTTACTAGAC 871  
 DB 573 SerTyrGluLeuIleLysAspGlyValTyrIleLysLysLysIleAsnAsnAsnAsn 592  
 QY 872 ACTACTGACATCCAGAGGAAGAAATTGGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931  
 DB 593 AsnAsnAsnIleLys---GlnGluSerSerSerSerLeuValTyrAsnAsnLeuSer----- 609

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QY 932 AAACAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACAATCTTTA 991
Db 610 -----SerProHisile 613
QY 992 AATTACTTCAAAATAAAGCATGTAAGTACTGTTTTCACAGAAATGTGT 1045
Db 614 ASnGlnGlyLeuAsnAsnThrArgTyrValSerCysGluLysAlaLysLeuCys 631

RESULT 5
Q9J861
ID Q9J861 PRELIMINARY; PRT; 461 AA.
AC Q9J861;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF76 CG30.
OS Spodoptera exigua nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10454;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20036646; PubMed=10567663;
RA IJkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
RA Goldbach R.W., Vlak J.M.;
RT "Sequence and organization of the spodoptera exigua multicapsid
RT nucleopolyhedrovirus genome."
RL J. Gen. Virol. 80:3289-3304 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA IJkel W.F., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
RA Goldbach R.W., Vlak J.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF169823; RAF33605.1; -.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 461 AA; 50820 MW; 6C062A3B43DD5D06 CRC64;

Alignment Scores:
Pred. No.: 0.484 Length: 461
Score: 100.50 Matches: 72
Percent Similarity: 36.23% Conservative: 53
Best Local Similarity: 20.87% Mismatches: 121
Query Match: 3.49% Indels: 99
DB: 12 Gaps: 13

US-09-771-161A-2 (1-1669) x Q9J861 (1-461)
QY 189 CAGTTATATGTTATCTCACTCTTATATTTCTTCCATGTTATTTGTACAAACAT 248
Db 27 GlnMetPheVal-----ProLeuPheLeuLeuAspGluCys-----LysHis 41
QY 249 ATAAATGTGT-----AGATTGTTATTTTACTTCT 278
Db 42 ValLeuCysLeuMetCysCysLysSerIleGlnAspGlyArgArgAlaIleThrCys 61
QY 279 ATAAATTCCTAATCATCTCCAGTTAAAGTGTTATATATTTATTTATTTACAGTTAC 338
Db 62 ProThrCysArgValSerSerGluLysLeuPheSerTyr-----PheTyrGlySerAsn 79
QY 339 AGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATGGAATATCTCTGAACA 398
Db 80 GlyLeuValLysPheAsnPheThrLeuAsnSerAlaGluLysPheAspMetArgAlaAsn 99
QY 399 TACCTGTAAATCATGTCCTCCACAGAGGAATCAT-----GTGATCTCTTC 443
Db 100 -----IleuAlaHisValAsnGluArgPheLysPheAlaIleValAspSerLeu 116
QY 444 AGCTCCATGAAATAGTGTCTCTCTGAAACTTCAAGGTCCTG----- 487
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## RESULT 6

```
Q9QZC6
ID Q9QZC6 PRELIMINARY; PRT; 589 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=kidney;
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSP; Q13490; IQBH.
DR GO: GO:0005622; C:intracellular; IEA.
```

DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.  
DR GO; GO:0006916; P:anti-apoptosis; IEA.  
DR InterPro; IPR001370; BIR.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS0089; ZF\_RING\_1.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 589 AA; 66777 MW; E6812FBE3EA34142 CRC64;

Alignment Scores:  
Pred. No.: 0.564 Length: 589  
Score: 100.00 Matches: 32  
Percent Similarity: 42.54% Conservative: 25  
Best Local Similarity: 23.88% Mismatches: 61  
Query Match: 3.47% Indels: 16  
DB: 11 Gaps: 3

US-09-771-161A-2 (1-1669) x Q9QZC6 (1-589)

QY 713 ATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAGCCCTTACCAGTCG 772  
DB 432 IleArgLysAsnArgMetalalaLeuPheGlnLeuThr-----CysValIleProIle 449  
QY 773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATCAAGAGGACTATGAACTTTAGTACC 832  
DB 450 LeuAspAspLeuLeuGluAlaSerValLeuThrLysGluHisAspIleIleArgGln 469  
QY 833 AAGCTTCAAGAGCCCTCAAAAGTCAGCAATTAAGTACTGACACTGACATCCAAAGAGAA 892  
DB 470 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleLeuValLysGlyAsn 489  
QY 893 GAATTTGCCAAAGTTATAGTACAAAATTCAGAGAT----- 928  
DB 490 AlaAlaAlaSerValPheLysAsnSerLeuLysGluValAspSerThrLeuTyrGluHis 509  
QY 929 -----AACAAACAAATGGGTCTTCCAGCTTACCCTGCGGAAATCTTGTGGTTCTAGA 979  
DB 510 LeuPheValGluLysThrMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 529  
QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAA 1039  
DB 530 GluGluGlnLeuArgArgLeuGlnGluArgThrCysLysValCysMetAspArgGlu 549  
QY 1040 ATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072  
DB 550 ValSerIleValPheIleProCysGlyHisLeuValValCys 563

RESULT 7

Q9E58 PRELIMINARY; PRT; 589 AA.  
ID Q9E58  
AC Q9E58  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inhibitor of apoptosis protein 2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;  
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of  
RT Apoptosis Protein 1, 2, and 3 Genes."

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL; AF183431; AAG22971.1; --  
DR HSSP; OL3490; 1QBH.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.  
DR GO; GO:0006916; P:anti-apoptosis; IEA.  
DR InterPro; IPR001370; BIR.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF00653; BIR; 3.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR SMART; SM00238; BIR; 3.  
DR SMART; SM00114; CARD; 1.  
DR SMART; SM00184; CARD; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS0089; ZF\_RING\_2; 1.  
KW Metal-binding; Zinc; Zinc-finger.  
SQ SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B-CRC64;

Alignment Scores:  
Pred. No.: 0.564 Length: 589  
Score: 100.00 Matches: 32  
Percent Similarity: 42.54% Conservative: 25  
Best Local Similarity: 23.88% Mismatches: 61  
Query Match: 3.47% Indels: 16  
DB: 11 Gaps: 3

US-09-771-161A-2 (1-1669) x Q9ESE8 (1-589)

QY 713 ATCCAGAGCAAAAGGAGACATTTGTAACCAATGACAGAGCCCTTACCAGTCG 772  
DB 432 IleArgLysAsnArgMetalalaLeuPheGlnLeuThr-----CysValIleProIle 449  
QY 773 CTAGATGCCCTTCTGTCCAGGGACTTGATCATCAAGAGGACTATGAACTTTAGTACC 832  
DB 450 LeuAspAspLeuLeuGluAlaSerValLeuThrLysGluHisAspIleIleArgGln 469  
QY 833 AAGCTTCAAGAGCCCTCAAAAGTCAGCAATTAAGTACTGACACTGACATCCAAAGAGAA 892  
DB 470 LysThrGlnIleProLeuGlnAlaArgGluLeuIleAspThrIleLeuValLysGlyAsn 489  
QY 893 GAATTTGCCAAAGTTATAGTACAAAATTCAGAGAT----- 928  
DB 490 AlaAlaAlaSerValPheLysAsnSerLeuLysGluValAspSerThrLeuTyrGluHis 509  
QY 929 -----AACAAACAAATGGGTCTTCCAGCTTACCCTGCGGAAATCTTGTGGTTCTAGA 979  
DB 510 LeuPheValGluLysThrMetLysTyrIleProThrGluAspValSerGlyLeuSerLeu 529  
QY 980 TCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAA 1039  
DB 530 GluGluGlnLeuArgArgLeuGlnGluArgThrCysLysValCysMetAspArgGlu 549  
QY 1040 ATGTGTTTCATA-----AAAGGATATTTATCTCTGT 1072  
DB 550 ValSerIleValPheIleProCysGlyHisLeuValValCys 563

RESULT 8

Q9IN63 PRELIMINARY; PRT; 799 AA.  
ID Q9IN63  
AC Q9IN63  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG12249-PB (LD02989p).  
GN MIRA OR CG12249.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea: Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazew R.G., Chang M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.H., Helt G., Nelson C.R., Gabor G.L.,  
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J.J., Brokstein P., Brostetter P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh N.V., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Hanson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp W., Drysdale R., Emert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003728; AANI3815.1; -;  
 DR EMBL; BT004903; AAO47881.1; -;  
 DR FlyBase; FBgn0021776; mira;  
 DR GO; GO:0045180; C:basal cortex; NAS;  
 DR GO; GO:0008105; P:asymmetric protein localization; IGI;  
 SQ SEQUENCE 799 AA; 89816 MW; AE00B9F2C7F654B6 CRC64;  
 Alignment Scores:  
 Pred. No.: 0.662 Length: 799  
 Score: 99.50 Matches: 59  
 Percent Similarity: 37.50% Conservative: 49  
 Best Local Similarity: 20.49% Mismatches: 111  
 Query Match: 3.45% Indels: 69  
 DB: 5 Gaps: 10  
 US-09-771-161a-2 (1-1669) x Q8IN63 (1-799)  
 QY 353 GCATTCACCTATGTGACAAAGAAATGGAATATTCTCTGACATACCTGTAAATCAT 412  
 DB 64 AlavalArgPheAlaSerSerSerLysGluAlaLysGluPheAlaIlePro----- 80  
 QY 413 GTCCACAAAGAGGAATCATGTGGATCTCTCAGTCCATGAAATAGTGGTCTCTCTGAA 472  
 DB 81 ---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGin 99  
 QY 473 ACTTCAAGGTCCCTCCAGCTCTCTCAAGACATGATTTTTTATCTAGAAAGCTCAAGAC 532  
 DB 100 ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly----- 117  
 QY 533 TGTATTATTAAGAGCTGCATCACTGCTCCTGGAATACAGTTGGATAGCACCATTCT 592  
 DB 118 -----Ser 118  
 QY 593 GGATCTCAAGGGCTGCATTCTGTGATCAAGACACATCCATGCTCTTTCAGCAATAATA 652  
 DB 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133  
 QY 653 ATCCACTCTCACTGCAGGAACCTCAGAACCTGTCAGCTGTCAGCTGGTATATGCCAGAGTGG 712  
 DB 134 ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153  
 QY 713 ---ATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACAGAGCC---TGCCTTAAC 766  
 DB 154 GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg 173  
 QY 767 CAGTCGTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAGCATATGAACCTGTT 826  
 DB 174 ArgHisValAspGlnLysGluAlaLysLeuArgLysGluLysGluLeuAla 193  
 QY 827 AGTACCAAGCTTACAGG-----ACCTCAAAAGTCAGACAATTACTAGAC 871  
 DB 194 ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGlnLeuSerHisLysAla 213  
 QY 872 ACTACTGACATCCAAGGGAAGAATTTGCCAAGATTATAGTACAAAATTTGAAAGATAAC 931  
 DB 214 LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaMet 232



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Db 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133
QY 653 AATCCACTCTCAACTGCAGAAACTCAGAACGCTGCAGCCCTGGTATAGCCAGAGTGG 712
Db 134 ThrProValGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153
QY 713 ---ATCCAGAGCAAGGAGACATTGTGAACCAATAGACAGAGCC---TGCCTTAAC 766
Db 154 GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg 173
QY 767 CAGTCGCTAGATCCCTCTGCTCCAGGAGCTGTATCATGAAAGAGGACTATCACTTGT 826
Db 174 ArgHisValAspGlnLeuLysGluAlaLysLeuArgGluGluHisGluLeuAla 193
QY 827 AGTACCAAGCCTACCAAG-----ACCTCAAAAGTCCAGCAATTAAGTAC 871
Db 194 ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla 213
QY 872 ACTACTGACATCCCAAGAGAGAAATTTGCCAAAGATTATAGTACAAAATTTGAAAGATAAC 931
Db 214 LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaMet 232
QY 932 AAACAAATGGGTCTTCAGCCCTTACCCGGAA-----ATACTTGTGGTCTTCT 976
Db 233 GluGlnGlnLeuGlnGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla 252
QY 977 AGATCACCATCTTTA-----AATTTCCTCAAAATATAAAGCATTAAGTGACT 1024
Db 253 GluSerGluAlaLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln 272
QY 1025 GTTTTTCAGAGAAATATGTGTTTCAATAAAGGATATTATATCTCTGTGCTTTGACTTT 1084
Db 273 LysValGluGluGln----- 277
QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCTTATTGAAGCTTCTTTGGGTAATATTAGT 1144
Db 278 -----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla 290
QY 1145 CTCCTCCATGACACTGCAGTATT 1168
Db 291 GlnAlaArgGluHisCysSerLeu 298
RESULT 11
O45116 PRELIMINARY; PRT; 830 AA.
AC O45116;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MIRANDA.
GN MIRA OR CG12249.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=97410310; PubMed=9267025;
RA Shen C.P., Jan L.Y., Jan Y.N.;
RT "Miranda is required for the asymmetric localization of Prospero
during mitosis in Drosophila.";
RL Cell 90:449-458(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RA Shen C.P., Jan L.Y., Jan Y.N.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF045771; AAC02621.1; -.
DR Flybase; FBgn0021776; mira.
DR GO; GO:0045180; C:basal cortex; NAS.
DR GO; GO:0008105; P:asymmetric protein localization; IGI.
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SQ SEQUENCE 830 AA; 93112 MW; 72F80EDC3FE6113B CRC64;
Alignment Scores:
Pred. No.: 0.666 Length: 830
Score: 99.50 Matches: 59
Percent Similarity: 37.50% Conservative: 49
Best Local Similarity: 20.49% Mismatches: 111
Query Match: 3.45% Indels: 69
DB: 5 Gaps: 10
US-09-771-161A-2 (1-1669) x O45116 (1-830)
QY 353 GCCATTACCTATGTGACAAAGAAATGAATATTCTCGAACATACCTGTAAATCAT 412
Db 64 AlaValArgPheAlaSerSerLysGluAlaLysGluPheAlaIlePro----- 80
QY 413 GGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAA 472
Db 81 ---LysGluAspLysLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln 99
QY 473 ACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGAC 532
Db 100 ArgLeuArgPheArgProThrProSerHisThrAspThrAlaThrGlySerGly----- 117
QY 533 TGTATTTTATGAAGCTGCATCACTGTCTGGAATACAGTTGGATAGCACCATTCT 592
Db 118 -----Ser 118
QY 593 GGATCTCAAGGGCTGCATTCTGTGATCAAGACCCTCCATGCTCTTCAGCAATAATA 652
Db 119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133
QY 653 AATCACCCTCAACTGCAGGAAACTCAGAACGCTCTGCAGCCCTGTATAGCCAGAGTGG 712
Db 134 ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153
QY 713 ---ATCCAGAGCAAGGAGAGACATTGTGAACCAATAGACAGAGCC---TGCCTTAAC 766
Db 154 GluIleArgHisLysAsnGluLeuIleGluSerGlnLeuSerGlnLeuAspValLeuArg 173
QY 767 CAGTCGCTAGATCCCTCTGCTCCAGGAGCTGTATCATGAAAGAGGACTATCACTTGT 826
Db 174 ArgHisValAspGlnLeuLysGluAlaLysLeuArgGluGluHisGluLeuAla 193
QY 827 AGTACCAAGCCTACCAAG-----ACCTCAAAAGTCCAGCAATTAAGTAC 871
Db 194 ThrSerLysThrAspArgLeuIleGluAlaLeuThrSerGluAsnLeuSerHisLysAla 213
QY 872 ACTACTGACATCCCAAGAGAGAAATTTGCCAAAGATTATAGTACAAAATTTGAAAGATAAC 931
Db 214 LeuAsnGluGlnMetGlyGlnGluHisAlaAsp---LeuLeuGluArgLeuAlaMet 232
QY 932 AAACAAATGGGTCTTCAGCCCTTACCCGGAA-----ATACTTGTGGTCTTCT 976
Db 233 GluGlnGlnLeuGlnGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla 252
QY 977 AGATCACCATCTTTA-----AATTTCCTCAAAATATAAAGCATTAAGTGACT 1024
Db 253 GluSerGluAlaLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln 272
QY 1025 GTTTTTCAGAGAAATATGTGTTTCAATAAAGGATATTATATCTCTGTGCTTTGACTTT 1084
Db 273 LysValGluGluGln----- 277
QY 1085 TTTTATATAAATCCGTGAGTATTAAAGCTTATTGAAGCTTCTTTGGGTAATATTAGT 1144
Db 278 -----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla 290
QY 1145 CTCCTCCATGACACTGCAGTATT 1168
Db 291 GlnAlaArgGluHisCysSerLeu 298
RESULT 11
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O04224
ID O04224 PRELIMINARY; PRT; 830 AA.
AC
AD O44224;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MIRANDA.
GN MIRA OR CG12249.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=9805952; PubMed=9403694;
RA Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.Q.,
RA Matsuzaki F.;
RT "Miranda directs Prospero to a daughter cell during Drosophila
RT asymmetric divisions."
RL Nature 390:625-629(1997).
DR ENBL; AB005861; BAA24111.1; -.
DR PIR; T00029; T00029.
DR FlyBase; FBgn0021776; mira.
DR GO; GO:0045180; C:basal cortex; NAS.
DR GO; GO:0008105; P:asymmetric protein localization; IGI.
SQ SEQUENCE 830 AA; 93171 MW; F7AD159AA58F178A CRC64;

Alignment Scores:
Pred. No.: 0.666 Length: 830
Score: 99.50 Matches: 59
Percent Similarity: 37.50% Conservative: 49
Best Local Similarity: 20.49% Mismatches: 111
Query Match: 3.45% Indels: 69
DB: 5 Gaps: 10

US-09-771-161A-2 (1-1669) x O44224 (1-830)
QY 353 GCCATTCACCTATGTGACAGAGAAATGGAATATCTCTGACATACCTGTAATCAT 412
Db |||||
64 AlaValArgPheAlaSerSerLysGluAlaLysGluPheAlaLeuPro----- 80
QY 413 GGTCCACAGAGGAATCATGTGGCTCTCAGCTCCATCAAAATAGTGGTCTCTCGAA 472
Db |||||
81 ---LysGluAspLysSerLysGlyLeuArgLeuPheArgThrProSerLeuProGln 99
QY 473 ACTTCAGGTCCTGCGGAGCTCTCAAGACAATGATTTTATCTAGAAAAGCTCAAGAC 532
Db |||||
100 ArgLeuArgPheArgProThrProSerHisThrAlaThrGlySerGly----- 117
QY 533 TGTATTATTAAGCTGCATCACTGCTCTGGAATCACAGTTGGGATAGCACCATTTCT 592
Db |||||
118 -----Ser 118
QY 593 GGATCTCAAGGGCTGCATTTCTGTGATCAAGACCACTCCATCTCTCAGCAATAATA 652
Db |||||
119 GlyAlaSerThrAlaAla-----SerThrProLeuHisSerAlaAlaThr 133
QY 653 AATCCATCTCACTCAGGAACTCAGACGCTGAGCTGCTGATAGCCAGCAGTGG 712
Db |||||
134 ThrProValLysGluAlaLysSerAlaSerArgLeuLysGlyLysGluAlaLeuGlnTyr 153
QY 713 ---ATCCAGAGCAAAAGGAGACATGTGAAACCAATGACAGAACCC---TGCCCTTAAC 766
Db |||||
154 GluLeuArgHisLysAsnGluLeuLeuLeuSerGlnLeuSerGlnLeuAspValLeuArg 173
QY 767 CAGTCGTAGATGCCCTTCTGTCAGGACTTGTATCATGAAGAGAGCACTATGAAGTGT 826
Db |||||
174 ArgHisValAspGlnLeuLysGluAlaGluAlaLysLeuArgGluGluHisGluLeuAla 193
QY 827 AGTACCAGCCTACAAGG-----ACCTCAAAGTCAGACAATTACTAGAC 871
Db |||||

194 ThrSerLysThrAspArgLeuLeuGluAlaLeuThrSerGluAsnLeuSerHisLysAla 213
872 ACTACTGACATCCAGGAGAGAAATTTGCAAAAGTTATAGTACAAAATTTGAAGATAAC 931
Db |||||
214 LeuAsnGluGlnMetGlyGlnGlnHisAlaAsp---LeuLeuGluArgLeuAlaMet 232
QY 932 AAACAAATGGTCTTCCAGCTTACCCGAA-----ATACTGTGGTTTCT 976
Db |||||
233 GluGlnGlnLeuGlnGlnGlnHisAspGluHisGluArgGlnValGluAlaLeuValAla 252
QY 977 AGATCACCATCTTTA-----AATTACTTCAAAATAAAGCATGTAGTGACT 1024
Db |||||
253 GluSerGluAlaLeuArgLeuAlaAsnGluLeuGlnThrAlaAsnGluAspArgGln 272
QY 1025 GTTTTTCAGAGAAATGTGTTTCATAAAAGGATATTTATATCTCTGTTGCTTGTACTT 1084
Db |||||
273 LysValGluGluGln----- 277
QY 1085 TTTTATATAAAATCCGTGAGTATTAAAGCTTTATTGAAGGTTCTTTGGGTAATATTAGT 1144
Db |||||
278 -----LeuGlnAlaGlnLeuSerAlaLeuGlnAlaAspValAla 290
QY 1145 CTCCTCCATGACACTGCAGTATT 1168
Db |||||
291 GlnAlaArgGluHisCysSerLeu 298

RESULT 12
Q9FTV4 PRELIMINARY; PRT; 869 AA.
ID Q9FTV4
AC Q9FTV4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0407B12.26 protein.
GN P0407B12.26.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nitponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0407B12."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR ENBL; AP002843; BAB17189.1; -.
DR Gramene; Q9FTV4; -.
SQ SEQUENCE 869 AA; 97064 MW; E2E59640E0BE63B2 CRC64;

Alignment Scores:
Pred. No.: 0.67 Length: 869
Score: 99.50 Matches: 59
Percent Similarity: 37.83% Conservative: 42
Best Local Similarity: 22.10% Mismatches: 83
Query Match: 3.45% Indels: 83
DB: 10 Gaps: 14

US-09-771-161A-2 (1-1669) x Q9FTV4 (1-869)
QY 317 TTTATGTATTCATACAGTTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAAG 376
Db |||||
298 PheGluHisGlnLeuAsnGluPheAlaAsnSerAlaPheArgLeuAsnGluHisSer 317
QY 377 AAAATCGAATTA-----TCTCTGAACATACCTGTAATCAT 412
Db |||||
318 SerMetMetLeuAsnLeuAspPheGlyAspHisSerSerSerSerHis 337
QY 413 GGTCCACAGAGGAATCATGTGATGCTCTCT-----CAGCTCCATGAAATAGTGT 463
Db |||||
338 AspArgThrGluLysGlyCysGlySerArgSerArgSerIleGlnLeu---LysThrAspGly 356
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QY 464 -----TCTCTGAACACTTCAAGTCCCTGCAGCTCCTCAAGACAAATGATTTT 514
Db 357 LeuLeuLeuSerProSerArgSerGlyAspIleGluSerProLys-----AspIleLeu 374
QY 515 TCTAGAAAGCTCAAGACTGTTTATTATGAAGCTGCATCACTGCTCTGGAATCACAGT 574
Db 375 CysGluArgAspAlaGluCys----- 381
QY 575 TGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATCTGTGATCACAAAGCACTCCA 634
Db 382 -----GlnValGluProSerAspAlaArgValSerPro 392
QY 635 TGCTCT-----TCAGCAATATAATCACTCTCAACTGCA-----GGA 673
Db 393 CysSerProValLeuGluAspLysLeuValAspProLeuCysSerGlnGluLysAspAsn 412
QY 674 AACTCAGACGCTGCAGCTGTATAGCCAG-----CAGTGGATCCAGAGCAAGGAA 730
Db 413 AsnSerGluAspLeu-----GlyMetAlaAsnIleSerAspValAsnCysLysGlyGlu 430
QY 731 GACATTTGAAACCAATGACAGAGCTCGCTTAACAGCTCGCTA----- 775
Db 431 HisLysValAsnAspAspAspGlySerLeuSerMetGlySerGluGlnLysArgLys 450
QY 776 -----GATCCCTCTGCTCCAGGACTTGATC-----ATG 805
Db 451 GluCysAspGluAspSerLeuValAspGluSerMetCysLysThrHisGluGlnLysSer 470
QY 806 AAAGAGGAC-----TATGAACCTTGTAGTACCAAG 835
Db 471 LysAspAspHisSerSerProGluAspValSerLysThrHisGluPheAspSerThrLys 490
QY 836 CCTACAAGGACCTCAAAAGTC-----AGACAAATTACTA 868
Db 491 AspAsnIleSerSerAlaValAspGlyAsnGluLysHisGluPheGluSerLysLysAsp 510
QY 869 GACACTACTGACATCAACAGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAAGAT 928
Db 511 AspThrAsnSerLeuGluGlyGluSerLeuAsnLysGluHisGluGlnLysSerLysGlu 530
QY 929 ACAACAACAAATGGCTTTCAG 949
Db 531 AspGluAsnSerGlyLeuGlu 537

RESULT 13
Q810W9
ID Q810W9 PRELIMINARY; PRT; 949 AA.
AC Q810W9;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Stearoyl-CoA desaturase (Acyl-CoA desaturase, fatty acid desaturase),
DE putative (EC 1.14.99.5).
GN PF0555W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1] Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feitwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
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RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sultson J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531 (2002).
DR EMBL; AL929352; CAD51476.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003677; E:DNA binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004768; F:stearoyl-CoA 9-desaturase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001522; Desaturase.
DR InterPro; IPR005804; FA desat. fam.
DR InterPro; IPR002052; N6 Mtase.
DR Pfam; PF00487; FA desaturase; 1.
DR PRINTS; PR00075; FACDSDSATRAE.
DR ProDom; PD002221; Desaturase; 1.
DR PROSITE; PS00092; N6_MTASE; 1.
KW Oxidoreductase.
SQ SEQUENCE 949 AA; 114072 MW; CB8C77E6A60DA605 CRC64;

Alignment Scores:
Pred. No.: 0.762 Length: 949
Score: 99.00 Matches: 81
Percent Similarity: 37.08% Conservative: 84
Best Local Similarity: 18.20% Mismatches: 131
Query Match: 3.44% Indels: 149
DB: 5 Gaps: 18

US-09-771-161A-2 (1-1669) x Q810W9 (1-949)
QY 149 GTTNCATAAAGTTATTTCCTGCTTCACTGCTCTTTCTCTTCAAGTT---ATATGTTATATT 205
Db 16 ValLeuHisThrLeuAsnLysSerTyrrLeuAspIleLysAspIleValThrTyrrLeu 35
QY 206 CTCAACTCTTATATTTCTTCCATGATTTTGTACAAACATATAAATGTTAGATT 265
Db 36 ThrTyrrPheIlePheLeuIleSerCysTyrrLeuLysAsnTyrr-----Phe 51
QY 266 GTATTTTACTTCTATAATTTCTCTAATCATCTCCAGTTAAAGTGATATATATTTATGTAT 325
Db 52 SerPheLysPheLeuAsnPheIleArgIleValLysSerSerIleValLeuIleLysCys 71
QY 326 TCATTACAGTTACAGAGTGTTTCAAGTGCCATTCACTATGTGACAAAGAGAAATGGAA 385
Db 72 LeuIleSerLeu-----LysTyrrLeuAsp 79
QY 386 TTATCTCTGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGGATCTCTCAG 445
Db 80 LeuAsnLeuThrLeuSerIleAsnPhe----- 88
QY 446 CTCATGAAATAGTGGTGTCTCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAAT 505
Db 88 ----- 88
QY 506 GATTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGTCTCTGGA 565
Db 89 PheTyrrLeuTyrrAsnIleLeuGlnLeuSerAsnPheLeuGlu----- 102
QY 566 AATCAGTGGGATAGCACCATTCTGGATCTCAAGGGGCTGCATTTCTGTGATCAAG 625
Db 103 -----ValSerThrSerGlnAsnLysLys---SerAsnAsnLys 114
QY 626 ACCACTCCATGCTCTTCCAGCAATAATAATCCACTCTCACTCACTGACGAGAACTCAGACGT 695
Db ----- 695
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Db 208 uileasnSerSerGlnLeuGlnCysLeuGluClyLeuLeuAspAsnLeuValSerSerAs 228  
QY 796 C-----TTGATCATGAAGAGCATGTAACCTTGTAGTACCAAGCCTACCAAGACCTC 849  
Db 228 pSerProLeuAsnIleSerGluAsp---GluIleIleAspArgMetProValIleThrAl 247  
QY 850 AAAAGTCAGACAATTAAGTACACTACTGACATCCCAAGGAGAGAAATTTGCC 901  
Db 247 aProIleAspGluLeuValProLeu-----GluGlnPheAla 259  
RESULT 15  
Q8R489 PRELIMINARY; PRT; 537 AA.  
AC Q8R489  
DT 01-JUN-2002 (TRENBLrel. 21, Created)  
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Syntaxin-interacting protein OCSYN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Safieddine S., Ly D., Wang Y.-X., Wang C.-Y., Kachar B., Petralia R.,  
RA Wenthold R.;  
RT "OCSYN, A novel syntaxin-interacting protein enriched in the subapical  
RT region of inner hair cells.";  
RL Mol. Cell. Neurosci. 0:0-0(2002).  
DR EMBL; AF494296; RMI14616.1;  
SQ SEQUENCE 537 AA, 58735 MW, EA9DFPD9AADDECD4 CRC64;

## Alignment Scores:

Pred. No.:	0.786	Length:	537
Score:	98.50	Matches:	51
Percent Similarity:	41.81%	Conservative:	46
Best Local Similarity:	21.98%	Mismatches:	76
Query Match:	3.42%	Indels:	59
DB:	11	Gaps:	12

US-09-771-161A-2 (1-1669) x Q8R489 (1-537)

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Db 54 AsnArgGlyProHisGlyArgSerAsnGlyAlaSer---LeuHisLysProGlySerSer 72  
QY 467 CCTGAACCTTCAAGGTCCTCCAGCTCCTCAAGACAATGATTTTATCTAGAAAAAGCT 526  
Db 73 Pro-----ProSerProArgGluLysAspLeuLeuSerMetLeuCys 86  
QY 527 CAAGACTGTTATTTT---ATGAAGCTGCATCACTGTCTCGAAATCACAGTTGGGATAGC 583  
Db 87 ArgAsnGlnLeuGlyProIleAsnValHisProSerTyrAlaProSerSerProSerSer 106  
QY 584 ACCATTCTGGATCTCAAGGGCTGATCTGTGATCAAGACCACTCCATCTCTTCA 643  
Db 107 SerAsnSerGlySer-----TyrLysGluSerAspCysSerPro 119  
QY 644 GCAATAATAATCCA-----CTCTCAACTGCAGGAACTCAGAACTCTGCAGCTGTG 697  
Db 120 ValMetArgProGlyArgTyrMetSerCysGlyGluAsnHisGlyValLysProPro 139  
QY 698 ATAGCCACAGCAGTGGATCCAGAGC-----AAAAGGAGACATTTGTGAACCAAAATGACAGAA 754  
Db 140 AsnProGluGlnThrProLeuGlnLysGluValThrValArgHisLeuLys 159  
QY 755 GCGTGCCTTAACAGTCG-----CTA 775  
Db 160 ThrLysLeuLysGluSerGluArgArgLeuHisGluArgSerGluIleValGluLeu 179  
QY 776 GATGCCCTTCTGTCAGGGACTTGATCATCAAGAGGACTAT----- 817  
Db 180 LysSerGlnLeuAlaArg-----MetArgGluAspIrpIleGluGluCysHis 196

QY 818 -----GAACTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTA 868  
Db 197 ArgValGluAlaGlnLeuAlaLeuLysGluAlaArg---LysGluIleLysGlnLeu--- 214  
QY 869 GACACTACTGACATCCAAAGGAGAGAATTTGCCAAAGTTATAGTACAAAAAATTGAAAGAT 928  
Db 215 -----LysGlnValIleGluThrMetArgAsp 223  
QY 929 AAC-----AAACAAATGGCTTCCAGCCTTACCCGGAATACTTGTGTGTTCTTCTAGA 979  
Db 224 AsnLeuAlaAspLysAspLysGlyIleGlnLysTyrPheValAspIleAsnIleGlnAsn 243  
QY 980 TCACCATCTTTAAATTTTACTTCAAAATAAAAGCATG 1015  
Db 244 LysLysLeuGluAlaLeuLeuGlnSerMetGluMet 255

Search completed: March 29, 2004, 14:23:34

Job time : 101.5 secs

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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 12, 2004, 11:14:14 ; Search time 292 Seconds  
(without alignments)  
3.125 Million cell updates/sec

Title: AF027706  
Perfect score: 4369  
Sequence: 1 ggcaccagtctctagaaag.....aaagtcaacagcctgatgtg 2501

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0  
Searched: 874 seqs, 182427 residues

Total number of hits satisfying chosen parameters: 1748

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 7 summaries

Command line parameters:  
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-OUT=af027706.pep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1  
-END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=7 -DOALIGN=200  
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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY  
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : \*pep\*  
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2: /home/sdavid/sdavid-tmp/apr04/swopel61/6348573.pep.\*  
3: /home/sdavid/sdavid-tmp/apr04/swopel61/6033855.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2849	65.2	544	1	US-09-925-301-1015
2	2827	64.7	540	2	US-09-069-023-27
3	2821	64.6	540	3	US-09-019-942-1
4	2778	63.6	531	2	US-09-069-023-1
5	2749.5	62.9	530	2	US-09-069-023-3
6	2501	57.2	478	2	US-09-069-023-4
7	1475	33.8	284	2	US-09-069-023-5

ALIGNMENTS

RESULT 1  
US-09-925-301-1015  
; Sequence 1015, Application US/09925301  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1015  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-301-1015

Alignment Scores:  
Pred. No.: 1.13e-190 Length: 544  
Score: 2849.00 Matches: 544  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 65.21% Indels: 0  
DB: 1 Gaps: 0

AF027706 (1-2501) x US-09-925-301-1015 (1-544)

Qy	213	CGCCCGGACCATGAACGGGAGGCCATCTGAGCGCCCTGCCACCATTCCCTACCAC	272
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Qy	273	AAACTCGCGACCTGCGCTACCTGAGCGGGCGGCTGCGACTGCTGCTCGCGCCGC	332
Db	21	LysLeuAlaAspLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerAlaArg	40
Qy	333	CACGACGACGCGCGCTCCAGTGGCGCTGAAGCACCTGCACATCCACACTCCGCTGCTC	392
Db	41	HisAlaAspTrpArgValGlnValAlaValIleHisLeuHisIleHisThrProLeuLeu	60
Qy	393	GACAGTGAAGAAAGAGATGCTTAAAGAGAGCTGAAATTTTACACAAAGCTAGATTAGT	452
Db	61	AspSerGluArgIysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSer	80
Qy	453	TACATCTCTCCAAATTTGGGAATTTGCAATGAGCTCAATTTTGGGAATAGTTACTGAA	512
Db	81	TyrIleLeuProIleLeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGlu	100
Qy	513	TACATGCAATGATCATTAATAATGAATCTCTACATAGGAAATGAATATCTCTGATGT	572
Db	101	TyrMetProAsnGlySerLeuAsnGluLeuHisArgIysThrGluTyrProAspVal	120
Qy	573	GTTTGGCATGAGATTTGCGATCTCTGCATGAAATTCGCCCTTGGTGTAAATTACTGCAC	632
Db	121	AlaTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHis	140
Qy	633	AATATGACTCTCTCTTACTTCTCATGACTTGAAGCTCAGATATCTTATTCGACAAT	692
Db	141	AsnMetThrProProLeuLeuHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn	160
Qy	693	GAATTTTCATGTTAAGATTTGCGATTTTGGTTTATCAAGTGGCGCATGATCTCTCTCA	752
Db	161	GluPheHisValIysIleAlaAspPheGlyLeuSerIysTrpArgMetMetSerLeuSer	180
Qy	753	CAGTCAGAGATGACAAATCTGCACACAGAGAGGAGGACAATTATCTATATGCCACCTGAA	812
Db	181	GlnSerArgSerSerLeuSerAlaProGluGlyThrIleIleTyrMetProProGlu	200
Qy	813	AACATGACTCGACAAAATCAAGGCGGAGTATCAAGCAGCATATATAGCTATGCA	872
Db	201	AsnTyrGluProGlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAla	220
Qy	873	GTTATCATCGGGAAGTGTATTCAGAAAAACAGCCTTTTGAAGATGTCAACCAATCTTTG	932
Db	221	ValIleThrTrpGluValLeuSerArgIysGlnProPheGluAspValThrAsnProLeu	240
Qy	933	CAGATAATGATAGTGTGTCAAGGACATCGACCTGTTATTATTAAGAAAGTTTGCA	992

Db 241 GlnIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluSerLeuPro 260  
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Db 261 TyrAspIleProHisArgAlaArgMetIleSerLeuIleGluSerGlyTyrAlaGlnAsn 280  
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Qy 1113 TTTGAAGAGATAACTTTCTTGAAGCTGTTATTCAGCTTAAGAAAAACAAAGTTACAGAGT 1172  
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Qy 1173 GTTTCAAGTGCATTCACCTATGTCAGAAAGAAATGGAATATCTCTGAAACATACCT 1232  
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Qy 1293 TCTCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAAATGATTTTTTATCTAGAAA 1352  
Db 361 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnArgPheLeuSerArgLys 380  
Qy 1353 GCTCAAGACTGTTATTTATGAAGTGCATCATCTGCTCGGAAATCACAGTTGGATAGC 1412  
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Qy 1473 GCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACCTGCTCAGCCCTGGTATAGC 1532  
Db 421 AlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 440  
Qy 1533 CAGCAGTGGATCCAGACAAAGGAGACATGTTGAACCAATGACAGAGCCTGCTT 1592  
Db 441 GlnGlnThrIleGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 460  
Qy 1593 AACCACTGCTAGATGCCCTCTCTGTCAGGGACTTGATCAAGAGAGACTATGAACTT 1652  
Db 461 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 480  
Qy 1653 GTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAAGACACTACTGACATC 1712  
Db 481 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 500  
Qy 1713 CAAGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAACAAACAATGGGT 1772  
Db 501 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 520  
Qy 1773 CTTACAGCTTACCCGGAATACTCTGTTTCTAGATCACCATCTTTAAATTTACTTCAA 1832  
Db 521 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuGln 540  
Qy 1833 AATAAAGCATG 1844  
Db 541 AsnLysSerMet 544

RESULT 2

US-09-069-023-27  
; Sequence 27, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-27  
Alignment Scores:  
Pred. No.: 3,69e-189 Length: 540  
Score: 2827.00 Matches: 540  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 64.71% Indels: 0  
DB: 2 Gaps: 0  
AF027706 (1-2501) x US-09-069-023-27 (1-540)  
Qy 225 ATGAACGGGAGGCCATCTGCAGCGCCCTCCACCATTCCTTACCACAACTCGCGAC 284  
Db 1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLysLeuAlaAsp 20  
Qy 285 CTGCGCTTACCTGAGCGCGCGCTCTGCGACTGTGTCTGCCCTCCCGCCACGAGACTGG 344  
Db 21 LeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTyr 40  
Qy 345 CGGCTCAGGTGGCGTGAAGCAGCTGCACATCCACACCTCCGCTGCTCCGACAGTGAAGA 404  
Db 41 ArgValGlnValAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60  
Qy 405 AAGGATGCTTAAGAGAAGCTGAAATTTTACAAAGCTAGATTTAGTTACATCTTCCA 464  
Db 61 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIleLeuPro 80  
Qy 465 ATTTTGGGAATTTGCAATGAGCTGAAATTTTGGGAATAGTTACTGTAATCATGCGCAAT 524  
Db 81 IleLeuGlyIleCysAsnGluProCysGluPheLeuGlyIleValThrGluTyrMetProAsn 100  
Qy 525 GGATCATTAAATGAACTCTACATAGAAACCTGAAATATCTGATGTTGCTTGGCCATTG 584  
Db 101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTyrProLeu 120  
Qy 585 AGATTTCCGATCTCTGATGAAATTTGCCCTTGGTGTAAATTTACCTGCAATATGACTCCT 644  
Db 121 ArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrPro 140  
Qy 645 CTTTACTTCAATCATGACTTGAAGACTCAGAAATCTTATTTGGCAATGAATTTTCATGTT 704  
Db 141 ProLeuLeuHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisVal 160  
Qy 705 AAGATTTCCAGATTTTGGTTTATCAAGTGGCGATGATGTCCTCTCCAGTCTACGAAGT 764  
Db 161 LysIleAlaAspPheGlyLeuSerLysTyrArgMetMetSerLeuSerGlnSerArgSer 180  
Qy 765 AGCAAACTGCACAGAGGAGGACAAATTTATCTATATGCCACCTGAAAACTATGAACCT 824  
Db 181 SerLysSerAlaProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro 200  
Qy 825 GGACAAAATCAAGGGCCAGTATCAAGCAGATATATAGCTATGAGTTATGATCATGAGTGG 884  
Db 201 GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTyr 220  
Qy 885 GAAGTGTATCCAGAAAACAGCTTTTGAAGATGTCACCAATCTTTCAGATAATGTAT 944  
Db 221 GluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyr 240  
Qy 945 AGTGTGTCAAGGACATCGACCTGTTTATTAATGAAGAAAGTTTCCCATATGATATACCT 1004  
Db 241 SerValSerGlnGlyHisArgProValIleAsnGluSerLeuProTyrAspIlePro 260

QY 1005 CACCAGACGATGATCTCTCTAATAGAAAGTGATGGGCACAAAATCCAGATGAAGA 1064  
Db HisArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArg 280  
QY 1065 CCATCTTTCTTAATGTTTAAATAGAACTCAACAGTTTGTGAGACATTTGAGAGNTA 1124  
Db ProSerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300  
QY 1125 ACTTTTCTGAAGCTGTTATTACAGTAAAGAAAACAAAGTTTACAGAGTGTTCAGTGCC 1184  
Db ThrPheLeuGluAlaValIleGlnLeuLysThrLysLeuGlnSerValSerSerAla 320  
QY 1185 ATTCACCTATGTGACAAAGAAAATGAATATCTCTGAACATACCTGTAAATCATGGT 1244  
Db 321 IleHisLeuCysAspLysLysMetGluLeuSerLeuAsnIleProValAsnHisGly 340  
QY 1245 CCACAGAGGAATCATGTGGATCTCTCAGTCCATGAAATAGTGTCTCCTGAACT 1304  
Db ProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThr 360  
QY 1305 TCAAGGTCCCTGCCAGCTCTCAAGACAATGATTTTTTATCTAGAAAAGCTCAAGACTGT 1364  
Db SerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCys 380  
QY 1365 TATTTTATGAAGTCATCATCTGCTCTGGAATCACAGTGGATAGCACCATTTCTGGT 1424  
Db TyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly 400  
QY 1425 TCTCAAGGGTGTGATTTCTGTGATCACAAGACCCTCATCTCTTCAGCAATATAAT 1484  
Db SerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerAlaIleAsn 420  
QY 1485 CCACCTCTCACTGACGAGAACTCAGAAGCTCTGACAGCTGTGATAGCCACAGTGGATC 1544  
Db ProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnTrpIle 440  
QY 1545 CAGACAAAAGGAGACATTTGTGAACCAATGACAGAAAGCTGCTTAAACAGTCGCTA 1604  
Db GlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeu 460  
QY 1605 GATGCCCTTCTGTCGAGGACTTGATCATGAAGAGGACTATGAATGTTAGTACCAAG 1664  
Db AspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLys 480  
QY 1665 CCTACAAGGACTCAAAAGTCAGACAATTTACTAGACACTACTGACATCCAAAGGAGAGAA 1724  
Db ProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu 500  
QY 1725 TTGCCAAAGTTATAGTACAAAATTGAAGATACAAACAAATGGGTCTTCAGCCTTAC 1784  
Db PheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyr 520  
QY 1785 CCGAATACTGTGGTTCTTAGATCACCACATTTAAATTTTACTTCAAAATAAAGCATG 1844  
Db ProGluIleLeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 540

## RESULT 3

US-09-019-942-1  
; Sequence 1, Application US/09019942  
; Patent No. 6033855  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT  
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P. C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA: US/09/019,942  
APPLICATION NUMBER: 06-FEB-1998  
FILING DATE: 06-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/068001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-019-942-1  
Alignment Scores:  
Pred. No.: 9,53e-189 Length: 540  
Score: 2821.00 Matches: 539  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 64.57% Indels: 0  
DB: 3 Gaps: 0  
AF027706 (1-2501) x US-09-019-942-1 (1-540)  
QY 225 ATGAACGGGAGGCGCATCTGCAGCGCCCTGCCACCAATTCCTTACCACAACTCCCGAC 284  
Db 1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLysLeuAlaAsp 20  
QY 285 CTGGCTTACTGAGCCGCGGCGCTCTGGCACTGTGTCTGCGCCGCCCGCCGAGACTGG 344  
Db 21 LeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrp 40  
QY 345 CGCTCCAGGTGGCGGTGAAGAGCCTGCACATCCACACTCGCTGCTCGACAGTGAAGA 404  
Db 41 ArgValGlnValAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60  
QY 405 AAGGATCTCTTAAGAGAGCTGAAATTTTACAAAAGCTAGATTAGTTACATTTCTTCCA 464  
Db 61 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIleLeuPro 80  
QY 465 ATTTTGGGAATTTGCAATGAGCCCTGAATTTTGGGAATAGTTACTGATGATCATCATCCAAAT 524  
Db 81 IleLeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100  
QY 525 GGATCATTAAATGAATCTTACATAGGAAACTGAATATCTGATGTTGCTTGGCCATTG 584  
Db 101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLeu 120  
QY 585 AGATTTCCGATCTTCATGAAATTTGCGTGGTGTAAATTTACCTGCGCAATATGACTCCT 644  
Db 121 ArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrPro 140  
QY 645 CCITTACTTCTCATGACTTGAAGACTCAGATATCTTATGGCAATGATTTTCATGTT 704  
Db 141 ProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisVal 160  
QY 705 AAGATTGCAGATTTTGGTTTATCAAGTGGCGCATGATGTCCCTCTCACAGTTCACGAAT 764  
Db 161 LysIleAlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSer 180  
QY 765 AGCAAAATCTGCACCAAGAGGAGGACAAATTTATCTATATGCACCTGAAACACTATGAACCT 824





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QY 912 GAAGATGTCACCAATCTTTGGCAGATAATGTATAGTGTCTCAGAGCATCGACTGTT 971
Db 221 GluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHisArgProVal 240
QY 972 ATTAATGAAGAAGTTTGCATATATATACCTCACCAGACGATGATCTCTCTAATA 1031
Db 241 IleAsnGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSerLeuIle 260
QY 1032 GAAAGTGGATGGCCACAAATCCAGATGAAGACCATCTTTCTTAAATGTTTAAAGAA 1091
Db 261 GluSerGlyTyrAlaGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGlu 280
QY 1092 CTTGAACCACTTTTGAGAACATTTGAAGAGATACTTTCTTGAAGCTGTATTACAGCTA 1151
Db 281 LeuGluProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleGlnLeu 300
QY 1152 AAGAAACAAAGTTCACAGAGTCTTCAAGTGCCTTACCTATGTGACAGAGAAAGATG 1211
Db 301 LysLysThrLysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMet 320
QY 1212 GAATTATCTCTGAACATACCTCTAAATCATGTCTCACAAGAGGAATCATGTGGATCCTCT 1271
Db 321 GluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSer 340
QY 1272 CAGCTCCATGAATAATAGTGGTCTCTCTGAACTTCAAGTCTCCAGCTCCTCAAGAC 1331
Db 341 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAsp 360
QY 1332 ATGATATTTTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCTGCTCT 1391
Db 361 AsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysPro 380
QY 1392 GGAATTCACAGTTGGATGACCACTTCTCTGTTCTTCAAGGCTGCATCTTGTGATCAC 1451
Db 381 GlyAsnHisSerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHis 400
QY 1452 AAGACCACTCCATGCTCTTACCAATAATAAATCACTCTCAACTGCAGGAACTCAGAA 1511
Db 401 LysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGlu 420
QY 1512 CQTCTGCAGCTGGTATAGCCAGCAGTGGATCCAGAGCAAGAGGAGACATCTGTGAC 1571
Db 421 ArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsn 440
QY 1572 CAAATGCACAGAGCTGCTTAAACCAAGTCGTAGATGCCCTTCTCTCCAGGACTTGATC 1631
Db 441 GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIle 460
QY 1632 ATGAAGAGGACTATGAATCTTTAGTACCAAGCCTACAGGACCTCAAAAGTCAAGCAA 1691
Db 461 MetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGln 480
QY 1692 TTACTAGACACTACTGACATCCAAAGGAGAGAAATTTGCCAAGTTATAGTACAAATG 1751
Db 481 LeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu 500
QY 1752 AAAGATAACAAACAAATGGTCTTACAGCTTACCCGGAATACTTGTGGTCTTACAGTCA 1811
Db 501 LysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSer 520
QY 1812 CCATCTTAAATTTACTTCAAAATAAAGCATG 1844
Db 521 ProSerLeuAsnLeuLeuGlnAsnLysSerMet 531
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## RESULT 5

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US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
```

```
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-069-023-3
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## Alignment Scores:

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Pred. No.: 7,84e-184 Length: 530
Score: 2749.50 Matches: 528
Percent Similarity: 99.62% Conservative: 1
Best Local Similarity: 99.44% Mismatches: 1
Query Match: 62.93% Indels: 1
DB: 2 Gaps: 1
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AF027706 (1-2501) x US-09-069-023-3 (1-530)

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QY 252 CTGCCCCACCATTCCTTACCACAAACTCGCCGACCTGCGCTACCTGAGCGCGGCGCTCT 311
Db 1 MetProThrIleProTyr---LysLeuAlaAspLeuArgTyrLeuSerArgGlyAlaSer 19
QY 312 GGCACCTGTGTCCTCGCCCGCCGACGACACTGGCGCGTCCAGGTGGCGCTGAAGCACCTG 371
Db 20 GlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnValAlaValLysMetLeu 39
QY 372 CACATCCACACTCCGCTGCTCGACAGTGAAGAAAGAGTGTCTTAAGAGAAGCTGAAATT 431
Db 40 HisIleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAlaGluIle 59
QY 432 TTACACAAAGCTAGATTAGTTACATCTTCCATTTTGGGAATTTGCAATTTGCAATGAGCTCAA 491
Db 60 LeuHisLysAlaArgPheSerTyrIleLeuProIleLeuGlyIleCysAsnGluProGlu 79
QY 492 TTTTGGGAATAGTTACTGAAATACATGCAAAATGGATGATTAATAATGAACTCTCATAGAGG 551
Db 80 PheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeuLeuHisArg 99
QY 552 AAAACTGAATATCTGTATGTTGCTTGGCCATTGAGATTTCCGATCTCTGCATGAAATGCC 611
Db 100 LysThrGluTyrProAspValAlaTrpProLeuArgPheArgIleLeuHisGluIleAla 119
QY 612 CTTGGTGTAAATTTACCTGCAATATGACTCTCTCTTTTACTTCTCATGACTTGAGACT 671
Db 120 LeuGlyValAsnTyrLeuHisAsnMetThrProProLeuLeuHisAspLeuLysThr 139
QY 672 CAGAAATCTTATTGGACAATGAATTTTCATGTTAAGATTGAGATTGTTTGTATCAAG 731
Db 140 GlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLeuSerLys 159
QY 732 TGGCGCATGATGTCCTCTCACTGACAGAGTGAAGAAATCTGCACCAAGAGAGGAGACA 791
Db 160 TrpArgMetSerLeuSerGlnSerArgSerLysSerAlaProGluGlyGlyThr 179
QY 792 ATTATCTATATGCACTGAGTTATCACATGGGAAGTGTATTATCCAGAAAAACAGGCTTTT 851
Db 180 IleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSerArgAlaSerIleLys 199
QY 852 CACGATATATATGCTATGCAAGTTATCACATGGGAAGTGTATTATCCAGAAAAACAGGCTTTT 911
Db 200 HisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe 219
QY 912 GAAGATGTCACCAATCTTTTGCAGATAATGTATAGTGTGTGCACAAAGGACATCGACTGTT 971
Db 220 GluAspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGlyHisArgProVal 239
QY 972 ATTAATGAAGAAGTTTGGCAGATATGATATACCTCAGGAGCACGATGATCTCTAATA 1031
Db 240 IleAsnGluGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSerLeuIle 259
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QY 1032 GAAAGTGGATGGGCACAAATCCAGATGAGAGACATCTTTCTTAAATGTTTAAATAGAA 1091
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QY 1092 CTGGAACAGATTTTGAAGAACATTTGAAGAGATAACTTTCTTGAAGCTGTTATTACAGCTA 1151
Db 280 LeuGluProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleGlnLeu 299
QY 1152 AAGAAAAACAAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGTGACAGAGAAAAATG 1211
Db 300 LysLysThrLysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMet 319
QY 1212 GAAATTTATCTCAACATACCTGTAATCATGTCACAGAGAGGAATCATGTGGATCTCTCT 1271
Db 320 GluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSer 339
QY 1272 CAGCTCCCATGAAATAGTGGTTCTCTGAAATCTCAAGTCCCTCCGACCTCTCAAGAC 1331
Db 340 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAsp 359
QY 1332 AATGATTTTATCTAGAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCCTGCTCT 1391
Db 360 AsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysPro 379
QY 1392 CGAAATCAGTGGGATAGACCACTTCTGCTCTCAAGGGCTGCATTCCTGTGATCAC 1451
Db 380 GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHis 399
QY 1452 AAGACCACTCCATGCTCTTCAAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAA 1511
Db 400 LysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGlu 419
QY 1512 CQTCTGACCTGGTATAGCCAGCAGTGCATCCAGACCAAAAGGAGAGACATGTGAAAC 1571
Db 420 ArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsn 439
QY 1572 CAAATGACAGAGCTGCTTAAACAGTCCGATGATGCTCTCTCCAGGAGCTTGATC 1631
Db 440 GlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIle 459
QY 1632 ATGAAAGAGGACTATCAACTCTTGTATCAAGCTTACCAAGCTTCAAGGACCTCAAAAGTCA 1691
Db 460 MetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGln 479
QY 1692 TTACTAGACACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTG 1751
Db 480 LeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu 499
QY 1752 AAAGATAACAAACAAATGGTCTTCAAGCTTACCCGGAATACTTGTGTTTCTAGATCA 1811
Db 500 LysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSer 519
QY 1812 CCATCTTTAAATTTACTTCAAAATAAAGCATG 1844
Db 520 ProSerLeuAsnLeuLeuGlnAsnLysSerMet 530
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RESULT 6

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US-09-069-023-4
; Sequence 4, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
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; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-4

Alignment Scores:
Pred. No.: 9,4e-167 Length: 478
Score: 2501.00 Matches: 478
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.24% Indels: 0
DB: 2 Gaps: 0

AF027706 (1-2501) x US-09-069-023-4 (1-478)
QY 411 GTCTTAAGAGACGCTGAAATTTTACACAAAGCTAGATTAGTTACATCTTCCAAATTTTG 470
Db 1 ValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIleLeuProIleLeu 20
QY 471 GGAATTTGCAATGAGCTGAAATTTTGGGAATAGTTACTGAATACATGCAAAATGATCA 530
Db 21 GlyIleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySer 40
QY 531 TTAATGAACTCCTACATAGGAAACTGAATATCCTGATGTTGCTTGGCCATTCAGATTT 590
Db 41 LeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaIleThrProLeuArgPhe 60
QY 591 CGCATCTGCTGATGAAATTTGCTTGGTGTAAATTTACTGACAAATATGACTCCTCCTTTA 650
Db 61 ArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrProLeu 80
QY 651 CTTTCATCATGACTTGAAGACTCAGAATATCTTATGGACAATGAATTCATGTTAAGATT 710
Db 81 LeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIle 100
QY 711 GCAGATTTTGGTTATCAAGTGGCGCATCATCTCCTCTCACAGTCACCAAGTAGCAAA 770
Db 101 AlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLys 120
QY 771 TCTCCACAGAGAGGAGGACAAATTTATCTATATGCTCCACTGAAAACTATGAACCTGGCAA 830
Db 121 SerAlaProGluGlyGlyThrIleIleTyrMetProGluAsnTyrGluProGlyGln 140
QY 831 AAATCAAGGCGCAGTATCAAGCAGCATATATATAGCTATCAGTTATCATCATGGGAAGTG 890
Db 141 LysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTrpGluVal 160
QY 891 TTATCCAGAAAACAGCCTTTTGAAGATGTCACCAATCCTTTGCAAGATAATGTATAGTGTG 950
Db 161 LeuSerArgLysGlnProPhePheGluAspValThrAsnProLeuGlnIleMetTyrSerVal 180
QY 951 TCACAAGGACATCGACCTGTTTATTAATGAAGAAAGTTTGGCATATATATACCTCACCGA 1010
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QY 1011 GCACGTATGATCTCTTAATAGAAAGTGGATGGGCACAAAATCCAGATGAAGACCATCT 1070
Db 201 AlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSer 220
QY 1071 TTCTTAAATGTTTAAATAGAACTTGAACCACTTTTGAACATTTTGAAGAGATAACTTTT 1130
Db 221 PheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIleThrPhe 240
QY 1131 CTTGAAGCTGTTTATTCAGCTAAAGAAACAAAGTTACAGAGTGTTCAGAGTGCATTCAC 1190
Db 241 LeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerValSerSerAlaIleHis 260
QY 1191 CTATGTGACAAGAGAAATTCGAATTTATCTCTGACATACCTGTAAATCATGGTCCCAAA 1250
Db 261 LeuCysAspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGln 280
QY 1251 GAGGAATCATGTGGATCCTCTCAGCTCCATCAAAATAGTGTTCCTCTGAAACTTCAGG 1310
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Db 281 GluGluSerCysGlySerSerGlnLeuHisGluLeuSerGlySerProGluThrSerArg 300  
QY 1311 TCCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAGCTCAAGACTGTTATTTT 1370  
Db 301 SerLeuProAlaProGlnAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPhe 320  
QY 1371 ATGAAGCTGCATCACTGCTCGGAATACACAGTTGGGATAGACCATTTCTGGTTCTCAA 1430  
Db 321 MetLysLeuHisCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGln 340  
QY 1431 AGGCGTGCATTCGTGATCACAGACCACTCCATGCTCTCAGCAATAATAAATCCACTC 1490  
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QY 1491 TCAACTGCAGGAACTCAGAACGCTGTCAGCGCTGTATAGCCAGCAGTGGATCCAGAGC 1550  
Db 361 SerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSer 380  
QY 1551 AAAAGGGAAGCATTTGTGAACAAATGACAGAGCTCGCTTAACCACTCGCTAGATGCC 1610  
Db 381 LysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAla 400  
QY 1611 CTTCTGTCAGGACTTCATCATGAAGAGGACTATGAATGTTAGTACCAAGCCTACA 1670  
Db 401 LeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThr 420  
QY 1671 AGGACTCAAAAGTCAGACAAATTAAGAGGACTATGAATGTTAGTACCAAGCCTACA 1730  
Db 421 ArgThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluPheAla 440  
QY 1731 AAAGTTATAGTACAAAAATTGAAGATAACAAATAATGGGTCTTACGCTTACCCGGAA 1790  
Db 441 LysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGlu 460  
QY 1791 ATACTTGGGTCTTCAGATCACCATTCTTAATTTACTTCAAAATAAAGCATG 1844  
Db 461 IleLeuValValSerArgSerProSerLeuAsnLeuLeuGlnAsnLysSerMet 478  
RESULT 7  
US-09-069-023-5  
; Sequence 5, Application US/09069023A  
; Patent No.: 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Nachiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-5

Alignment Scores:  
Pred. No.: 2,98e-96 Length: 284  
Score: 1475.00 Matches: 284  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 33.76% Indels: 0  
DB: 2 Gaps: 0

AF027706 (1-2501) x US-09-069-023-5 (1-284)

QY 993 TATGATATACCTCCAGGACGATGATCTCTCTAATAGAAAGTGGATGGCCACAAAT 1052  
Db 1 TyrAspIleProHisArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsn 20

QY 1053 CCAGATGAAGACCATCTTCTTAAATGTTTAAATAGAACTTGAAACCAAGTTTGTGAGAAC 1112  
Db 21 ProAspGluArgProSerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThr 40  
QY 1113 TTTCAAGAGATAACTTTCTTGAAGCTGTTATTCAGCTTAAGAAACAAACAGTTACAGAGT 1172  
Db 41 PheGluGluIleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSer 60  
QY 1173 GTTTCAAGTGCATTTCACCTATGTGACAAAGAAAAATGGAATTTATCTCTGAACATACCT 1232  
Db 61 ValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerLeuAsnIlePro 80  
QY 1233 GTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGGT 1292  
Db 81 ValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHisGluAsnSerGly 100  
QY 1293 TCTCCTCAAACTTCAAGGTCCTCCAGCTCCTCAAGACATGATTTTATCTAGAAAA 1352  
Db 101 SerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLys 120  
QY 1353 GCTCAAGACTGTTATTTTATGAAGCTGCATCAGCTGCTCTGGAAATCAGAGTTGGATAGC 1412  
Db 121 AlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHisSerTrpAspSer 140  
QY 1413 ACCATTCTGTTCTCAAAAGGCTGCAATCTGTGATCACAAGACCACTTCCATGCTCTTCA 1472  
Db 141 ThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSer 160  
QY 1473 GCATATATAATCCACTCTCACTGCGAGGAACCTCAGAACGCTCTGCAGCCTGTATAGCC 1532  
Db 161 AlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAla 180  
QY 1533 CAGCAGTGGATCCAGAGCAAAAGGAAGACATTTCTGAACCAAAATGACAGAACGCTGCCTT 1592  
Db 181 GlnGlnTrpIleGlnSerLysArgLysAspIleValAsnGlnMetThrGluAlaCysLeu 200  
QY 1593 AACCACTGCTAGATGCCCTTCTCTCAGGAGCTTGATCATGAAAGAGGACTATGAACTT 1652  
Db 201 AsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 220  
QY 1653 GTTAGTACCAGCCTACAGGACCTCAAAAGTCAAGCAATTTACTAGACACTACTGACATC 1712  
Db 221 ValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThrThrAspIle 240  
QY 1713 CAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAACAAACAAATGGGT 1772  
Db 241 GlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGly 260  
QY 1773 CTTCAAGCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAATTTACTTCAA 1832  
Db 261 LeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnLeuLeuGln 280  
QY 1833 AATRAAAGCATG 1844  
Db 281 AsnLysSerMet 284

Search completed: April 12, 2004, 11:24:10  
Job time : 303 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2004, 09:56:56 ; Search time 154 Seconds  
(without alignments)  
4.025 Million cell updates/sec

Title: AF027706  
Perfect score: 2501  
Sequence: 1 ggcaccagtctctagaaag.....aaagtcaacagcctgatgtg 2501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 123919 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 5 summaries

Database : a\*\*  
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2: /home/sdavid/sdavid-tmp/apr04/swopel61/aa48762.genesegm2000s.\*  
3: /home/sdavid/sdavid-tmp/apr04/swopel61/aa48762.genesegm1990s.\*  
4: /home/sdavid/sdavid-tmp/apr04/swopel61/aa48762.genesegm1990s.\*  
5: /home/sdavid/sdavid-tmp/apr04/swopel61/ac004003.gb\_pr.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2490.5	99.6	2	AAZ48762 Human RICK coding
2	2017.8	80.7	3	AAZ02558 Human B1 cDNA.Ho
3	1864	74.5	4	AAZ09246 Human CARD-3 cDNA.
4	969.2	38.8	5	AC004003 ACCESSION:AC004003
5	709	28.3	1	AI824070 ACCESSION:AI824070

ALIGNMENTS

RESULT 1  
AAZ48762  
ID AAZ48762 standard; cDNA; 2502 BP.  
XX  
AC AAZ48762;  
XX  
DT 21-MAR-2000 (first entry)  
XX  
DB Human RICK coding sequence.  
XX  
KW RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;  
KW caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway;  
KW CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation;  
KW gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;  
KW aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.  
OS Homo sapiens.  
XX

Db 301 CGCGCGCTCTGGACATGTGTCTGTCGCGCGCCACGACAGCTGGCGCGTCAGGTGCC 360  
Qy 360 GTGAAGCACCTGCACATCCACATCCGCTGCTCGACAGTGAAGAAAGGATGCTTAA 419  
Db 361 GTGAAGCACCTGCACATCCACATCCGCTGCTCGACAGTGAAGAAAGGATGCTTAA 420  
Qy 420 GAAGCTGAATTTTACACAAAGCTAGATTTAGTTACATCTTCCAAATTTGGGAATTTGC 479  
Db 421 GAAGCTGAATTTTACACAAAGCTAGATTTAGTTACATCTTCCAAATTTGGGAATTTGC 480  
Qy 480 AATGAGCTGAATTTTGGGAATAGTTTACTGAAATACATGCGCAAAATGGATCATTTAAATCAA 539  
Db 481 AATGAGCTGAATTTTGGGAATAGTTTACTGAAATACATGCGCAAAATGGATCATTTAAATGAA 540  
Qy 540 CTCCTACATAGAAATCGAATATCTTGATATCTTGATGCTTGGCGCAATGAGATTCGATCCTG 599  
Db 541 CTCCTACATAGAAATCGAATATCTTGATATCTTGATGCTTGGCGCAATGAGATTTGCGATCCTG 600  
Qy 600 CATGAAATTCGCTGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 659  
Db 601 CATGAAATTCGCTGGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660  
Qy 660 GACTTGAAGACTCAGATATCTTATTTGCAATGAATTTTCATGTTTGAAGATTCAGATTTT 719  
Db 661 GACTTGAAGACTCAGATATCTTATTTGCAATGAATTTTCATGTTTGAAGATTCAGATTTT 720  
Qy 720 GCTTTATCAAGTGGCGATGATGCTCTCACAGTCAAGATGAGTACCTCTCTTACTTTCATCAT 779  
Db 721 GCTTTATCAAGTGGCGATGATGCTCTCACAGTCAAGATGAGTACCTCTCTTACTTTCATCAT 780  
Qy 780 GAAGGAGGACAAATTTATCTATATGCGACCTGAAATTAATTAATTAATTAATTAATTAATTAAT 839  
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Qy 840 GCCAGTATCAAGCAGATATATATAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
Db 900 AAACAGCTTTTGAAGATGTCACCAATCTTTGCGAGATTAATTAATTAATTAATTAATTAATTAAT 959  
Qy 901 AAACAGCTTTTGAAGATGTCACCAATCTTTGCGAGATTAATTAATTAATTAATTAATTAATTAAT 960  
Qy 960 CATGACCTGTTTAAATGAAGAAAGTTTGCATATGATATACCTCACCGAGCAGTATG 1019  
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Qy 1080 TGTTTAATAGAACTTGAACCAAGTTTGAACCAATTTGAAGAGATTAATTAATTAATTAATTAATTAAT 1139  
Db 1081 TGTTTAATAGAACTTGAACCAAGTTTGAACCAATTTGAAGAGATTAATTAATTAATTAATTAATTAAT 1140  
Qy 1140 GTTATTCAGCTAAAGAAACAAAGTTTACAGAGTGTTCAGGTGCCATTCACCTATGTCAC 1199  
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Qy 1200 AAGAGAAATGGAATTTCTGACATACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1259  
Db 1201 AAGAGAAATGGAATTTCTGACATACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1260  
Qy 1260 TGTGGATCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAAATTTCAAGTCCCTGCCA 1319  
Db 1261 TGTGGATCTCTCAGCTCCATGAAATAGTGGTCTCTCTGAAATTTCAAGTCCCTGCCA 1320  
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Db 1321 GCTCTCAAGACAAATGATTTTATCTGAAGAGCTCAAGAGCTGTTATTTATGAGCTG 1380  
Qy 1380 CATCAGTCTCTGGAATCAGCTGGGATAGCACCATTCTTGTTCTCAAGGCTGCA 1439

1381 CATCACTGTCTGGAAATCACAGTTGGGATAGACACATTTCTGGTTCTCAAAAGGGCTGCA 1440  
Qy 1440 TTCTGTGATCACAAAGACCACTCCATGCTCTTCAAGCAATAATAAATCACTCTCAACTGCA 1499  
Db 1441 TTCTGTGATCACAAAGACCACTCCATGCTCTTCAAGCAATAATAAATCACTCTCAACTGCA 1500  
Qy 1500 GGAAATCTCAGAACGCTCTGCAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAA 1559  
Db 1501 GGAAATCTCAGAACGCTCTGCAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAA 1560  
Qy 1560 GACATTTGTGAAACCAATGACAGAGCCTGCCTTAACCACTGCTAGATCCCTTCTGTCTCC 1619  
Db 1561 GACATTTGTGAAACCAATGACAGAGCCTGCCTTAACCACTGCTAGATCCCTTCTGTCTCC 1620  
Qy 1620 AGGAGCTTGATCATGAAAGAGGACTATGAATCTGTTAGTACCAAGGCTCAAGAGCCTCA 1679  
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Qy 1680 AAAGTCAAGCAATTAATAGACACTAGTACATCCAAAGGAGAGAAATTTGCAAAAGTTATA 1739  
Db 1681 AAAGTCAAGCAATTAATAGACACTAGTACATCCAAAGGAGAGAAATTTGCAAAAGTTATA 1740  
Qy 1740 GTCAAAATTTGAAAGATTAACAAATGGGCTTTCAGCCTTACCGGAAATTAATTTG 1799  
Db 1741 GTCAAAATTTGAAAGATTAACAAATGGGCTTTCAGCCTTACCGGAAATTAATTTG 1800  
Qy 1800 GTTCTTAGATCACCATCTTTTAAATTTTACTTTCAAAAATAAAGCATGTAAGTGAATGTTTT 1859  
Db 1801 GTTCTTAGATCACCATCTTTTAAATTTTACTTTCAAAAATAAAGCATGTAAGTGAATGTTTT 1860  
Qy 1860 CAAGAGAAATGTGTTTCATAAAAGATTTATATATCTCTGTTGCTTGAATCTTTTTTAT 1919  
Db 1861 CAAGAGAAATGTGTTTCATAAAAGATTTATATATCTCTGTTGCTTGAATCTTTTTTAT 1920  
Qy 1920 ATAAATCCGCTGAGTATTAAGCTTTTATGCAAGCTTTTATGCAAGCTTTTGGGTAATATAGTCTCCCT 1979  
Db 1921 ATAAATCCGCTGAGTATTAAGCTTTTATGCAAGCTTTTATGCAAGCTTTTGGGTAATATAGTCTCCCT 1980  
Qy 1980 CCATGACACTGCACTATTTTTTAAATTAATAAAGTAAAGTGAATGTAATTTGGTGAAT 2039  
Db 1981 CCATGACACTGCACTATTTTTTAAATTAATAAAGTAAAGTGAATTTGGTGAAT 2040  
Qy 2040 TGCTACATAGTTCATTTTATGCTCTTTTATGCTTTTACAGAAACCACTTTTAAAGGATAGT 2099  
Db 2041 TGCTACATAGTTCATTTTATGCTCTTTTATGCTTTTACAGAAACCACTTTTAAAGGATAGT 2100  
Qy 2100 AATTAATTTCTGTTTATTAACAGTGCCTTTAAGGTATGATTTCTGATGGAAGCCTTTT 2159  
Db 2101 AATTAATTTCTGTTTATTAACAGTGCCTTTAAGGTATGATTTCTGATGGAAGCCTTTT 2160  
Qy 2160 CACATTCATGTTCTTCATGGAATTTATTTGTTTACTTGTCTAAGATGCAATTTGATTTATGA 2219  
Db 2161 CACATTCATGTTCTTCATGGAATTTATTTGTTTACTTGTCTAAGATGCAATTTGATTTATGA 2220  
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Qy 2280 AATTTGCCCTCAAAAGGTTTAAATTTAAATCTCCATTTATGAGTATCAATTTTAAAGTT 2339  
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Qy 2340 TTATTTATGAATTTCCCTTTAAATATGATTTTCAAGGTAAACCAATATCAATATAAAGAA 2399  
Db 2341 TTATTTATGAATTTCCCTTTAAATATGATTTTCAAGGTAAACCAATATCAATATAAAGAA 2400  
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Qy 2460 GTCCACCAACCAAGCTTAAATTAAGTCAACAGGCTGATGTG 2501  
Db 2461 GTCCACCAACCAAGCTTAAATTAAGTCAACAGGCTGATGTG 2502



1381 ATCACTGTCTGGAAATCACAGTTGGGATAGCACCATTTCTGGTTCTCAAGGGCTGCAT 1440  
1416 ATCACTGTCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCAT 1475  
1441 TCTGTGATCACAGACCACTCCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAG 1500  
1476 TCTGTGATCACAGACCACTCCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAG 1535  
1501 GAAACTCAGAACGCTCTGAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAG 1560  
1536 GAAACTCAGAACGCTCTGAGCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAG 1595  
1561 ACATTGTGAACCAATGACAGAGCCTGCTTAACCACTGCTAGATGCGCTTCTGTCCA 1620  
1596 ACATTGTGAACCAATGACAGAGCCTGCTTAACCACTGCTAGATGCGCTTCTGTCCA 1655  
1621 GGGACTTGATCATGAAGAGGACTATGAACCTTTAGTACCAAGCCTACAGGACCTCAA 1680  
1656 GGGACTTGATCATGAAGAGGACTATGAACCTTTAGTACCAAGCCTACAGGACCTCAA 1715  
1681 AAGTCAGACAATTAAGTACACTACTGACATCACTCAAGGAGAGAAATTTGCCAAAGTTATAG 1740  
1716 AAGTCAGACAATTAAGTACACTACTGACATCACTCAAGGAGAGAAATTTGCCAAAGTTATAG 1775  
1741 TACAAAATTTGAAGATTAACAAACAAATGGCTCTTACGCTTACCCGGAAATACTTGTGG 1800  
1776 TACAAAATTTGAAGATTAACAAACAAATGGCTCTTACGCTTACCCGGAAATACTTGTGG 1835  
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1836 TTCTTAGATCACCACTCTTTAAATTTACTTCAAAATATAAGCATGTAAGTACTGTTTTTC 1895  
1861 AAGAAAGAAATGTTTCAATAAGAAATATATATCTCTGTTGCTTCACTTTTTTATA 1920  
1896 AAGAAAGAAATGTTTCAATAAGAAATATATATCTCTGTTGCTTCACTTTTTTATA 1955  
1921 TAAATTCGTTGATTAAGCTTTTCAAGGTTCTTTGGTAAATATATAGTCTCCCTC 1980  
1956 TAAATTCGTTGATTAAGCTTTTCAAGGTTCTTTGGTAAATATATAGTCTCCCTC 2015  
1981 CATGACACTGCAATTTTTTTTAAATTAATCAAGTAAAAAGTTGAATTTG 2031  
2016 CATGACACTGCAATTTTTTTTAAATTAATCAAGTAAAAAGTTGAATTTG 2066

RESULT 3  
AAZ09246  
ID AAZ09246 standard; cdna; 1931 BP.

AC AAZ09246;

XX 25-OCT-1999 (first entry)

XX Human CARD-3 cdna.

KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;  
KW caspase activation; detection; screening; therapy; diagnosis; disease;  
KW apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex;  
KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;  
KW hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;  
KW systemic lupus erythematosus; immune-mediated glomerulonephritis; stroke;  
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;  
KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;  
KW myelodysplastic syndrome; myocardial infarction; cell proliferation;  
KW cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y; CARD-4Z;  
KW human; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 214..1836

FT /\*tag= a

/product= "CARD-3"

WO9940102-A1.

12-AUG-1999.

05-FEB-1999; 99WO-US002544.

06-FEB-1998; 98US-00019942.

17-JUN-1998; 98US-00093041.

08-DEC-1998; 98US-00207359.

(MILL-) MILLENNIUM PHARM INC.

Bertin J;

WPI; 1999-494269/41.

P-PSDB; AAY31140.

Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell survival.

Example 2; Fig 1; 181pp; English.

This invention describes the isolation of novel human caspase recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins and a partial murine CARD-4L protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation. The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the TNF receptor complex, or abnormal activity of a caspase. Diseases that may be treated/include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4L, a short transcript that encodes CARD-4S or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence encodes the human CARD-3 protein described in the method of the invention

Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 U; 0 Other;

Query Match 74.5%; Score 1864; DB 4; Length 1931;

Best Local Similarity 99.7%; Pred. No. 5.3e-06;

Matches 1867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 23 GTCAGCTCTGTTTCGAGAAACACGCGTGGCGCATCCGGGAATGGGGCCCTC 82

Db 12 GTCAGCTCTGTTTCGAGAAACACGCGTGGCGCATCCGGGAATGGGGCCCTC 71

QY 83 GTGACCTAGTCTTCGGGGGAAAAGGCTTTGCCGCTCGCTCGTCAGGGCGGTATC 142

Db 72 GTGACCTAGTCTTCGGGGGAAAAGGCTTTGCCGCTCGCTCGTCAGGGCGGTATC 131

QY 143 TGGGCGCTGAGCGCGCATGGGAGCCCTTGGAGCCCGCCGAGGGGGGCACCCCGGA 202

Db 132 TGGGCGCTGAGCGCGCATGGGAGCCCTTGGAGCCCGCCGAGGGGGGCACCCCGGA 191

QY 203 ACCGCGCTGAGCGCGCCGGGACCATGAACGGGAGGCCATCTGCAGCGCCCTGCCACCAT 262

Db 192 ACCGCGCTGAGCGCGCCGGGACCATGAACGGGAGGCCATCTGCAGCGCCCTGCCACCAT 251



QY 263 TCCCTACCAAACTCGCGGACCTGCGCTACTGAGCGCGCGCGCTCTCGGACATGTGTC 322  
Db 252 TCCCTTACCACAACTCGCGGACCTGCGCTACTGAGCGCGCGCGCTCTCGGACATGTGTC 311  
QY 323 GTCGCGCGCGCAGCAGACTCGCGGCTGAGGTGCGGTGAGCAGCAGCTGCACATCCACAC 382  
Db 312 GTCGCGCGCGCAGCAGACTCGCGGCTGAGGTGCGGTGAGCAGCAGCTGCACATCCACAC 371  
QY 383 TCCGCTGCTCGACAGTGAAGAAAGGATGTCTTAAGAGAAGCTGAAATTTTACACAAAGC 442  
Db 372 TCCGCTGCTCGACAGTGAAGAAAGGATGTCTTAAGAGAAGCTGAAATTTTACACAAAGC 431  
QY 443 TAGATTAGTTACATCTTCCATTTTGGGAATTTGGGAATTTGGGAATTTGGGAAT 502  
Db 432 TAGATTAGTTACATCTTCCATTTTGGGAATTTGGGAATTTGGGAATTTGGGAAT 491  
QY 503 AGTTACTGAATACATGCGCAATGGAATCAATTAAGTAACTCTTACATAGGAAACTGAATA 562  
Db 492 AGTTACTGAATACATGCGCAATGGAATCAATTAAGTAACTCTTACATAGGAAACTGAATA 551  
QY 563 TCCTGAGTTGCTTGGCCATTTGAGATTTTGCATCTCGATGAAATTTGCCCTTGGTGTAAA 622  
Db 552 TCCTGATGTTGCTTGGCCATTTGAGATTTTGCATCTCGATGAAATTTGCCCTTGGTGTAAA 611  
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Db 612 TTACTGCAATATGACTCTCTTCTTACTTCACTGACTGAGACTGCAATATCTT 671  
QY 683 ATTGACAAATGAATTTTCAATTTAGATTGCAATTTTGGTTTATCAAGTGGCGCATGAT 742  
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QY 1643 CTATGAATCTTGTAGTACCAAGCTTCAAGGACCTCAAAAGTCAAGAAATTTACTAGACAC 1702  
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RESULT 4  
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LOCUS Homo sapiens BAC clone CTA-437L15 from 8q21, complete sequence.  
DEFINITION AC004003  
ACCESSION AC004003.1 GI:2772557  
VERSION HTG.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 116650)  
Ozersky, P., Holmes, A. and Brody, M.  
The sequence of Homo sapiens BAC clone CTA-437L15  
Unpublished  
REFERENCE  
2 (bases 1 to 116650)  
Waterston, R.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
3 (bases 1 to 116650)  
Submitted (15-JAN-1998) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
Waterston, R.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
4 (bases 1 to 116650)  
Submitted (27-JUN-1998) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
Waterston, R.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
-----  
Submitted (21-DEC-1999) Department of Genetics, Washington  
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@watson.wustl.edu](mailto:sapiens@watson.wustl.edu)  
----- Summary Statistics -----  
Center project name: H RG437L15

**NOTICE:** This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**  
This chromosome 8 clone was provided by Dr. Patrick Concannon (natcon@ummc.org) at the Virginia Mason Research Institute.

**SOURCE INFORMATION:**  
Clone CTA-437115 is from a release of the human BAC library  
CIBT-HS-A. The library contains cloned DNA from human sperm. Seqs:  
Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.  
Kim et al., Genomics 34:213-8 (1996). The clone is available from  
Research Genetics, Inc. (<http://www.resgen.com>).

RESEARCH GENETICS, INC. (INC)  
VECTOR: pBelOBAc11  
selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is CTA-237G1. The actual start of  
this clone is at base position 1 of CTA-437L15; actual end is at  
116650 of CTA-437L15.

This clone contains STS HS275YE1 (NID:q1051703).

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Best Local Similarity 98.9%; Pred. NO. 0.00049;

Matches 985; Conservative 0; Mismatches 3; Indels 8; Gaps 1;

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Qy 1566 GTGAACCAAAATGACAGAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGGAC 1625
Db 39937 GTGAACCAAAATGACAGAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGGAC 39996
Qy 1626 TTGATCATGAAAGGAGTAACTGATGAACTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTC 1685
Db 39997 TTGATCATGAAAGGAGTAACTGATGAACTGTTAGTACCAAGCTTCAAGGACCTCAAAAGTC 40056
Qy 1686 AGCAATTAATGACACACTGACATCAAGGAGAGAAATTCGCAAGTTATAGTACAA 1745
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Qy 1746 AAATGTAAGATACAAACAAATGGCTTTCAGGCTTACCCGGAATATAGTCCCTCAATGA 1805
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Qy 1806 AGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAA 1865
Db 40177 AGATCACCATCTTTAAATTTACTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAA 40236
Qy 1866 GAATGTTGTTTCATAAAGGATATATATCTCTGTTGCTTGAATTTTATATATAAA 1925
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Qy 1926 TCCGTGAGTATTAAGCTTTTATGAAGTCTCTTGGGTAAATATATAGTCCCTCCATGA 1985
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Qy 2046 ATAGTTCAATTTTTATGCTCTTTTGTGTTTAAAGAACCACTTTTAAAGGATAGTAATAT 2105
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Db 40829 AACAAACCAAGCTAAATAAAGTCAACAGCTGATGTG 40864
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#### RESULT 5

AI824070/c

LOCUS

DEFINITION  
wJ35907.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2404860 3',  
similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA  
sequence.

ACCESSION  
AI824070

VERSION  
AI824070.1

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 738)

AUTHORS  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
Unpublished (1997)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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/clone\_lib="NCI CGAP Kid12"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site: 1: Not 1; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI CGAP Kids was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clones 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo. "

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Query Match      28.3%; Score 709; DB 1; Length 738;
Best Local Similarity 98.0%; Pred. No. 0.96;
Matches 726; Conservative 0; Mismatches 7; Indels 8; Gaps 1;
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Qy 1821 AATTACTTCAAAATAAAGCATGTAGTGAAGTGTCTTCAAGAGAAATGTCTTCATA 1880
Db 678 AATTACTTCAAAATAAAGCATGTAGTGAAGTGTCTTCAAGAGAAATGTCTTCATA 619
Qy 1801 AAAGGATATTTATATCTCTGTCTTCTGACCTTTTATATAAAATCCGTGAGTATTAAA 1940
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Qy 1941 GCTTTATTGAAGGTTCTTTGGGTAATAATTAGTCTCCCTCATGACACTGCAGTATTTT 2000
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Db 386 TGCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTCATTCATGTTCTTCATGGA 327
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Search completed: April 12, 2004, 09:59:33  
Job time : 156 secs